

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 21, 2001, 13:23:59 : Search time 393.89 Seconds  
(without alignments)  
3013.345 Million cell updates/sec

Title: US-09-138-735-1\_COPY\_1232\_1825

Perfect score: 594

Sequence: 1 caggtacagcgtacgctt.....aaacgagctccgtgagcata 594

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 1746710 seqs, 999096356 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3493420

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

Pending\_Patents\_MN\_New:\*  
1: /cgn1\_7/ptodata/1/pna/PCR\_NEW\_COMB.seq:\*  
2: /cgn1\_7/ptodata/1/pna/US06\_NEW\_COMB.seq:\*  
3: /cgn1\_7/ptodata/1/pna/US07\_NEW\_COMB.seq:\*  
4: /cgn1\_7/ptodata/1/pna/US08\_NEW\_COMB.seq:\*  
5: /cgn1\_7/ptodata/1/pna/US09\_NEW\_COMB.seq:\*  
6: /cgn1\_7/ptodata/1/pna/US09\_NEW\_COMB.seq1:\*  
7: /cgn1\_7/ptodata/1/pna/US09\_NEW\_COMB.seq2:\*  
8: /cgn1\_7/ptodata/1/pna/US60\_NEW\_COMB.seq:\*

Pred. NO. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description         |
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| 1          | 594   | 100.0       | 3402   | 6  | US-09-138-735-1     |
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| 3          | 20    | 3.4         | 91470  | 6  | US-09-803-736-19    |
| 4          | 18    | 3.0         | 18     | 6  | US-09-138-735-5     |
| 5          | 18    | 3.0         | 18     | 6  | US-09-138-735-8     |
| 6          | 18    | 3.0         | 261    | 6  | US-09-866-555-4980  |
| 7          | 18    | 3.0         | 297    | 7  | US-09-864-524-3874  |
| 8          | 18    | 3.0         | 328    | 6  | US-09-764-891-1027  |
| 9          | 18    | 3.0         | 348    | 7  | US-09-540-213-5492  |
| 10         | 18    | 3.0         | 371    | 6  | US-09-667-188A-4578 |
| 11         | 18    | 3.0         | 468    | 7  | US-09-864-761-52    |
| 12         | 18    | 3.0         | 476    | 6  | US-09-904-809-19378 |
| 13         | 18    | 3.0         | 476    | 6  | US-09-909-627-11623 |
| 14         | 18    | 3.0         | 478    | 7  | US-09-864-761-16893 |
| 15         | 18    | 3.0         | 506    | 7  | US-09-840-145-13709 |
| 16         | 18    | 3.0         | 1431   | 8  | US-60-312-544-4166  |
| 17         | 18    | 3.0         | 1485   | 1  | PCR-US01-16450-789  |
| 18         | 18    | 3.0         | 2817   | 6  | US-09-836-472-1298  |
| 19         | 18    | 3.0         | 15270  | 7  | US-09-764-905-28829 |
| 20         | 18    | 3.0         | 15270  | 7  | US-09-764-905-40566 |
| 21         | 18    | 3.0         | 96424  | 6  | US-09-803-736-1397  |
| 22         | 17    | 2.9         | 241    | 7  | US-09-724-671-11298 |
| 23         | 17    | 2.9         | 241    | 7  | US-09-540-213-52685 |
| 24         | 17    | 2.9         | 264    | 7  | US-09-540-213-44587 |
| 25         | 17    | 2.9         | 300    | 7  | US-09-540-213-33702 |

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|----|----|-----|--------|----|----------------------|--------------------|
| 26 | 17 | 2.9 | 301    | 7  | US-09-724-671-8427   | Sequence 8427, Ap  |
| 27 | 17 | 2.9 | 303    | 7  | US-09-724-671-8448   | Sequence 8448, Ap  |
| 28 | 17 | 2.9 | 322    | 7  | US-09-863-524-3604   | Sequence 3604, Ap  |
| 29 | 17 | 2.9 | 353    | 7  | US-09-724-671-5748   | Sequence 5748, Ap  |
| 30 | 17 | 2.9 | 396    | 7  | US-09-724-671-4945   | Sequence 4945, Ap  |
| 31 | 17 | 2.9 | 398    | 6  | US-09-804-730-15348  | Sequence 15348, A  |
| 32 | 17 | 2.9 | 402    | 6  | US-09-904-703-4316   | Sequence 4316, Ap  |
| 33 | 17 | 2.9 | 404    | 6  | US-09-866-555-6918   | Sequence 6918, Ap  |
| 34 | 17 | 2.9 | 419    | 7  | US-09-692-257A-6664  | Sequence 6664, Ap  |
| 35 | 17 | 2.9 | 426    | 6  | US-09-804-730-8833   | Sequence 8833, Ap  |
| 36 | 17 | 2.9 | 430    | 6  | US-09-904-809-4385   | Sequence 4385, Ap  |
| 37 | 17 | 2.9 | 439    | 7  | US-09-881-797-3357   | Sequence 3357, Ap  |
| 38 | 17 | 2.9 | 444    | 7  | US-09-724-671-4408   | Sequence 4408, Ap  |
| 39 | 17 | 2.9 | 468    | 6  | US-09-758-463-219    | Sequence 219, App  |
| 40 | 17 | 2.9 | 474    | 7  | US-09-881-797-3356   | Sequence 3356, Ap  |
| 41 | 17 | 2.9 | 481    | 8  | US-60-253-652-24408  | Sequence 24408, A  |
| 42 | 17 | 2.9 | 492    | 6  | US-09-823-241-6683   | Sequence 6683, Ap  |
| 43 | 17 | 2.9 | 500    | 7  | US-09-850-147-15830  | Sequence 15830, A  |
| 44 | 17 | 2.9 | 501    | 7  | US-09-834-366-4311   | Sequence 4311, Ap  |
| 45 | 17 | 2.9 | 514    | 6  | US-09-758-463-239    | Sequence 239, App  |
| 46 | 17 | 2.9 | 562    | 7  | US-09-821-837-4107   | Sequence 4107, Ap  |
| 47 | 17 | 2.9 | 643    | 7  | US-09-823-327-3606   | Sequence 3606, Ap  |
| 48 | 17 | 2.9 | 697    | 6  | US-09-623-746A-60    | Sequence 60, App1  |
| 49 | 17 | 2.9 | 771    | 1  | PCR-US01-08631-9801  | Sequence 9801, Ap  |
| 50 | 17 | 2.9 | 781    | 1  | PCR-US01-08631-9802  | Sequence 9802, Ap  |
| 51 | 17 | 2.9 | 790    | 6  | US-09-883-152-20     | Sequence 20, App1  |
| 52 | 17 | 2.9 | 812    | 8  | US-60-278-561-2143   | Sequence 2143, Ap  |
| 53 | 17 | 2.9 | 954    | 1  | PCR-US01-18569-775   | Sequence 775, App  |
| 54 | 17 | 2.9 | 1269   | 1  | PCR-US01-08631-10338 | Sequence 10338, A  |
| 55 | 17 | 2.9 | 1513   | 6  | US-09-898-888-7596   | Sequence 7596, Ap  |
| 56 | 17 | 2.9 | 1707   | 1  | PCR-US01-08631-29984 | Sequence 29984, A  |
| 57 | 17 | 2.9 | 1959   | 8  | US-60-278-561-12846  | Sequence 12846, A  |
| 58 | 17 | 2.9 | 1970   | 1  | PCR-US01-08631-21764 | Sequence 21764, A  |
| 59 | 17 | 2.9 | 2205   | 1  | PCR-US01-08631-8851  | Sequence 8851, Ap  |
| 60 | 17 | 2.9 | 2211   | 7  | US-09-764-874-12555  | Sequence 12555, A  |
| 61 | 17 | 2.9 | 2914   | 8  | US-60-278-256-10032  | Sequence 10032, A  |
| 62 | 17 | 2.9 | 3465   | 8  | US-60-278-233-8890   | Sequence 8890, Ap  |
| 63 | 17 | 2.9 | 3617   | 7  | US-09-764-874-12556  | Sequence 12556, A  |
| 64 | 17 | 2.9 | 3618   | 7  | US-09-764-874-12554  | Sequence 12554, A  |
| 65 | 17 | 2.9 | 3846   | 7  | US-09-902-540-2520   | Sequence 2520, Ap  |
| 66 | 17 | 2.9 | 4815   | 1  | PCR-US01-08631-24178 | Sequence 24178, A  |
| 67 | 17 | 2.9 | 4815   | 1  | PCR-US01-08631-26102 | Sequence 26102, A  |
| 68 | 17 | 2.9 | 4826   | 8  | US-60-260-483-126    | Sequence 126, App  |
| 69 | 17 | 2.9 | 4835   | 8  | US-60-278-258-4418   | Sequence 4418, Ap  |
| 70 | 17 | 2.9 | 5491   | 17 | PCR-US01-08631-21772 | Sequence 21772, A  |
| 71 | 17 | 2.9 | 6238   | 1  | PCR-US01-08631-4045  | Sequence 4045, Ap  |
| 72 | 17 | 2.9 | 6266   | 8  | US-60-278-232-9933   | Sequence 9933, Ap  |
| 73 | 17 | 2.9 | 7714   | 6  | US-09-760-457-438    | Sequence 438, App  |
| 74 | 17 | 2.9 | 7714   | 6  | US-09-760-457-463    | Sequence 463, App  |
| 75 | 17 | 2.9 | 17503  | 7  | US-09-902-540-1114   | Sequence 1114, Ap  |
| 76 | 17 | 2.9 | 32189  | 6  | US-09-764-874-3391   | Sequence 3391, Ap  |
| 77 | 17 | 2.9 | 32189  | 7  | US-09-764-874-8672   | Sequence 8672, Ap  |
| 78 | 17 | 2.9 | 32189  | 7  | US-09-764-874-9823   | Sequence 9823, Ap  |
| 79 | 17 | 2.9 | 32189  | 7  | US-09-764-874-10121  | Sequence 10121, A  |
| 80 | 17 | 2.9 | 46626  | 6  | US-09-803-736-184    | Sequence 184, App  |
| 81 | 17 | 2.9 | 80099  | 6  | US-09-803-736-1287   | Sequence 1287, Ap  |
| 82 | 17 | 2.9 | 94029  | 6  | US-09-803-736-147    | Sequence 147, App  |
| 83 | 17 | 2.9 | 240825 | 6  | US-09-790-288-1      | Sequence 1, App1   |
| 84 | 16 | 2.7 | 73     | 8  | US-60-253-457-27313  | Sequence 27313, A  |
| 85 | 16 | 2.7 | 139    | 7  | US-09-864-761-27193  | Sequence 27193, A  |
| 86 | 16 | 2.7 | 235    | 7  | US-09-724-671-4668   | Sequence 4668, Ap  |
| 87 | 16 | 2.7 | 236    | 7  | US-09-863-524-4502   | Sequence 4502, Ap  |
| 88 | 16 | 2.7 | 236    | 8  | US-60-253-376-35947  | Sequence 35947, A  |
| 89 | 16 | 2.7 | 239    | 8  | US-60-253-376-35896  | Sequence 35896, A  |
| 90 | 16 | 2.7 | 241    | 7  | US-09-853-366-7523   | Sequence 7523, Ap  |
| 91 | 16 | 2.7 | 245    | 7  | US-09-877-486-3351   | Sequence 3351, Ap  |
| 92 | 16 | 2.7 | 275    | 7  | US-09-912-292-55592  | Sequence 55592, A  |
| 93 | 16 | 2.7 | 279    | 7  | US-09-853-366-1403   | Sequence 1403, Ap  |
| 94 | 16 | 2.7 | 285    | 7  | US-09-859-499-835    | Sequence 835, App  |
| 95 | 16 | 2.7 | 290    | 6  | US-09-617-681A-3535  | Sequence 3535, App |
| 96 | 16 | 2.7 | 293    | 8  | US-60-252-833-38373  | Sequence 38373, A  |
| 97 | 16 | 2.7 | 297    | 7  | US-09-867-716-7328   | Sequence 7328, Ap  |
| 98 | 16 | 2.7 | 302    | 6  | US-09-783-587-1286   | Sequence 1286, Ap  |

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|-------|----|-----|------|---|-----------------------|---------------------|-------|----|-----|--------|---|-----------------------|--------------------|
| 99    | 16 | 2.7 | 302  | 7 | US-09-912-292-38493   | Sequence 38493, A   | 172   | 16 | 2.7 | 1324   | 7 | US-09-850-118-1432    | Sequence 1432, Ap  |
| C 100 | 16 | 2.7 | 306  | 7 | US-09-853-369-3588    | Sequence 3588, Ap   | 173   | 16 | 2.7 | 1403   | 6 | US-09-760-466-560     | Sequence 560, App  |
| C 101 | 16 | 2.7 | 311  | 7 | US-09-877-486-3861    | Sequence 3861, Ap   | C 174 | 16 | 2.7 | 1692   | 1 | PCT-US01-08631-122519 | Sequence 22519, A  |
| C 102 | 16 | 2.7 | 315  | 7 | US-09-867-716-6790    | Sequence 6790, Ap   | C 175 | 16 | 2.7 | 1770   | 1 | US-09-902-540-4547    | Sequence 4547, Ap  |
| 103   | 16 | 2.7 | 326  | 7 | US-09-724-671-18201   | Sequence 18201, A   | C 176 | 16 | 2.7 | 1975   | 6 | US-09-760-466-4452    | Sequence 4452, App |
| 104   | 16 | 2.7 | 328  | 8 | US-60-253-456-26975   | Sequence 26975, A   | C 177 | 16 | 2.7 | 1992   | 1 | PCT-US01-08631-26331  | Sequence 26331, A  |
| 105   | 16 | 2.7 | 331  | 7 | US-09-724-671-4901    | Sequence 4901, Ap   | C 178 | 16 | 2.7 | 2058   | 1 | US-09-758-468-1199    | Sequence 1199, App |
| 106   | 16 | 2.7 | 335  | 7 | US-09-724-671-5022    | Sequence 5022, Ap   | C 179 | 16 | 2.7 | 2140   | 8 | US-60-278-258-11997   | Sequence 11997, A  |
| 107   | 16 | 2.7 | 337  | 8 | US-60-253-457-29711   | Sequence 29711, A   | C 180 | 16 | 2.7 | 2268   | 1 | PCT-US01-08631-119259 | Sequence 19259, A  |
| 108   | 16 | 2.7 | 338  | 7 | US-09-724-671-18461   | Sequence 18461, A   | C 181 | 16 | 2.7 | 2310   | 6 | US-09-603-207-25      | Sequence 25, App1  |
| 109   | 16 | 2.7 | 346  | 7 | US-09-912-292-8604    | Sequence 8604, Ap   | C 182 | 16 | 2.7 | 2337   | 8 | US-60-278-561-12029   | Sequence 12029, A  |
| 110   | 16 | 2.7 | 353  | 7 | US-09-724-671-18790   | Sequence 18790, A   | C 183 | 16 | 2.7 | 2372   | 1 | PCT-US01-08631-22280  | Sequence 22380, A  |
| C 111 | 16 | 2.7 | 371  | 6 | US-09-888-888-12001   | Sequence 12081, A   | C 184 | 16 | 2.7 | 2345   | 8 | US-60-278-258-4998    | Sequence 4998, Ap  |
| C 112 | 16 | 2.7 | 371  | 6 | US-09-886-555-19255   | Sequence 19255, A   | C 185 | 16 | 2.7 | 2450   | 1 | PCT-US01-08631-20712  | Sequence 20712, A  |
| C 113 | 16 | 2.7 | 372  | 8 | US-60-252-833-35457   | Sequence 35457, A   | C 186 | 16 | 2.7 | 2550   | 7 | US-09-902-540-8526    | Sequence 8526, Ap  |
| C 114 | 16 | 2.7 | 382  | 8 | US-60-252-833-13311   | Sequence 13311, A   | C 187 | 16 | 2.7 | 2668   | 6 | US-09-598-075-154     | Sequence 154, App  |
| C 115 | 16 | 2.7 | 387  | 7 | US-09-724-750-24153   | Sequence 24153, A   | C 188 | 16 | 2.7 | 2688   | 6 | US-09-598-075-154     | Sequence 154, App  |
| C 116 | 16 | 2.7 | 396  | 1 | PCT-US01-08631-116672 | Sequence 16672, A   | C 189 | 16 | 2.7 | 3331   | 6 | US-09-325-810-31      | Sequence 31, App1  |
| C 117 | 16 | 2.7 | 397  | 6 | US-09-904-703-2778    | Sequence 2778, Ap   | C 190 | 16 | 2.7 | 3331   | 6 | US-09-373-658-31      | Sequence 31, App1  |
| C 118 | 16 | 2.7 | 401  | 7 | US-09-850-147-3027    | Sequence 3027, Ap   | C 191 | 16 | 2.7 | 3331   | 6 | US-60-171-503-31      | Sequence 31, App1  |
| C 119 | 16 | 2.7 | 409  | 8 | US-60-253-654-23916   | Sequence 23916, A   | C 192 | 16 | 2.7 | 3342   | 8 | US-60-278-258-11917   | Sequence 11917, A  |
| C 120 | 16 | 2.7 | 409  | 8 | US-60-253-592-23916   | Sequence 23916, A   | C 193 | 16 | 2.7 | 3429   | 1 | PCT-US01-08631-229177 | Sequence 229177, A |
| C 121 | 16 | 2.7 | 410  | 8 | US-60-253-456-7084    | Sequence 7084, Ap   | C 194 | 16 | 2.7 | 3684   | 8 | US-60-278-258-6146    | Sequence 6146, Ap  |
| C 122 | 16 | 2.7 | 421  | 7 | US-09-692-257A-6018   | Sequence 6018, Ap   | C 195 | 16 | 2.7 | 3718   | 6 | US-09-620-3128-74     | Sequence 74, App1  |
| C 123 | 16 | 2.7 | 422  | 7 | US-09-724-750-22736   | Sequence 22736, A   | C 196 | 16 | 2.7 | 4369   | 6 | US-09-764-891-8870    | Sequence 8870, Ap  |
| C 124 | 16 | 2.7 | 425  | 7 | US-09-724-750-21484   | Sequence 21484, A   | C 197 | 16 | 2.7 | 4641   | 1 | PCT-US01-08631-22587  | Sequence 2587, A   |
| C 125 | 16 | 2.7 | 427  | 6 | US-09-667-188A-11299  | Sequence 11299, Ap  | C 198 | 16 | 2.7 | 7213   | 7 | US-09-764-905-39933   | Sequence 39933, A  |
| C 126 | 16 | 2.7 | 431  | 6 | US-09-909-629-35857   | Sequence 35857, A   | C 199 | 16 | 2.7 | 7671   | 8 | US-60-278-232-8827    | Sequence 8827, Ap  |
| C 127 | 16 | 2.7 | 437  | 7 | US-09-773-476-127     | Sequence 127, App   | C 200 | 16 | 2.7 | 8066   | 1 | PCT-US01-08631-29175  | Sequence 29175, A  |
| C 128 | 16 | 2.7 | 441  | 7 | US-09-834-366-36358   | Sequence 36358, A   | C 201 | 16 | 2.7 | 9321   | 7 | US-09-902-540-898     | Sequence 898, App  |
| C 129 | 16 | 2.7 | 443  | 6 | US-09-909-629-37049   | Sequence 37049, A   | C 202 | 16 | 2.7 | 15172  | 7 | US-09-902-540-1086    | Sequence 1086, App |
| C 130 | 16 | 2.7 | 446  | 6 | US-09-909-629-32826   | Sequence 32826, A   | C 203 | 16 | 2.7 | 18339  | 7 | US-09-881-797-808     | Sequence 808, App  |
| C 131 | 16 | 2.7 | 451  | 8 | US-60-253-654-23636   | Sequence 23636, A   | C 204 | 16 | 2.7 | 19222  | 7 | US-09-902-540-11192   | Sequence 1192, Ap  |
| C 132 | 16 | 2.7 | 451  | 8 | US-60-253-592-23636   | Sequence 23636, A   | C 205 | 16 | 2.7 | 21988  | 6 | US-09-803-736-347     | Sequence 347, App  |
| C 133 | 16 | 2.7 | 461  | 7 | US-09-834-366-12022   | Sequence 12022, A   | C 206 | 16 | 2.7 | 24757  | 6 | US-09-764-868-1347    | Sequence 1347, Ap  |
| C 134 | 16 | 2.7 | 473  | 7 | US-09-864-761-2646    | Sequence 2646, Ap   | C 207 | 16 | 2.7 | 25497  | 7 | US-09-902-540-1224    | Sequence 1224, Ap  |
| C 135 | 16 | 2.7 | 475  | 8 | US-60-253-652-14488   | Sequence 14488, A   | C 208 | 16 | 2.7 | 29859  | 7 | US-09-902-540-1265    | Sequence 1265, Ap  |
| C 136 | 16 | 2.7 | 476  | 8 | US-60-253-653-3489    | Sequence 3489, A    | C 209 | 16 | 2.7 | 39678  | 7 | US-09-764-905-39808   | Sequence 39808, A  |
| C 137 | 16 | 2.7 | 482  | 7 | US-09-864-761-10572   | Sequence 10572, A   | C 210 | 16 | 2.7 | 41927  | 7 | US-09-902-540-1268    | Sequence 1268, Ap  |
| C 138 | 16 | 2.7 | 486  | 7 | US-09-824-518-5079    | Sequence 5079, Ap   | C 211 | 16 | 2.7 | 76304  | 8 | US-09-803-736-951     | Sequence 951, App1 |
| C 139 | 16 | 2.7 | 487  | 7 | US-09-864-761-5298    | Sequence 5298, Ap   | C 212 | 16 | 2.7 | 81662  | 6 | US-09-803-736-951     | Sequence 951, App1 |
| C 140 | 16 | 2.7 | 488  | 7 | US-09-912-292-43627   | Sequence 43627, A   | C 213 | 16 | 2.7 | 84702  | 6 | US-09-803-736-474     | Sequence 474, App  |
| C 141 | 16 | 2.7 | 491  | 8 | US-60-252-833-13471   | Sequence 13471, A   | C 214 | 16 | 2.7 | 87210  | 6 | US-09-803-736-767     | Sequence 767, App  |
| C 142 | 16 | 2.7 | 497  | 6 | US-09-866-555-6172    | Sequence 6172, Ap   | C 215 | 16 | 2.7 | 99547  | 6 | US-09-803-736-1121    | Sequence 1121, App |
| C 143 | 16 | 2.7 | 501  | 6 | US-09-796-692-4449    | Sequence 4449, Ap   | C 216 | 16 | 2.7 | 101647 | 6 | US-09-803-736-380     | Sequence 380, App  |
| C 144 | 16 | 2.7 | 503  | 6 | US-09-796-692-5825    | Sequence 5825, Ap   | C 217 | 16 | 2.7 | 114505 | 6 | US-09-803-736-129     | Sequence 129, App  |
| C 145 | 16 | 2.7 | 507  | 7 | US-09-840-145-11795   | Sequence 11795, A   | C 218 | 16 | 2.7 | 145744 | 6 | US-09-803-736-1465    | Sequence 1465, Ap  |
| C 146 | 16 | 2.7 | 525  | 7 | US-09-902-540-9559    | Sequence 9559, Ap   | C 219 | 16 | 2.7 | 165200 | 6 | US-09-803-110-205     | Sequence 205, App  |
| C 147 | 16 | 2.7 | 553  | 6 | US-09-804-730-6011    | Sequence 6011, Ap   | C 220 | 16 | 2.7 | 186449 | 7 | US-09-881-797-715     | Sequence 715, App  |
| C 148 | 16 | 2.7 | 556  | 7 | US-09-861-478-273     | Sequence 273, App   | C 221 | 16 | 2.7 | 199268 | 7 | US-09-881-797-697     | Sequence 697, App  |
| C 149 | 16 | 2.7 | 558  | 7 | US-09-861-478-29      | Sequence 29, App1   | C 222 | 16 | 2.7 | 342340 | 6 | US-09-803-110-219     | Sequence 219, App  |
| C 150 | 16 | 2.7 | 601  | 6 | US-09-758-450-458     | Sequence 458, App   | C 223 | 16 | 2.7 | 51     | 8 | US-60-278-232-1843    | Sequence 1843, Ap  |
| C 151 | 16 | 2.7 | 614  | 8 | US-60-253-378-36311   | Sequence 36331, A   | C 224 | 15 | 2.5 | 57     | 5 | US-60-278-232-3958    | Sequence 3958, Ap  |
| C 152 | 16 | 2.7 | 624  | 8 | US-60-253-652-11254   | Sequence 11254, A   | C 225 | 15 | 2.5 | 51     | 8 | US-60-278-232-3958    | Sequence 4, App1   |
| C 153 | 16 | 2.7 | 638  | 7 | US-09-834-366-10416   | Sequence 10416, A   | C 226 | 15 | 2.5 | 65     | 7 | US-09-908-975-28318   | Sequence 28318, A  |
| C 154 | 16 | 2.7 | 651  | 6 | US-09-738-626-982     | Sequence 982, App   | C 227 | 15 | 2.5 | 65     | 8 | US-60-287-724-28318   | Sequence 28318, A  |
| C 155 | 16 | 2.7 | 713  | 7 | US-09-861-478-316     | Sequence 316, App   | C 228 | 15 | 2.5 | 106    | 7 | US-09-834-366-33225   | Sequence 33225, A  |
| C 156 | 16 | 2.7 | 756  | 7 | US-09-902-540-5475    | Sequence 5475, App  | C 229 | 15 | 2.5 | 118    | 7 | US-09-692-257A-2050   | Sequence 2050, Ap  |
| C 157 | 16 | 2.7 | 876  | 6 | US-09-760-451-93      | Sequence 93, App1   | C 230 | 15 | 2.5 | 155    | 8 | US-60-253-457-40041   | Sequence 40041, A  |
| C 158 | 16 | 2.7 | 909  | 6 | US-09-758-474-223     | Sequence 223, App1  | C 231 | 15 | 2.5 | 167    | 6 | US-09-804-730-21002   | Sequence 21002, A  |
| C 159 | 16 | 2.7 | 919  | 6 | US-09-760-451-45      | Sequence 45, App1   | C 232 | 15 | 2.5 | 213    | 4 | US-08-798-074B-605    | Sequence 605, App  |
| C 160 | 16 | 2.7 | 930  | 6 | US-09-902-540-5570    | Sequence 5570, Ap   | C 233 | 15 | 2.5 | 213    | 4 | US-08-798-074B-605    | Sequence 605, App  |
| C 161 | 16 | 2.7 | 976  | 6 | US-09-760-466-85      | Sequence 85, App1   | C 234 | 15 | 2.5 | 213    | 4 | US-08-798-074B-605    | Sequence 605, App  |
| C 162 | 16 | 2.7 | 1030 | 7 | US-09-902-540-3902    | Sequence 3902, Ap   | C 235 | 15 | 2.5 | 222    | 7 | US-09-540-213-38267   | Sequence 38267, A  |
| C 163 | 16 | 2.7 | 1038 | 6 | US-09-803-110-6914    | Sequence 6914, Ap   | C 236 | 15 | 2.5 | 222    | 7 | US-09-877-486-4991    | Sequence 4991, Ap  |
| C 164 | 16 | 2.7 | 1070 | 7 | US-09-867-716-17316   | Sequence 17316, A   | C 237 | 15 | 2.5 | 224    | 7 | US-09-877-486-2809    | Sequence 2809, Ap  |
| C 165 | 16 | 2.7 | 1107 | 8 | US-60-309-870-59      | Sequence 857, App1  | C 238 | 15 | 2.5 | 224    | 7 | US-09-877-486-7019    | Sequence 7019, Ap  |
| C 166 | 16 | 2.7 | 1146 | 6 | US-09-803-110-2857    | Sequence 2857, App1 | C 239 | 15 | 2.5 | 225    | 5 | US-09-824-559-3218    | Sequence 3218, Ap  |
| C 167 | 16 | 2.7 | 1178 | 7 | US-09-881-797-4070    | Sequence 4070, Ap   | C 240 | 15 | 2.5 | 226    | 7 | US-09-877-486-588     | Sequence 588, App  |
| C 168 | 16 | 2.7 | 1236 | 1 | PCT-US01-16450-742    | Sequence 742, App   | C 241 | 15 | 2.5 | 236    | 8 | US-60-253-378-36188   | Sequence 36188, A  |
| C 169 | 16 | 2.7 | 1238 | 8 | US-60-309-870-58      | Sequence 58, App1   | C 242 | 15 | 2.5 | 246    | 7 | US-09-853-369-5124    | Sequence 5124, Ap  |
| C 170 | 16 | 2.7 | 1266 | 8 | US-60-279-526-251     | Sequence 251, App   | C 243 | 15 | 2.5 | 246    | 7 | US-09-724-671-20713   | Sequence 20713, A  |
| C 171 | 16 | 2.7 | 1267 | 1 | PCT-US01-16450-1306   | Sequence 1306, App  | C 244 | 15 | 2.5 | 249    | 6 | US-09-758-470-98      | Sequence 98, App1  |



|       |    |     |     |   |                     |                      |       |    |     |     |   |                      |                     |
|-------|----|-----|-----|---|---------------------|----------------------|-------|----|-----|-----|---|----------------------|---------------------|
| C 245 | 15 | 2.5 | 256 | 7 | US-09-773-476-37    | Sequence 37, App1    | C 318 | 15 | 2.5 | 347 | 5 | US-09-824-559-7087   | Sequence 7087, App  |
| C 246 | 15 | 2.5 | 256 | 7 | US-09-864-761-18722 | Sequence 18722, A    | C 319 | 15 | 2.5 | 348 | 7 | US-09-770-791-739    | Sequence 739, App   |
| C 247 | 15 | 2.5 | 256 | 7 | US-09-540-213-46447 | Sequence 46447, A    | C 320 | 15 | 2.5 | 351 | 8 | US-60-253-654-2279   | Sequence 2279, App  |
| C 248 | 15 | 2.5 | 259 | 7 | US-09-540-213-12022 | Sequence 12022, A    | C 321 | 15 | 2.5 | 351 | 8 | US-60-253-592-2279   | Sequence 2279, App  |
| C 249 | 15 | 2.5 | 266 | 7 | US-09-853-807-2007  | Sequence 2007, App   | C 322 | 15 | 2.5 | 352 | 7 | US-09-764-874-7543   | Sequence 7543, App  |
| C 250 | 15 | 2.5 | 269 | 7 | US-09-540-213-53081 | Sequence 53081, A    | C 323 | 15 | 2.5 | 352 | 8 | US-60-252-833-3404   | Sequence 3404, App  |
| C 251 | 15 | 2.5 | 277 | 7 | US-09-850-147-6491  | Sequence 6491, App   | C 324 | 15 | 2.5 | 353 | 8 | US-60-253-654-183328 | Sequence 183328, A  |
| C 252 | 15 | 2.5 | 277 | 7 | US-09-894-949-6094  | Sequence 6094, App   | C 325 | 15 | 2.5 | 353 | 8 | US-60-255-592-183328 | Sequence 183328, A  |
| C 253 | 15 | 2.5 | 279 | 7 | US-09-894-949-6140  | Sequence 6140, App   | C 326 | 15 | 2.5 | 354 | 6 | US-09-878-722-118    | Sequence 118, App   |
| C 254 | 15 | 2.5 | 279 | 8 | US-60-253-653-17410 | Sequence 17410, App  | C 327 | 15 | 2.5 | 354 | 7 | US-09-904-436-138    | Sequence 138, App   |
| C 255 | 15 | 2.5 | 281 | 7 | US-09-540-213-19496 | Sequence 19496, A    | C 328 | 15 | 2.5 | 356 | 7 | US-09-859-490-12486  | Sequence 12486, A   |
| C 256 | 15 | 2.5 | 282 | 7 | US-09-724-671-4888  | Sequence 4888, App   | C 329 | 15 | 2.5 | 359 | 6 | US-09-878-178-2119   | Sequence 2119, App  |
| C 257 | 15 | 2.5 | 282 | 7 | US-09-783-590-7613  | Sequence 7613, App   | C 330 | 15 | 2.5 | 359 | 8 | US-60-253-457-13176  | Sequence 13176, A   |
| C 258 | 15 | 2.5 | 282 | 7 | US-09-839-976-288   | Sequence 288, App    | C 331 | 15 | 2.5 | 360 | 8 | US-60-252-833-37830  | Sequence 37830, A   |
| C 259 | 15 | 2.5 | 284 | 7 | US-09-764-874-9875  | Sequence 9875, App   | C 332 | 15 | 2.5 | 362 | 7 | US-09-912-292-24508  | Sequence 24508, A   |
| C 260 | 15 | 2.5 | 284 | 8 | US-60-253-653-6571  | Sequence 6571, App   | C 333 | 15 | 2.5 | 364 | 7 | US-09-912-292-35540  | Sequence 35540, A   |
| C 261 | 15 | 2.5 | 285 | 7 | US-09-853-807-3263  | Sequence 3263, App   | C 334 | 15 | 2.5 | 364 | 8 | US-60-253-455-22138  | Sequence 22138, A   |
| C 262 | 15 | 2.5 | 287 | 6 | US-09-790-435-2160  | Sequence 2160, App   | C 335 | 15 | 2.5 | 365 | 6 | US-09-504-576A-2428  | Sequence 2428, App  |
| C 263 | 15 | 2.5 | 287 | 8 | US-60-253-652-24155 | Sequence 24155, A    | C 336 | 15 | 2.5 | 367 | 6 | US-09-804-730-2839   | Sequence 2839, App  |
| C 264 | 15 | 2.5 | 289 | 8 | US-60-253-378-36075 | Sequence 36075, A    | C 337 | 15 | 2.5 | 367 | 6 | US-09-758-442-1172   | Sequence 1172, App  |
| C 265 | 15 | 2.5 | 290 | 7 | US-09-867-716-2318  | Sequence 2318, App   | C 338 | 15 | 2.5 | 370 | 7 | US-09-724-671-18825  | Sequence 18825, A   |
| C 266 | 15 | 2.5 | 292 | 7 | US-09-880-107-1581  | Sequence 1581, App   | C 339 | 15 | 2.5 | 371 | 7 | US-09-724-671-1222   | Sequence 1222, App  |
| C 267 | 15 | 2.5 | 292 | 7 | US-09-823-327-5530  | Sequence 5530, App   | C 340 | 15 | 2.5 | 371 | 8 | US-60-253-652-20359  | Sequence 20359, A   |
| C 268 | 15 | 2.5 | 292 | 7 | US-09-540-213-38802 | Sequence 38802, A    | C 341 | 15 | 2.5 | 373 | 6 | US-09-898-888-3587   | Sequence 3587, App  |
| C 269 | 15 | 2.5 | 293 | 7 | US-09-840-145-5109  | Sequence 5109, App   | C 342 | 15 | 2.5 | 373 | 6 | US-09-804-730-13731  | Sequence 13731, A   |
| C 270 | 15 | 2.5 | 293 | 8 | US-60-253-653-283   | Sequence 283, App    | C 343 | 15 | 2.5 | 374 | 6 | US-09-757-034-653    | Sequence 653, App   |
| C 271 | 15 | 2.5 | 294 | 6 | US-09-803-110-7207  | Sequence 7207, App   | C 344 | 15 | 2.5 | 375 | 1 | PCT-US01-08631-2528  | Sequence 2528, App  |
| C 272 | 15 | 2.5 | 294 | 7 | US-09-863-524-3586  | Sequence 3586, App   | C 345 | 15 | 2.5 | 375 | 7 | US-09-724-671-12222  | Sequence 12222, App |
| C 273 | 15 | 2.5 | 296 | 7 | US-09-540-213-47736 | Sequence 47732, A    | C 346 | 15 | 2.5 | 377 | 8 | US-09-783-590-10476  | Sequence 10476, A   |
| C 274 | 15 | 2.5 | 297 | 7 | US-09-839-976-1736  | Sequence 1736, App   | C 347 | 15 | 2.5 | 378 | 8 | US-60-253-378-6338   | Sequence 6338, App  |
| C 275 | 15 | 2.5 | 297 | 8 | US-09-922-217-31    | Sequence 31, App1    | C 348 | 15 | 2.5 | 381 | 7 | US-09-692-257A-1435  | Sequence 1435, App  |
| C 276 | 15 | 2.5 | 297 | 8 | US-60-253-652-19466 | Sequence 19466, A    | C 349 | 15 | 2.5 | 381 | 8 | US-60-253-378-1838   | Sequence 1838, App  |
| C 277 | 15 | 2.5 | 300 | 7 | US-09-894-949-2547  | Sequence 2547, App   | C 350 | 15 | 2.5 | 381 | 8 | US-60-253-455-568    | Sequence 568, App   |
| C 278 | 15 | 2.5 | 301 | 7 | PCT-US01-08656-4893 | Sequence 4893, App   | C 351 | 15 | 2.5 | 384 | 6 | US-09-611-527A-96    | Sequence 96, App    |
| C 279 | 15 | 2.5 | 301 | 7 | US-09-877-486-3646  | Sequence 3646, App   | C 352 | 15 | 2.5 | 384 | 7 | US-09-611-527A-1813  | Sequence 1813, App  |
| C 280 | 15 | 2.5 | 301 | 8 | US-60-253-653-342   | Sequence 342, App    | C 353 | 15 | 2.5 | 388 | 7 | US-09-912-292-54559  | Sequence 54559, A   |
| C 281 | 15 | 2.5 | 302 | 8 | US-60-253-378-22144 | Sequence 22144, A    | C 354 | 15 | 2.5 | 390 | 7 | US-09-834-366-47296  | Sequence 47296, A   |
| C 282 | 15 | 2.5 | 303 | 6 | US-09-804-730-20147 | Sequence 20147, A    | C 355 | 15 | 2.5 | 390 | 7 | US-09-864-761-4279   | Sequence 4279, App  |
| C 283 | 15 | 2.5 | 304 | 8 | US-60-252-833-12574 | Sequence 12574, A    | C 356 | 15 | 2.5 | 390 | 7 | US-09-864-761-21032  | Sequence 21032, A   |
| C 284 | 15 | 2.5 | 307 | 8 | US-60-253-378-36054 | Sequence 36054, A    | C 357 | 15 | 2.5 | 391 | 7 | US-09-864-761-3379   | Sequence 3379, App  |
| C 285 | 15 | 2.5 | 312 | 8 | US-60-253-619-6598  | Sequence 6598, App   | C 358 | 15 | 2.5 | 393 | 6 | US-09-909-628-15965  | Sequence 15965, A   |
| C 286 | 15 | 2.5 | 313 | 7 | US-09-724-671-13915 | Sequence 13915, A    | C 359 | 15 | 2.5 | 393 | 6 | US-09-834-366-46608  | Sequence 46608, A   |
| C 287 | 15 | 2.5 | 314 | 6 | US-09-866-555-13756 | Sequence 13756, A    | C 360 | 15 | 2.5 | 394 | 6 | US-09-866-555-11628  | Sequence 11628, A   |
| C 288 | 15 | 2.5 | 314 | 7 | US-09-764-905-25631 | Sequence 25631, A    | C 361 | 15 | 2.5 | 394 | 6 | US-60-252-833-37793  | Sequence 37793, A   |
| C 289 | 15 | 2.5 | 314 | 8 | US-60-253-456-4867  | Sequence 4867, App   | C 362 | 15 | 2.5 | 396 | 5 | US-09-824-555-4703   | Sequence 4703, App  |
| C 290 | 15 | 2.5 | 317 | 8 | US-09-912-292-28740 | Sequence 28740, A    | C 363 | 15 | 2.5 | 397 | 6 | US-09-907-452-18     | Sequence 18, App1   |
| C 291 | 15 | 2.5 | 317 | 8 | US-60-253-456-6564  | Sequence 6564, App   | C 364 | 15 | 2.5 | 397 | 6 | US-09-611-527A-95    | Sequence 95, App    |
| C 292 | 15 | 2.5 | 318 | 7 | US-09-764-905-8323  | Sequence 8323, App   | C 365 | 15 | 2.5 | 397 | 7 | US-09-840-145-10176  | Sequence 10176, A   |
| C 293 | 15 | 2.5 | 319 | 8 | US-60-253-456-23377 | Sequence 23377, A    | C 366 | 15 | 2.5 | 398 | 6 | US-09-904-703-2817   | Sequence 2817, App  |
| C 294 | 15 | 2.5 | 321 | 7 | US-09-724-671-3935  | Sequence 3935, App   | C 367 | 15 | 2.5 | 399 | 6 | US-09-611-527A-866   | Sequence 866, App   |
| C 295 | 15 | 2.5 | 321 | 7 | US-09-912-292-28740 | Sequence 28740, A    | C 368 | 15 | 2.5 | 399 | 8 | US-60-253-456-2997   | Sequence 2997, App  |
| C 296 | 15 | 2.5 | 322 | 8 | US-60-253-653-22384 | Sequence 22384, A    | C 369 | 15 | 2.5 | 400 | 6 | US-09-898-888-9289   | Sequence 9289, App  |
| C 297 | 15 | 2.5 | 323 | 6 | US-09-922-279-286   | Sequence 286, App    | C 370 | 15 | 2.5 | 400 | 7 | US-09-850-147-1568   | Sequence 1568, A    |
| C 298 | 15 | 2.5 | 328 | 8 | US-60-252-833-23255 | Sequence 23255, A    | C 371 | 15 | 2.5 | 400 | 8 | US-60-253-457-12676  | Sequence 12676, A   |
| C 299 | 15 | 2.5 | 329 | 8 | US-60-253-654-24353 | Sequence 24353, A    | C 372 | 15 | 2.5 | 401 | 7 | US-09-724-671-11990  | Sequence 11990, A   |
| C 300 | 15 | 2.5 | 329 | 8 | US-60-255-592-24353 | Sequence 24353, A    | C 373 | 15 | 2.5 | 401 | 7 | US-09-764-905-21194  | Sequence 21194, App |
| C 301 | 15 | 2.5 | 334 | 7 | US-09-724-671-10249 | Sequence 10249, A    | C 374 | 15 | 2.5 | 402 | 6 | US-09-667-188A-6861  | Sequence 6861, App  |
| C 302 | 15 | 2.5 | 334 | 7 | US-09-859-490-10762 | Sequence 10762, A    | C 375 | 15 | 2.5 | 403 | 6 | US-09-904-703-6175   | Sequence 6175, App  |
| C 303 | 15 | 2.5 | 334 | 8 | US-60-253-456-22763 | Sequence 22763, A    | C 376 | 15 | 2.5 | 403 | 6 | US-09-611-527A-2636  | Sequence 2636, App  |
| C 304 | 15 | 2.5 | 335 | 6 | US-09-823-241-7965  | Sequence 7965, App   | C 377 | 15 | 2.5 | 403 | 6 | US-09-617-681A-1429  | Sequence 1429, App  |
| C 305 | 15 | 2.5 | 339 | 6 | US-09-540-213-28886 | Sequence 28886, A    | C 378 | 15 | 2.5 | 405 | 7 | US-09-692-257A-1123  | Sequence 1123, App  |
| C 306 | 15 | 2.5 | 339 | 8 | US-60-253-378-2631  | Sequence 2631, App   | C 379 | 15 | 2.5 | 405 | 7 | US-09-824-518-1921   | Sequence 1921, App  |
| C 307 | 15 | 2.5 | 340 | 6 | US-09-804-730-16368 | Sequence 16368, A    | C 380 | 15 | 2.5 | 405 | 7 | US-09-824-556-5594   | Sequence 5594, App  |
| C 308 | 15 | 2.5 | 341 | 6 | US-09-718-454-130   | Sequence 130, App    | C 381 | 15 | 2.5 | 405 | 7 | US-09-824-628-5594   | Sequence 5594, App  |
| C 309 | 15 | 2.5 | 341 | 8 | US-60-253-457-16677 | Sequence 16677, App  | C 382 | 15 | 2.5 | 408 | 5 | US-09-824-555-7947   | Sequence 7947, App  |
| C 310 | 15 | 2.5 | 342 | 4 | US-08-798-074B-5584 | Sequence 5584, App   | C 383 | 15 | 2.5 | 410 | 6 | US-09-898-888-37682  | Sequence 37682, A   |
| C 311 | 15 | 2.5 | 342 | 4 | US-08-798-074B-5584 | Sequence 5584, App   | C 384 | 15 | 2.5 | 410 | 6 | US-09-804-730-3741   | Sequence 3741, App  |
| C 312 | 15 | 2.5 | 342 | 4 | US-08-798-074C-5584 | Sequence 5584, App   | C 385 | 15 | 2.5 | 411 | 1 | PCT-US01-04926A-431  | Sequence 431, App   |
| C 313 | 15 | 2.5 | 342 | 6 | US-09-667-188A-234  | Sequence 234, App    | C 386 | 15 | 2.5 | 411 | 1 | PCT-US01-04926A-432  | Sequence 432, App   |
| C 314 | 15 | 2.5 | 344 | 7 | US-09-724-671-5541  | Sequence 5341, App   | C 387 | 15 | 2.5 | 411 | 1 | PCT-US01-04926A-433  | Sequence 433, App   |
| C 315 | 15 | 2.5 | 344 | 7 | US-09-850-147-15518 | Sequence 15518, App  | C 388 | 15 | 2.5 | 412 | 6 | US-09-909-628-22790  | Sequence 22790, App |
| C 316 | 15 | 2.5 | 345 | 7 | US-09-834-366-7468  | Sequence 7468, App   | C 389 | 15 | 2.5 | 412 | 7 | US-09-813-155-10939  | Sequence 10939, A   |
| C 317 | 15 | 2.5 | 346 | 7 | US-09-540-213-38719 | Sequence 38719, App1 | C 390 | 15 | 2.5 | 412 | 7 | US-09-923-779-23     | Sequence 23, App1   |

|       |    |     |     |   |                      |                    |       |    |     |     |   |                      |                    |
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| C 391 | 15 | 2.5 | 412 | 8 | US-60-253-654-11685  | Sequence 11685, A  | 464   | 15 | 2.5 | 449 | 7 | US-09-912-292-22281  | Sequence 22281, A  |
| C 392 | 15 | 2.5 | 413 | 8 | US-60-253-592-11685  | Sequence 11685, A  | 465   | 15 | 2.5 | 450 | 7 | US-09-821-710-44229  | Sequence 44229, A  |
| C 393 | 15 | 2.5 | 413 | 6 | US-09-909-629-37     | Sequence 37, App1  | C 466 | 15 | 2.5 | 450 | 6 | US-09-909-629-916    | Sequence 916, App  |
| C 394 | 15 | 2.5 | 413 | 6 | US-09-909-629-37     | Sequence 45, App1  | C 467 | 15 | 2.5 | 451 | 6 | US-09-866-555-17982  | Sequence 17982, A  |
| C 395 | 15 | 2.5 | 413 | 6 | US-09-909-629-37     | Sequence 32493, A  | C 468 | 15 | 2.5 | 451 | 6 | US-09-909-629-932    | Sequence 932, App  |
| C 396 | 15 | 2.5 | 413 | 7 | US-09-692-257A-5534  | Sequence 5534, App | C 469 | 15 | 2.5 | 451 | 7 | US-09-692-257A-6939  | Sequence 6939, App |
| C 397 | 15 | 2.5 | 413 | 7 | US-09-922-217-676    | Sequence 676, App  | C 470 | 15 | 2.5 | 452 | 6 | US-09-909-627-19588  | Sequence 19588, A  |
| C 398 | 15 | 2.5 | 414 | 6 | US-09-904-703-4865   | Sequence 4865, App | C 471 | 15 | 2.5 | 452 | 6 | US-09-909-629-963    | Sequence 963, App  |
| C 399 | 15 | 2.5 | 414 | 6 | US-09-909-629-35     | Sequence 35, App1  | C 472 | 15 | 2.5 | 453 | 6 | US-09-866-555-1963   | Sequence 1963, App |
| C 400 | 15 | 2.5 | 414 | 6 | US-09-909-629-39     | Sequence 39, App1  | C 473 | 15 | 2.5 | 453 | 6 | US-09-866-555-13245  | Sequence 13245, A  |
| C 401 | 15 | 2.5 | 414 | 6 | US-09-909-629-81     | Sequence 81, App1  | C 474 | 15 | 2.5 | 453 | 6 | US-09-823-241-2237   | Sequence 2237, App |
| C 402 | 15 | 2.5 | 415 | 6 | US-09-804-730-2144   | Sequence 2144, App | C 475 | 15 | 2.5 | 453 | 7 | US-09-912-292-55435  | Sequence 55435, A  |
| C 403 | 15 | 2.5 | 415 | 6 | US-09-758-463-176    | Sequence 176, App  | C 476 | 15 | 2.5 | 454 | 7 | US-09-909-629-914    | Sequence 9346, A   |
| C 404 | 15 | 2.5 | 415 | 6 | US-09-904-809-18884  | Sequence 18884, A  | C 477 | 15 | 2.5 | 454 | 6 | US-09-909-629-925    | Sequence 9346, A   |
| C 405 | 15 | 2.5 | 416 | 1 | PCT-US01-14827-7046  | Sequence 7046, App | C 478 | 15 | 2.5 | 454 | 6 | US-09-909-629-925    | Sequence 925, App  |
| C 406 | 15 | 2.5 | 416 | 1 | US-09-824-559-2436   | Sequence 2436, App | C 479 | 15 | 2.5 | 455 | 6 | US-09-909-629-925    | Sequence 925, App  |
| C 407 | 15 | 2.5 | 416 | 6 | US-09-909-627-4339   | Sequence 4339, App | C 480 | 15 | 2.5 | 455 | 6 | US-09-909-629-925    | Sequence 925, App  |
| C 408 | 15 | 2.5 | 416 | 6 | US-09-909-629-19     | Sequence 19, App1  | C 481 | 15 | 2.5 | 455 | 6 | US-09-909-629-957    | Sequence 957, App  |
| C 409 | 15 | 2.5 | 416 | 6 | US-09-909-629-23     | Sequence 23, App1  | C 482 | 15 | 2.5 | 455 | 7 | US-09-834-366-6856   | Sequence 6856, App |
| C 410 | 15 | 2.5 | 417 | 6 | US-09-909-629-22     | Sequence 22, App1  | C 483 | 15 | 2.5 | 456 | 6 | US-09-764-891-1125   | Sequence 1125, App |
| C 411 | 15 | 2.5 | 417 | 6 | US-09-904-703-4703   | Sequence 4703, App | C 484 | 15 | 2.5 | 456 | 6 | US-09-909-629-34311  | Sequence 34311, A  |
| C 412 | 15 | 2.5 | 418 | 6 | US-09-909-629-83     | Sequence 83, App1  | C 485 | 15 | 2.5 | 457 | 7 | US-09-834-366-31993  | Sequence 31993, A  |
| C 413 | 15 | 2.5 | 418 | 6 | US-09-909-629-17     | Sequence 17, App1  | C 486 | 15 | 2.5 | 459 | 6 | US-09-909-627-20302  | Sequence 20302, A  |
| C 414 | 15 | 2.5 | 419 | 6 | US-09-540-213-20738  | Sequence 20738, A  | C 487 | 15 | 2.5 | 459 | 6 | US-09-909-627-20318  | Sequence 20318, A  |
| C 415 | 15 | 2.5 | 420 | 5 | US-09-824-559-8115   | Sequence 8115, App | C 488 | 15 | 2.5 | 459 | 6 | US-09-617-681A-44225 | Sequence 44225, A  |
| C 416 | 15 | 2.5 | 420 | 6 | US-09-760-469-357    | Sequence 357, App  | C 489 | 15 | 2.5 | 459 | 6 | US-09-617-681A-44225 | Sequence 44225, A  |
| C 417 | 15 | 2.5 | 420 | 6 | US-09-904-703-528    | Sequence 528, App  | C 490 | 15 | 2.5 | 459 | 6 | US-09-617-681A-44225 | Sequence 44225, A  |
| C 418 | 15 | 2.5 | 420 | 6 | US-09-909-627-3452   | Sequence 3452, App | C 491 | 15 | 2.5 | 461 | 6 | US-09-617-681A-3191  | Sequence 3191, A   |
| C 419 | 15 | 2.5 | 420 | 6 | US-09-909-627-3452   | Sequence 3452, App | C 492 | 15 | 2.5 | 461 | 7 | US-09-846-038-652    | Sequence 652, App  |
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| C 422 | 15 | 2.5 | 421 | 7 | US-09-850-147-11141  | Sequence 11141, A  | C 495 | 15 | 2.5 | 466 | 6 | US-09-504-703-16820  | Sequence 16820, A  |
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| C 425 | 15 | 2.5 | 422 | 6 | US-09-617-681A-908   | Sequence 908, App  | C 498 | 15 | 2.5 | 467 | 7 | US-09-834-366-6099   | Sequence 6099, App |
| C 426 | 15 | 2.5 | 422 | 7 | US-09-724-671-19895  | Sequence 19895, A  | C 499 | 15 | 2.5 | 468 | 6 | US-09-813-155-171    | Sequence 171, App  |
| C 427 | 15 | 2.5 | 422 | 7 | US-09-912-292-40783  | Sequence 40783, A  | C 500 | 15 | 2.5 | 468 | 6 | US-09-904-809-16387  | Sequence 16387, A  |
| C 428 | 15 | 2.5 | 423 | 6 | US-09-758-446-355    | Sequence 355, App  | C 501 | 15 | 2.5 | 471 | 6 | US-09-866-555-17936  | Sequence 17936, A  |
| C 429 | 15 | 2.5 | 423 | 6 | US-09-909-629-16210  | Sequence 16210, A  | C 502 | 15 | 2.5 | 472 | 6 | US-09-866-555-17936  | Sequence 17936, A  |
| C 430 | 15 | 2.5 | 423 | 6 | US-09-838-601-1588   | Sequence 1588, App | C 503 | 15 | 2.5 | 473 | 7 | US-09-866-555-17936  | Sequence 17936, A  |
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| C 432 | 15 | 2.5 | 426 | 8 | US-09-667-188A-5567  | Sequence 5567, App | C 505 | 15 | 2.5 | 475 | 6 | US-09-813-155-3575   | Sequence 3575, App |
| C 433 | 15 | 2.5 | 428 | 7 | US-09-834-366-46453  | Sequence 46453, A  | C 506 | 15 | 2.5 | 475 | 6 | US-09-813-155-3575   | Sequence 3575, App |
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| C 438 | 15 | 2.5 | 431 | 7 | US-09-821-710-6102   | Sequence 6102, App | C 511 | 15 | 2.5 | 478 | 6 | US-09-904-809-326    | Sequence 326, App  |
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| C 454 | 15 | 2.5 | 443 | 7 | US-09-724-671-3267   | Sequence 3267, App | C 527 | 15 | 2.5 | 494 | 7 | US-09-838-601-1312   | Sequence 1312, App |
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| C 463 | 15 | 2.5 | 449 | 6 | US-09-909-629-928    | Sequence 928, App  | C 536 | 15 | 2.5 | 500 | 7 | US-09-813-155-5726   | Sequence 5726, App |
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| 550 | 15 | 2.5 | 512 | 7 | US-09-838-601-1855   | Sequence 1855, Ap  | 623 | 15 | 2.5 | 677  | 6 | US-09-850-147-5398    | Sequence 5398, App |
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| 552 | 15 | 2.5 | 514 | 8 | US-60-279-526-983    | Sequence 983, App  | 625 | 15 | 2.5 | 696  | 6 | US-09-758-471-1941    | Sequence 1941, Ap  |
| 553 | 15 | 2.5 | 518 | 6 | US-09-504-576A-172   | Sequence 172, App  | 626 | 15 | 2.5 | 700  | 6 | US-09-898-888-11952   | Sequence 11952, A  |
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| 573 | 15 | 2.5 | 555 | 6 | US-09-796-692-8108   | Sequence 8108, Ap  | 646 | 15 | 2.5 | 873  | 7 | US-09-902-540-4045    | Sequence 4045, Ap  |
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| 575 | 15 | 2.5 | 560 | 7 | US-09-540-213-38806  | Sequence 38806, Ap | 648 | 15 | 2.5 | 925  | 6 | US-09-764-902-799     | Sequence 799, App  |
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| 579 | 15 | 2.5 | 569 | 7 | US-09-825-422-123    | Sequence 123, App  | 652 | 15 | 2.5 | 937  | 6 | US-09-898-888-12676   | Sequence 12676, A  |
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| 581 | 15 | 2.5 | 577 | 8 | US-60-253-652-6296   | Sequence 6296, Ap  | 654 | 15 | 2.5 | 989  | 7 | US-09-867-716-15773   | Sequence 15771, A  |
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| 583 | 15 | 2.5 | 587 | 8 | US-60-252-833-28454  | Sequence 28454, A  | 656 | 15 | 2.5 | 994  | 7 | US-09-861-478-4575    | Sequence 4575, Ap  |
| 584 | 15 | 2.5 | 588 | 8 | US-60-252-833-30247  | Sequence 30247, A  | 657 | 15 | 2.5 | 1005 | 8 | US-60-278-561-13631   | Sequence 13631, A  |
| 585 | 15 | 2.5 | 589 | 8 | US-60-252-833-42071  | Sequence 42071, A  | 658 | 15 | 2.5 | 1019 | 7 | US-09-867-716-16359   | Sequence 16359, A  |
| 586 | 15 | 2.5 | 594 | 7 | US-09-825-422-30     | Sequence 30, Appl  | 659 | 15 | 2.5 | 1029 | 6 | US-09-803-110-4766    | Sequence 4766, Ap  |
| 587 | 15 | 2.5 | 595 | 8 | US-60-253-378-2609   | Sequence 2609, Ap  | 660 | 15 | 2.5 | 1035 | 6 | PCT-US01-08631-6639   | Sequence 6039, Ap  |
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| 591 | 15 | 2.5 | 600 | 7 | US-09-825-422-243    | Sequence 243, App  | 664 | 15 | 2.5 | 1077 | 6 | US-09-738-626-2405    | Sequence 2405, Ap  |
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| 594 | 15 | 2.5 | 604 | 6 | US-09-898-888-15067  | Sequence 15067, A  | 667 | 15 | 2.5 | 1104 | 7 | PCT-US01-08631-4359   | Sequence 4359, Ap  |
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| 596 | 15 | 2.5 | 606 | 7 | US-09-724-671-4040   | Sequence 4040, Ap  | 669 | 15 | 2.5 | 1122 | 6 | US-09-803-110-7369    | Sequence 7369, Ap  |
| 597 | 15 | 2.5 | 607 | 7 | US-09-811-217-368    | Sequence 368, App  | 670 | 15 | 2.5 | 1134 | 6 | US-60-278-561-1563    | Sequence 1563, Ap  |
| 598 | 15 | 2.5 | 612 | 7 | US-09-825-422-624    | Sequence 624, App  | 671 | 15 | 2.5 | 1137 | 6 | US-09-898-888-13846   | Sequence 13846, A  |
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| 600 | 15 | 2.5 | 616 | 6 | US-60-253-653-19130  | Sequence 19130, A  | 673 | 15 | 2.5 | 1143 | 8 | US-60-312-544-4476    | Sequence 4476, Ap  |
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| 602 | 15 | 2.5 | 621 | 8 | US-60-253-378-20042  | Sequence 20042, Ap | 675 | 15 | 2.5 | 1155 | 6 | US-09-898-888-3424    | Sequence 3424, Ap  |
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| 604 | 15 | 2.5 | 624 | 8 | US-60-252-833-42032  | Sequence 42032, A  | 677 | 15 | 2.5 |      |   |                       |                    |
| 605 | 15 | 2.5 | 627 | 8 | US-09-825-422-496    | Sequence 496, App  | 678 | 15 | 2.5 |      |   |                       |                    |
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| 607 | 15 | 2.5 | 629 | 7 | US-09-692-257A-14827 | Sequence 14827, A  | 680 | 15 | 2.5 |      |   |                       |                    |
| 608 | 15 | 2.5 | 632 | 8 | US-60-252-833-28427  | Sequence 28427, A  | 681 | 15 | 2.5 |      |   |                       |                    |
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| C 683 | 15 | 2.5 | 1162 | 1 | PCT-US01-04926A-89   | Sequence 89, Appl  | 756   | 15 | 2.5 | 1930 | 6 | US-09-898-888-10346  | Sequence 10346, A   |
| C 684 | 15 | 2.5 | 1164 | 1 | PCT-US01-04631-14649 | Sequence 14649, A  | C 757 | 15 | 2.5 | 1935 | 7 | US-09-764-905-22338  | Sequence 22335, A   |
| C 685 | 15 | 2.5 | 1174 | 6 | US-09-758-442-356    | Sequence 356, App  | C 758 | 15 | 2.5 | 1957 | 1 | PCT-US01-14827-2693  | Sequence 2693, App  |
| C 686 | 15 | 2.5 | 1176 | 1 | PCT-US01-16450-925   | Sequence 925, App  | C 759 | 15 | 2.5 | 2010 | 8 | US-60-257-896-8      | Sequence 8, App1    |
| C 687 | 15 | 2.5 | 1200 | 6 | US-09-602-740-661    | Sequence 661, App  | C 760 | 15 | 2.5 | 2053 | 1 | PCT-US01-08631-5020  | Sequence 5020, App  |
| C 688 | 15 | 2.5 | 1207 | 1 | PCT-US01-04926A-88   | Sequence 88, App   | C 761 | 15 | 2.5 | 2070 | 1 | PCT-US01-08631-13250 | Sequence 13250, A   |
| C 689 | 15 | 2.5 | 1218 | 5 | US-09-546-547-3      | Sequence 3, App1   | C 762 | 15 | 2.5 | 2114 | 1 | PCT-US01-08631-455   | Sequence 455, App   |
| C 690 | 15 | 2.5 | 1220 | 8 | US-60-312-544-4164   | Sequence 4164, App | C 763 | 15 | 2.5 | 2178 | 1 | PCT-US01-14827-77    | Sequence 77, App1   |
| C 691 | 15 | 2.5 | 1223 | 5 | US-09-925-297-282    | Sequence 282, App  | C 764 | 15 | 2.5 | 2184 | 6 | US-09-760-443-290    | Sequence 290, App   |
| C 692 | 15 | 2.5 | 1224 | 5 | US-09-855-768-34     | Sequence 34, App   | C 765 | 15 | 2.5 | 2186 | 1 | US-60-312-544-2394   | Sequence 2394, App  |
| C 693 | 15 | 2.5 | 1240 | 8 | US-60-312-544-2176   | Sequence 2176, App | C 766 | 15 | 2.5 | 2188 | 1 | PCT-US01-14827-7990  | Sequence 7990, App  |
| C 694 | 15 | 2.5 | 1245 | 6 | US-09-738-626-89     | Sequence 89, App   | C 767 | 15 | 2.5 | 2221 | 7 | US-09-611-197-74     | Sequence 74, App    |
| C 695 | 15 | 2.5 | 1249 | 6 | US-09-758-446-297    | Sequence 297, App  | C 768 | 15 | 2.5 | 2231 | 6 | US-09-810-173-166    | Sequence 166, App   |
| C 696 | 15 | 2.5 | 1250 | 1 | PCT-US01-04926A-87   | Sequence 20852, A  | C 769 | 15 | 2.5 | 2237 | 6 | US-09-810-173-359    | Sequence 359, App   |
| C 697 | 15 | 2.5 | 1255 | 1 | PCT-US01-04926A-87   | Sequence 87, App   | C 770 | 15 | 2.5 | 2237 | 6 | US-09-757-028-551    | Sequence 551, App   |
| C 698 | 15 | 2.5 | 1275 | 6 | US-09-898-888-5936   | Sequence 5936, App | C 771 | 15 | 2.5 | 2311 | 5 | US-09-925-302-244    | Sequence 244, App   |
| C 699 | 15 | 2.5 | 1281 | 6 | US-09-647-472-3      | Sequence 3, App1   | C 772 | 15 | 2.5 | 2341 | 8 | US-60-278-258-12522  | Sequence 12522, A   |
| C 700 | 15 | 2.5 | 1281 | 6 | US-09-885-722-8      | Sequence 8, App1   | C 773 | 15 | 2.5 | 2347 | 1 | PCT-US01-08631-2250  | Sequence 250, App   |
| C 701 | 15 | 2.5 | 1287 | 6 | US-09-602-787A-179   | Sequence 179, App  | C 774 | 15 | 2.5 | 2356 | 1 | PCT-US01-08636-3426  | Sequence 3426, App  |
| C 702 | 15 | 2.5 | 1313 | 5 | US-09-827-110-4      | Sequence 4, App1   | C 775 | 15 | 2.5 | 2420 | 7 | US-09-850-118-1586   | Sequence 1, App1    |
| C 703 | 15 | 2.5 | 1313 | 6 | US-09-448-188-4      | Sequence 4, App1   | C 776 | 15 | 2.5 | 2420 | 6 | US-09-722-845-1      | Sequence 4231, App  |
| C 704 | 15 | 2.5 | 1334 | 6 | US-09-808-383-4380   | Sequence 4380, App | C 777 | 15 | 2.5 | 2424 | 7 | US-09-902-540-4231   | Sequence 5957, App  |
| C 705 | 15 | 2.5 | 1335 | 6 | US-09-803-110-3948   | Sequence 3948, App | C 778 | 15 | 2.5 | 2447 | 1 | PCT-US01-08631-5957  | Sequence 167, App   |
| C 706 | 15 | 2.5 | 1344 | 1 | PCT-US01-08631-18601 | Sequence 18601, A  | C 779 | 15 | 2.5 | 2459 | 6 | US-09-810-173-157    | Sequence 22086, A   |
| C 707 | 15 | 2.5 | 1347 | 1 | PCT-US01-08631-26354 | Sequence 26354, A  | C 780 | 15 | 2.5 | 2474 | 1 | PCT-US01-08631-22086 | Sequence 2577, A    |
| C 708 | 15 | 2.5 | 1350 | 7 | US-09-902-540-8545   | Sequence 4545, App | C 781 | 15 | 2.5 | 2477 | 1 | PCT-US01-08631-26577 | Sequence 10138, A   |
| C 709 | 15 | 2.5 | 1351 | 8 | US-60-278-258-8079   | Sequence 8079, App | C 782 | 15 | 2.5 | 2479 | 8 | US-60-278-561-10138  | Sequence 35, App1   |
| C 710 | 15 | 2.5 | 1354 | 6 | US-09-764-869-2118   | Sequence 2118, App | C 783 | 15 | 2.5 | 2510 | 7 | US-09-646-777A-35    | Sequence 8585, App1 |
| C 711 | 15 | 2.5 | 1355 | 6 | US-09-898-888-12961  | Sequence 12961, A  | C 784 | 15 | 2.5 | 2544 | 1 | PCT-US01-08631-85854 | Sequence 11683, A   |
| C 712 | 15 | 2.5 | 1359 | 6 | US-09-803-110-5000   | Sequence 5000, App | C 785 | 15 | 2.5 | 2554 | 6 | US-09-905-059-92     | Sequence 92, App1   |
| C 713 | 15 | 2.5 | 1364 | 6 | US-09-757-028-712    | Sequence 712, App  | C 786 | 15 | 2.5 | 2554 | 6 | US-09-598-075-25     | Sequence 25, App1   |
| C 714 | 15 | 2.5 | 1368 | 6 | US-09-898-888-14361  | Sequence 14361, A  | C 787 | 15 | 2.5 | 2579 | 6 | US-09-598-075-25     | Sequence 25, App1   |
| C 715 | 15 | 2.5 | 1416 | 7 | US-09-902-540-4687   | Sequence 4687, App | C 788 | 15 | 2.5 | 2579 | 6 | US-09-598-075-25     | Sequence 159, App   |
| C 716 | 15 | 2.5 | 1423 | 6 | US-09-229-911A-9     | Sequence 9, App1   | C 789 | 15 | 2.5 | 2598 | 6 | US-09-893-133-159    | Sequence 408, App   |
| C 717 | 15 | 2.5 | 1428 | 8 | US-60-278-561-13845  | Sequence 13845, A  | C 790 | 15 | 2.5 | 2623 | 6 | US-09-760-469-457    | Sequence 467, App   |
| C 718 | 15 | 2.5 | 1443 | 6 | US-09-803-110-6442   | Sequence 6442, App | C 791 | 15 | 2.5 | 2635 | 6 | US-09-764-875-468    | Sequence 390, App   |
| C 719 | 15 | 2.5 | 1448 | 7 | US-09-673-395A-29    | Sequence 29, App1  | C 792 | 15 | 2.5 | 2655 | 7 | US-09-902-540-8965   | Sequence 8965, App  |
| C 720 | 15 | 2.5 | 1476 | 7 | US-09-902-540-220    | Sequence 220, App  | C 793 | 15 | 2.5 | 2659 | 7 | US-09-902-540-4695   | Sequence 4695, App  |
| C 721 | 15 | 2.5 | 1500 | 1 | PCT-US01-08631-21140 | Sequence 21140, A  | C 794 | 15 | 2.5 | 2678 | 6 | US-09-807-757A-8     | Sequence 8, App1    |
| C 722 | 15 | 2.5 | 1500 | 7 | US-09-902-540-7578   | Sequence 7578, App | C 795 | 15 | 2.5 | 2719 | 7 | US-09-881-797-4046   | Sequence 4046, App  |
| C 723 | 15 | 2.5 | 1501 | 6 | US-09-652-125A-9389  | Sequence 9389, App | C 796 | 15 | 2.5 | 2720 | 7 | US-09-646-777A-223   | Sequence 223, App   |
| C 724 | 15 | 2.5 | 1527 | 1 | PCT-US01-08656-3553  | Sequence 3553, App | C 797 | 15 | 2.5 | 2725 | 6 | US-09-764-875-166    | Sequence 166, App   |
| C 725 | 15 | 2.5 | 1535 | 6 | US-09-898-888-5742   | Sequence 5742, App | C 798 | 15 | 2.5 | 2754 | 8 | US-60-278-258-8606   | Sequence 8606, App  |
| C 726 | 15 | 2.5 | 1542 | 1 | PCT-US01-16450-1135  | Sequence 1125, App | C 799 | 15 | 2.5 | 2766 | 8 | US-09-738-626-1976   | Sequence 1976, App  |
| C 727 | 15 | 2.5 | 1556 | 1 | PCT-US01-08631-28034 | Sequence 28034, A  | C 800 | 15 | 2.5 | 2801 | 6 | US-60-312-544-4456   | Sequence 4456, App  |
| C 728 | 15 | 2.5 | 1587 | 7 | US-09-902-540-7908   | Sequence 7908, App | C 801 | 15 | 2.5 | 2828 | 1 | PCT-US01-08631-22891 | Sequence 22891, A   |
| C 729 | 15 | 2.5 | 1593 | 1 | PCT-US01-08631-10188 | Sequence 10188, A  | C 802 | 15 | 2.5 | 2840 | 8 | US-09-925-301-513    | Sequence 513, App   |
| C 730 | 15 | 2.5 | 1593 | 1 | PCT-US01-08631-12929 | Sequence 12929, A  | C 803 | 15 | 2.5 | 2840 | 1 | PCT-US01-08631-27475 | Sequence 27475, A   |
| C 731 | 15 | 2.5 | 1593 | 1 | PCT-US01-08631-23755 | Sequence 23755, A  | C 804 | 15 | 2.5 | 2867 | 8 | US-09-764-875-166    | Sequence 166, App   |
| C 732 | 15 | 2.5 | 1593 | 1 | PCT-US01-08631-27962 | Sequence 27962, A  | C 805 | 15 | 2.5 | 2928 | 8 | US-60-278-258-5199   | Sequence 5199, App  |
| C 733 | 15 | 2.5 | 1697 | 6 | US-09-663-119-1      | Sequence 1, App1   | C 806 | 15 | 2.5 | 2935 | 6 | US-09-760-466-1739   | Sequence 1739, App  |
| C 734 | 15 | 2.5 | 1737 | 1 | PCT-US01-08631-27544 | Sequence 27544, A  | C 807 | 15 | 2.5 | 2970 | 1 | PCT-US01-14827-6685  | Sequence 6685, App  |
| C 735 | 15 | 2.5 | 1752 | 7 | US-09-902-540-3394   | Sequence 3394, App | C 808 | 15 | 2.5 | 2999 | 5 | US-09-925-301-513    | Sequence 513, App   |
| C 736 | 15 | 2.5 | 1777 | 1 | PCT-US01-08656-3951  | Sequence 3951, App | C 809 | 15 | 2.5 | 3109 | 8 | US-60-278-561-11648  | Sequence 11648, A   |
| C 737 | 15 | 2.5 | 1781 | 1 | PCT-US01-18569-643   | Sequence 643, App  | C 810 | 15 | 2.5 | 3174 | 4 | PCT-US01-08631-8007  | Sequence 8007, App  |
| C 738 | 15 | 2.5 | 1781 | 6 | US-09-764-868-356    | Sequence 356, App  | C 811 | 15 | 2.5 | 3191 | 6 | US-09-652-125A-8832  | Sequence 8832, App  |
| C 739 | 15 | 2.5 | 1802 | 7 | US-09-902-540-6855   | Sequence 6855, App | C 812 | 15 | 2.5 | 3231 | 1 | PCT-US01-14827-2077  | Sequence 2077, App  |
| C 740 | 15 | 2.5 | 1831 | 6 | US-09-893-133-158    | Sequence 158, App  | C 813 | 15 | 2.5 | 3263 | 1 | PCT-US01-08631-3020  | Sequence 3020, App  |
| C 741 | 15 | 2.5 | 1831 | 6 | US-09-521-195-4      | Sequence 4, App1   | C 814 | 15 | 2.5 | 3263 | 1 | PCT-US01-18569-894   | Sequence 894, App   |
| C 742 | 15 | 2.5 | 1831 | 7 | US-09-798-743-2      | Sequence 2, App1   | C 815 | 15 | 2.5 | 3292 | 8 | US-60-278-232-6177   | Sequence 6177, App  |
| C 743 | 15 | 2.5 | 1850 | 1 | PCT-US01-08631-18557 | Sequence 18557, A  | C 816 | 15 | 2.5 | 3309 | 5 | US-09-925-298-273    | Sequence 273, App   |
| C 744 | 15 | 2.5 | 1850 | 1 | PCT-US01-08631-24141 | Sequence 24141, A  | C 817 | 15 | 2.5 | 3372 | 1 | PCT-US01-08631-26201 | Sequence 26201, A   |
| C 745 | 15 | 2.5 | 1853 | 7 | US-09-764-905-20522  | Sequence 20522, A  | C 818 | 15 | 2.5 | 3427 | 7 | US-09-808-384-759    | Sequence 759, App   |
| C 746 | 15 | 2.5 | 1860 | 7 | US-09-764-905-20520  | Sequence 20520, A  | C 819 | 15 | 2.5 | 3469 | 8 | US-60-278-258-4077   | Sequence 4077, App  |
| C 747 | 15 | 2.5 | 1869 | 5 | US-09-927-796-1      | Sequence 1, App1   | C 820 | 15 | 2.5 | 3639 | 7 | US-09-902-540-5646   | Sequence 5646, App  |
| C 748 | 15 | 2.5 | 1869 | 6 | US-09-511-631-1      | Sequence 1, App1   | C 821 | 15 | 2.5 | 3709 | 8 | US-60-278-258-1473   | Sequence 1473, App  |
| C 749 | 15 | 2.5 | 1876 | 6 | US-09-885-722-5      | Sequence 5, App1   | C 822 | 15 | 2.5 | 3758 | 7 | US-09-902-540-6742   | Sequence 6742, App  |
| C 750 | 15 | 2.5 | 1878 | 6 | US-09-803-110-7264   | Sequence 7264, App | C 823 | 15 | 2.5 | 3760 | 7 | US-09-902-540-543    | Sequence 543, App   |
| C 751 | 15 | 2.5 | 1883 | 1 | PCT-US01-08631-23939 | Sequence 23939, A  | C 824 | 15 | 2.5 | 3936 | 7 | US-09-919-172-49     | Sequence 49, App1   |
| C 752 | 15 | 2.5 | 1891 | 6 | US-09-922-279-1598   | Sequence 1598, App | C 825 | 15 | 2.5 | 4096 | 8 | US-60-278-258-16068  | Sequence 16068, A   |
| C 753 | 15 | 2.5 | 1894 | 5 | US-09-546-547-1      | Sequence 1, App1   | C 826 | 15 | 2.5 | 4151 | 7 | US-09-764-905-31116  | Sequence 31116, App |
| C 754 | 15 | 2.5 | 1900 | 1 | PCT-US01-08631-23217 | Sequence 23217, A  | C 827 | 15 | 2.5 | 4241 | 7 | US-09-764-874-9876   | Sequence 9876, App  |
| C 755 | 15 | 2.5 | 1901 | 8 | US-60-278-258-10537  | Sequence 10537, A  | C 828 | 15 | 2.5 | 4241 | 7 | US-09-764-874-9877   | Sequence 9877, App  |

|       |    |     |       |   |                      |                    |       |    |     |         |   |                     |                   |
|-------|----|-----|-------|---|----------------------|--------------------|-------|----|-----|---------|---|---------------------|-------------------|
| C 829 | 15 | 2.5 | 4386  | 1 | PCR-US01-21985-2     | Sequence 2, Appl1  | 902   | 15 | 2.5 | 28558   | 7 | US-09-902-540-1231  | Sequence 1231, Ap |
| C 830 | 15 | 2.5 | 4452  | 1 | PCR-US01-21985-1     | Sequence 1, Appl1  | C 903 | 15 | 2.5 | 28558   | 7 | US-09-902-540-1231  | Sequence 1231, Ap |
| C 831 | 15 | 2.5 | 4473  | 1 | PCR-US01-08631-24189 | Sequence 24189, A  | C 904 | 15 | 2.5 | 28974   | 7 | US-09-764-905-24789 | Sequence 24789, A |
| C 832 | 15 | 2.5 | 4751  | 7 | US-09-881-797-2510   | Sequence 2510, Ap  | C 905 | 15 | 2.5 | 32082   | 6 | US-09-764-891-9679  | Sequence 9679, A  |
| C 833 | 15 | 2.5 | 4935  | 1 | PCR-US01-08631-12167 | Sequence 12167, A  | C 906 | 15 | 2.5 | 32187   | 6 | US-09-764-874-12253 | Sequence 12253, A |
| C 834 | 15 | 2.5 | 5027  | 6 | US-09-760-469-1173   | Sequence 1173, App | C 907 | 15 | 2.5 | 32195   | 6 | US-09-764-866-1605  | Sequence 1605, A  |
| C 835 | 15 | 2.5 | 5216  | 6 | US-09-764-860-695    | Sequence 695, App  | C 908 | 15 | 2.5 | 32195   | 6 | US-09-764-875-1233  | Sequence 1233, Ap |
| C 836 | 15 | 2.5 | 5216  | 6 | US-09-764-870-607    | Sequence 607, App  | C 909 | 15 | 2.5 | 32195   | 6 | US-09-764-870-611   | Sequence 611, App |
| C 837 | 15 | 2.5 | 5338  | 8 | US-60-278-232-7796   | Sequence 7796, Ap  | C 910 | 15 | 2.5 | 32195   | 6 | US-09-764-870-617   | Sequence 617, App |
| C 838 | 15 | 2.5 | 5342  | 6 | US-09-807-757A-1     | Sequence 1, Appl1  | C 911 | 15 | 2.5 | 32195   | 6 | US-09-764-870-617   | Sequence 617, App |
| C 839 | 15 | 2.5 | 5593  | 6 | US-09-598-075-226    | Sequence 226, App  | C 912 | 15 | 2.5 | 34067   | 6 | US-09-803-736-437   | Sequence 437, App |
| C 840 | 15 | 2.5 | 5593  | 6 | US-09-598-075A-226   | Sequence 226, App  | C 913 | 15 | 2.5 | 34062   | 7 | US-09-902-540-1261  | Sequence 1261, Ap |
| C 841 | 15 | 2.5 | 5785  | 6 | US-09-764-902-2249   | Sequence 2249, Ap  | C 914 | 15 | 2.5 | 34842   | 6 | US-09-803-736-359   | Sequence 359, App |
| C 842 | 15 | 2.5 | 5785  | 6 | US-09-764-902-2251   | Sequence 2251, Ap  | C 915 | 15 | 2.5 | 35614   | 7 | US-09-902-540-1255  | Sequence 1255, Ap |
| C 843 | 15 | 2.5 | 5785  | 6 | US-09-760-475-4022   | Sequence 4022, Ap  | C 916 | 15 | 2.5 | 41768   | 7 | US-09-902-540-1365  | Sequence 1365, Ap |
| C 844 | 15 | 2.5 | 5785  | 6 | US-09-760-475-4024   | Sequence 4024, Ap  | C 917 | 15 | 2.5 | 49311   | 6 | US-09-803-736-1387  | Sequence 1387, Ap |
| C 845 | 15 | 2.5 | 5819  | 6 | US-09-764-902-2253   | Sequence 2253, Ap  | C 918 | 15 | 2.5 | 51354   | 7 | US-09-902-540-1270  | Sequence 1270, Ap |
| C 846 | 15 | 2.5 | 5819  | 6 | US-09-760-475-4026   | Sequence 4026, Ap  | C 919 | 15 | 2.5 | 54573   | 6 | US-09-803-736-542   | Sequence 542, App |
| C 847 | 15 | 2.5 | 5892  | 1 | PCR-US01-08631-21168 | Sequence 21168, A  | C 920 | 15 | 2.5 | 58857   | 6 | US-09-477-962-1     | Sequence 1, Appl1 |
| C 848 | 15 | 2.5 | 5898  | 1 | PCR-US01-08631-15924 | Sequence 15924, A  | C 921 | 15 | 2.5 | 61001   | 6 | US-09-803-736-799   | Sequence 799, App |
| C 849 | 15 | 2.5 | 6054  | 8 | US-60-278-561-11049  | Sequence 11049, A  | C 922 | 15 | 2.5 | 65325   | 6 | US-09-803-736-766   | Sequence 766, App |
| C 850 | 15 | 2.5 | 6375  | 7 | US-09-902-540-741    | Sequence 741, App  | C 923 | 15 | 2.5 | 67878   | 6 | US-09-803-736-27    | Sequence 27, Appl |
| C 851 | 15 | 2.5 | 6454  | 7 | US-09-764-874-12623  | Sequence 12623, A  | C 924 | 15 | 2.5 | 75106   | 6 | US-09-803-736-1382  | Sequence 1382, Ap |
| C 852 | 15 | 2.5 | 6500  | 6 | US-09-764-904-129    | Sequence 129, App  | C 925 | 15 | 2.5 | 77826   | 6 | US-09-803-110-189   | Sequence 189, App |
| C 853 | 15 | 2.5 | 6500  | 6 | US-09-764-860-1190   | Sequence 1190, Ap  | C 926 | 15 | 2.5 | 79046   | 6 | US-09-803-736-819   | Sequence 819, App |
| C 854 | 15 | 2.5 | 6896  | 7 | US-09-764-905-24790  | Sequence 24790, A  | C 927 | 15 | 2.5 | 81341   | 6 | US-09-803-736-155   | Sequence 155, App |
| C 855 | 15 | 2.5 | 6935  | 7 | US-09-902-540-865    | Sequence 865, App  | C 928 | 15 | 2.5 | 81677   | 6 | US-09-803-736-445   | Sequence 445, App |
| C 856 | 15 | 2.5 | 7367  | 8 | US-60-257-896-7      | Sequence 7, Appl1  | C 929 | 15 | 2.5 | 82214   | 6 | US-09-803-736-1166  | Sequence 1166, Ap |
| C 857 | 15 | 2.5 | 7482  | 7 | US-09-764-905-21773  | Sequence 21773, A  | C 930 | 15 | 2.5 | 82311   | 6 | US-09-803-736-484   | Sequence 484, App |
| C 858 | 15 | 2.5 | 7874  | 8 | US-60-278-232-2240   | Sequence 2240, A   | C 931 | 15 | 2.5 | 82460   | 6 | US-09-803-736-1448  | Sequence 1448, Ap |
| C 859 | 15 | 2.5 | 7994  | 7 | US-09-902-540-797    | Sequence 797, App  | C 932 | 15 | 2.5 | 83698   | 6 | US-09-803-736-806   | Sequence 806, App |
| C 860 | 15 | 2.5 | 8261  | 7 | US-09-764-905-19773  | Sequence 19773, A  | C 933 | 15 | 2.5 | 84294   | 6 | US-09-803-736-414   | Sequence 414, App |
| C 861 | 15 | 2.5 | 10311 | 7 | US-09-902-540-957    | Sequence 957, App  | C 934 | 15 | 2.5 | 84297   | 6 | US-09-803-736-34    | Sequence 34, Appl |
| C 862 | 15 | 2.5 | 10467 | 6 | US-09-764-891-6892   | Sequence 6892, Ap  | C 935 | 15 | 2.5 | 85214   | 6 | US-09-803-736-226   | Sequence 226, App |
| C 863 | 15 | 2.5 | 10549 | 6 | US-09-760-457-447    | Sequence 447, App  | C 936 | 15 | 2.5 | 86854   | 6 | US-09-803-736-422   | Sequence 422, App |
| C 864 | 15 | 2.5 | 10549 | 6 | US-09-760-475-3540   | Sequence 3540, Ap  | C 937 | 15 | 2.5 | 87090   | 6 | US-09-803-736-933   | Sequence 933, App |
| C 865 | 15 | 2.5 | 10549 | 6 | US-09-764-874-7773   | Sequence 7773, Ap  | C 938 | 15 | 2.5 | 88401   | 6 | US-09-803-736-71    | Sequence 71, Appl |
| C 866 | 15 | 2.5 | 10644 | 7 | US-09-902-540-1028   | Sequence 1028, Ap  | C 939 | 15 | 2.5 | 88904   | 6 | US-09-803-736-438   | Sequence 438, App |
| C 867 | 15 | 2.5 | 10835 | 7 | US-09-902-540-1031   | Sequence 1031, Ap  | C 940 | 15 | 2.5 | 88904   | 6 | US-09-803-736-630   | Sequence 630, App |
| C 868 | 15 | 2.5 | 10983 | 7 | US-09-764-874-10530  | Sequence 10530, A  | C 941 | 15 | 2.5 | 89934   | 6 | US-09-803-736-335   | Sequence 335, App |
| C 869 | 15 | 2.5 | 11573 | 7 | US-09-902-540-1052   | Sequence 1052, Ap  | C 942 | 15 | 2.5 | 91308   | 6 | US-09-803-736-1367  | Sequence 1367, Ap |
| C 870 | 15 | 2.5 | 11695 | 7 | US-09-902-540-1045   | Sequence 1045, Ap  | C 943 | 15 | 2.5 | 91608   | 6 | US-09-803-736-18    | Sequence 18, Appl |
| C 871 | 15 | 2.5 | 11922 | 7 | US-09-902-540-1063   | Sequence 1063, Ap  | C 944 | 15 | 2.5 | 91854   | 6 | US-09-803-736-379   | Sequence 379, App |
| C 872 | 15 | 2.5 | 12277 | 7 | US-09-902-540-1018   | Sequence 1018, Ap  | C 945 | 15 | 2.5 | 92569   | 6 | US-09-803-736-202   | Sequence 202, App |
| C 873 | 15 | 2.5 | 12886 | 7 | US-09-807-007-5      | Sequence 5, Appl1  | C 946 | 15 | 2.5 | 93724   | 6 | US-09-803-736-117   | Sequence 17, Appl |
| C 874 | 15 | 2.5 | 14518 | 7 | US-09-764-905-21997  | Sequence 21997, A  | C 947 | 15 | 2.5 | 94369   | 6 | US-09-803-736-334   | Sequence 334, App |
| C 875 | 15 | 2.5 | 14518 | 7 | US-09-764-905-21998  | Sequence 21998, A  | C 948 | 15 | 2.5 | 96801   | 6 | US-09-803-736-322   | Sequence 322, App |
| C 876 | 15 | 2.5 | 14519 | 7 | US-09-764-905-21999  | Sequence 21999, A  | C 949 | 15 | 2.5 | 96892   | 6 | US-09-803-736-1436  | Sequence 1436, Ap |
| C 877 | 15 | 2.5 | 15632 | 6 | US-09-760-466-1740   | Sequence 1740, Ap  | C 950 | 15 | 2.5 | 98412   | 6 | US-09-803-736-1010  | Sequence 1010, Ap |
| C 878 | 15 | 2.5 | 15914 | 6 | US-09-760-483-815    | Sequence 815, App  | C 951 | 15 | 2.5 | 104016  | 6 | US-09-803-736-137   | Sequence 137, App |
| C 879 | 15 | 2.5 | 15914 | 6 | US-09-760-457-580    | Sequence 580, App  | C 952 | 15 | 2.5 | 104738  | 6 | US-09-803-736-639   | Sequence 629, App |
| C 880 | 15 | 2.5 | 15914 | 6 | US-09-760-485-1355   | Sequence 1355, App | C 953 | 15 | 2.5 | 104661  | 6 | US-09-803-736-310   | Sequence 310, App |
| C 881 | 15 | 2.5 | 15914 | 6 | US-09-764-905-28034  | Sequence 28034, A  | C 954 | 15 | 2.5 | 107600  | 6 | US-09-803-736-571   | Sequence 571, App |
| C 882 | 15 | 2.5 | 16080 | 1 | PCR-US01-21354-2     | Sequence 2, Appl1  | C 955 | 15 | 2.5 | 109560  | 6 | US-09-803-736-1169  | Sequence 1169, Ap |
| C 883 | 15 | 2.5 | 16427 | 7 | US-09-902-540-1160   | Sequence 1160, Ap  | C 956 | 15 | 2.5 | 110974  | 6 | US-09-803-736-157   | Sequence 157, App |
| C 884 | 15 | 2.5 | 16448 | 7 | US-09-902-540-9686   | Sequence 9686, Ap  | C 957 | 15 | 2.5 | 110766  | 6 | US-09-803-736-681   | Sequence 681, App |
| C 885 | 15 | 2.5 | 16450 | 7 | US-09-902-540-1098   | Sequence 1098, Ap  | C 958 | 15 | 2.5 | 114738  | 6 | US-09-803-736-132   | Sequence 132, App |
| C 886 | 15 | 2.5 | 16489 | 6 | US-09-764-866-1483   | Sequence 1483, Ap  | C 959 | 15 | 2.5 | 115310  | 7 | US-09-803-736-368   | Sequence 368, App |
| C 887 | 15 | 2.5 | 17437 | 7 | US-09-764-874-13474  | Sequence 13474, A  | C 960 | 15 | 2.5 | 178520  | 7 | US-09-881-797-701   | Sequence 701, App |
| C 888 | 15 | 2.5 | 17458 | 7 | US-09-764-874-13473  | Sequence 13473, A  | C 961 | 15 | 2.5 | 181925  | 6 | US-09-803-736-143   | Sequence 143, App |
| C 889 | 15 | 2.5 | 18324 | 7 | US-09-902-540-1196   | Sequence 1196, Ap  | C 962 | 15 | 2.5 | 183147  | 6 | US-09-803-736-534   | Sequence 534, App |
| C 890 | 15 | 2.5 | 18664 | 7 | US-09-764-905-20233  | Sequence 20233, A  | C 963 | 15 | 2.5 | 184668  | 6 | US-09-803-110-207   | Sequence 207, App |
| C 891 | 15 | 2.5 | 18664 | 7 | US-09-764-905-39250  | Sequence 39250, A  | C 964 | 15 | 2.5 | 202868  | 6 | US-09-803-736-552   | Sequence 552, App |
| C 892 | 15 | 2.5 | 19372 | 6 | US-09-760-466-1741   | Sequence 1741, Ap  | C 965 | 15 | 2.5 | 204382  | 7 | US-09-881-797-702   | Sequence 702, App |
| C 893 | 15 | 2.5 | 20795 | 1 | PCR-US01-08631-28400 | Sequence 28400, A  | C 966 | 15 | 2.5 | 213788  | 6 | US-09-803-736-556   | Sequence 556, App |
| C 894 | 15 | 2.5 | 21129 | 6 | US-09-760-443-2150   | Sequence 2150, Ap  | C 967 | 15 | 2.5 | 226706  | 6 | US-09-855-768-1     | Sequence 1, Appl1 |
| C 895 | 15 | 2.5 | 21129 | 6 | US-09-764-869-1734   | Sequence 1734, Ap  | C 968 | 15 | 2.5 | 244769  | 6 | US-09-803-110-210   | Sequence 210, App |
| C 896 | 15 | 2.5 | 21710 | 6 | US-09-764-902-2311   | Sequence 2311, Ap  | C 969 | 15 | 2.5 | 300663  | 6 | US-09-803-110-213   | Sequence 213, App |
| C 897 | 15 | 2.5 | 22760 | 7 | US-09-764-874-7820   | Sequence 7820, Ap  | C 970 | 15 | 2.5 | 300663  | 6 | US-09-803-110-213   | Sequence 213, App |
| C 898 | 15 | 2.5 | 23394 | 7 | US-09-764-905-31985  | Sequence 31985, A  | C 971 | 15 | 2.5 | 308503  | 6 | US-09-803-110-216   | Sequence 216, App |
| C 899 | 15 | 2.5 | 24986 | 7 | US-09-902-540-1200   | Sequence 1200, Ap  | C 972 | 15 | 2.5 | 374732  | 6 | US-09-803-110-214   | Sequence 214, App |
| C 900 | 15 | 2.5 | 25871 | 7 | US-09-798-743-5      | Sequence 5, Appl1  | C 973 | 15 | 2.5 | 506113  | 6 | US-09-803-110-218   | Sequence 218, App |
| C 901 | 15 | 2.5 | 26064 | 7 | US-09-764-874-11517  | Sequence 11517, A  | C 974 | 15 | 2.5 | 3309400 | 6 | US-09-738-626-1     | Sequence 1, Appl1 |

|        |    |     |         |   |                     |                   |
|--------|----|-----|---------|---|---------------------|-------------------|
| C 975  | 15 | 2.5 | 3309400 | 6 | US-09-778-826-1     | Sequence 1, April |
| C 976  | 14 | 2.4 | 20      | 6 | US-09-198-452A-6030 | Sequence 6030, Ap |
| C 977  | 14 | 2.4 | 51      | 8 | US-60-278-258-1803  | Sequence 1803, Ap |
| C 978  | 14 | 2.4 | 51      | 8 | US-60-278-258-1803  | Sequence 3020, Ap |
| C 979  | 14 | 2.4 | 51      | 8 | US-60-278-258-8103  | Sequence 8103, Ap |
| C 980  | 14 | 2.4 | 51      | 8 | US-60-278-561-7706  | Sequence 7706, Ap |
| C 981  | 14 | 2.4 | 51      | 8 | US-60-278-561-12127 | Sequence 12127, A |
| C 982  | 14 | 2.4 | 51      | 8 | US-60-278-232-2159  | Sequence 2159, Ap |
| C 983  | 14 | 2.4 | 51      | 8 | US-60-278-232-11815 | Sequence 11815, A |
| C 984  | 14 | 2.4 | 60      | 7 | US-09-908-975-14472 | Sequence 14472, A |
| C 985  | 14 | 2.4 | 60      | 7 | US-09-908-975-20597 | Sequence 20597, A |
| C 986  | 14 | 2.4 | 60      | 8 | US-60-287-724-14472 | Sequence 14472, A |
| C 987  | 14 | 2.4 | 60      | 8 | US-60-287-724-20597 | Sequence 20597, A |
| C 988  | 14 | 2.4 | 63      | 8 | US-60-253-378-12103 | Sequence 12103, A |
| C 989  | 14 | 2.4 | 65      | 7 | US-09-908-975-26346 | Sequence 26346, A |
| C 990  | 14 | 2.4 | 65      | 8 | US-60-287-724-26346 | Sequence 26346, A |
| C 991  | 14 | 2.4 | 71      | 8 | US-60-253-654-18952 | Sequence 18952, A |
| C 992  | 14 | 2.4 | 71      | 8 | US-60-253-592-18952 | Sequence 18952, A |
| C 993  | 14 | 2.4 | 91      | 8 | US-60-253-654-29184 | Sequence 29184, A |
| C 994  | 14 | 2.4 | 91      | 8 | US-60-253-592-29184 | Sequence 29184, A |
| C 995  | 14 | 2.4 | 96      | 8 | US-60-253-654-7998  | Sequence 7998, Ap |
| C 996  | 14 | 2.4 | 96      | 8 | US-60-253-592-7998  | Sequence 7998, Ap |
| C 997  | 14 | 2.4 | 98      | 7 | US-09-834-366-33476 | Sequence 33476, A |
| C 998  | 14 | 2.4 | 103     | 7 | US-09-864-761-26081 | Sequence 26081, A |
| C 999  | 14 | 2.4 | 108     | 7 | US-09-917-292-20683 | Sequence 20683, A |
| C 1000 | 14 | 2.4 | 113     | 6 | US-09-688-848-3173  | Sequence 3173, Ap |

## ALIGNMENTS

```

RESULT 1
US-09-138-735-1
: Sequence 1, Application US/09138735
: GENERAL INFORMATION:
: APPLICANT: PARANHOS-BACCALA, Glaucia
: APPLICANT: LESENECHAL, Mylene
: APPLICANT: JOUVER, Michel
: TITLE OF INVENTION: TRYPANOSOMA CRUZI ANTIGEN, GENE ENCODING THEREFOR AND METHODS OF
: TITLE OF INVENTION: DETECTING AND TREATING CHAGAS DISEASE
: FILE REFERENCE: WPI 36400B
: CURRENT APPLICATION NUMBER: US/09/138,735
: CURRENT FILING DATE: 1998-08-24
: PRIOR APPLICATION NUMBER: US 08/480,917
: PRIOR FILING DATE: 1995-06-07
: PRIOR APPLICATION NUMBER: FR 94/10132
: PRIOR FILING DATE: 1994-08-12
: NUMBER OF SEQ ID NOS: 13
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 1
: LENGTH: 3402
: TYPE: DNA
: ORGANISM: Trypanosoma cruzi
: US-09-138-735-1

```

|            | Query Match | Similarity                                                       | Score | DB         | Length |
|------------|-------------|------------------------------------------------------------------|-------|------------|--------|
| Best Local | 594         | 100.0%                                                           | 594   | 6          | 3402   |
| Matches    | 594         | Conservative                                                     | 0     | Mismatches | 0      |
|            |             |                                                                  |       | Indels     | 0      |
|            |             |                                                                  |       | Gaps       | 0      |
| QY         | 1           | caagatacagcgtaacgagcttctgtctcaatcgttaacgcgaacgtaagctgtctgtgct    | 60    |            |        |
| Db         | 1232        | caagatacagcgtaacgagcttctgtctcaatcgttaacgcgaacgtaagctgtctgtgct    | 1291  |            |        |
| QY         | 61          | gactgttgcgtatcgattgacatcttcattctcgtctctcccgcaaggagaagaacgag      | 120   |            |        |
| Db         | 1292        | gactgttgcgtatcgattgacatcttcattctcgtctctcccgcaaggagaagaacgag      | 1351  |            |        |
| QY         | 121         | ccaaagccaaaataacatcgtatgtgcgcgcgcgaacccggggtgtgtctcccggcact      | 180   |            |        |
| Db         | 1352        | ccaaagccaaaataacatcgtatgtgcgcgcgcgaacccggggtgtgtgtctcccggcact    | 1411  |            |        |
| QY         | 181         | gaacgcgcgagtagcagatcacaacaatacgaattctgcgcgtcgtcgtacatccctcgtacat | 240   |            |        |

|    |      |                                                                   |      |
|----|------|-------------------------------------------------------------------|------|
| Db | 1412 | gagcgcgcggtatgcagtcctatccaatagactctgcgcgtcgctgcataccctctgaccca    | 1471 |
| QY | 241  | ccccctgtctcaagccagccaagcagccgcgcctctctgcgcgcgcgacatcgctgag        | 300  |
| Db | 1472 | cccccttctcaagccagccaagcagcagccgcctctctgcgcgcgcgatactcgctag        | 1531 |
| QY | 301  | ccgcagcgttggggagcaagatcatctgtctaactctagtgaaatcaactgggagataatgcc   | 360  |
| Db | 1532 | ccgcagcgttggggagcaagatcatctgtctaactctagtgaaatcaactgggagataatgcc   | 1591 |
| QY | 361  | caaaagagcgtctgtcaagcacttgagcgccgcgcagccagagagttctaagcgagtgaactcc  | 420  |
| Db | 1592 | caaaagagcgtctgtcaagcacttgagcgccgcgcagcagaggttctaagcgagtgaactcc    | 1651 |
| QY | 421  | acgactatccgcgcccgagcggaacaaatctcataagggcaaaatggccggaactgttgacgct  | 480  |
| Db | 1652 | acgactatccgcgcccgagcggaacaaatctcataagggcaaaatggccggaactgttgacgct  | 1711 |
| QY | 481  | ggaatcttgatggcagctaaatagttgtgcacagcgcgccctgtctctcccaacagccgcgcgaa | 540  |
| Db | 1712 | ggaatcttgatggcagctaaatagttgtgcacagcgcgccctgtctctcccaacagccgcgcgaa | 1771 |
| QY | 541  | ccaacagagaagaagaagagcctccgcgcgcatgtgaaacagctctcgtygcgata          | 594  |
| Db | 1772 | ccaacagagaagaagaagagcctccgcgcgcatgtgaaacagctctcgtygcgata          | 1825 |

## RESULT 2

```

GENERAL INFORMATION:
APPLICANT: PARANHOS-BACCALA, Glaucia
APPLICANT: LESENECHAL, Mylene
APPLICANT: JOLIVET, Michel
TITLE OF INVENTION: TYPANOSOMA CRUZI ANTIGEN, GENE ENCODING THEREFOR AND METHODS
TITLE OF INVENTION: DETECTING AND TREATING CHAGAS DISEASE
FILE REFERENCE: WPI 36400B
CURRENT APPLICATION NUMBER: US/09/138,735
CURRENT FILING DATE: 1998-08-24
PRIOR APPLICATION NUMBER: US 08/480,917
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: FR 94/10132
PRIOR FILING DATE: 1994-08-12
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.0
SEQ ID NO 9
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: probe/primer
US-09-138-735-9

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Query Match          3.7%; Score 22; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      35  cagccgacgctagctgcgtcct 56
          |||||
Db       1  cagccgacgctagctgcgtcct 22

RESULT      3
US-09-803-736-19/C
: Sequence 19, Application US/09803736
: GENERAL INFORMATION:
: APPLICANT: Bush, David F.
: APPLICANT: Levin, Irena M.
: APPLICANT: Norris, Susan R.
: APPLICANT: Rounsley, Steven D.
: APPLICANT: Wiegand, Roger C.

```

TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof  
FILE REFERENCE: 38-10(15493)D  
CURRENT APPLICATION NUMBER: US/09/803,736  
CURRENT FILING DATE: 2001-03-12  
PRIOR APPLICATION NUMBER: US 09/534,859  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: Identified by Attorney Docket number 04983.0206CPUS01 38-10  
PRIOR FILING DATE: 2000-10-20  
NUMBER OF SEQ ID NOS: 1582  
SEQ ID NO 19  
LENGTH: 91470  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
US-09-803-736-19

Query Match 3.4%; Score 20; DB 6; Length 91470;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 212 cttctgcgcgtcgtcgtcc 231  
|||||  
DB 42747 CTTCTGCCGCTGCTGCATCC 42728

RESULT 4  
US-09-138-735-5  
Sequence 5, Application US/09138735  
GENERAL INFORMATION:  
APPLICANT: PARANHOS-BACCALA, Glaucia  
APPLICANT: LESENECHAL, Mylene  
APPLICANT: JOLIVET, Michel  
TITLE OF INVENTION: TRYPANOSOMA CRUZI ANTIGEN, GENE ENCODING THEREFOR AND METHODS OF  
FILE REFERENCE: WPB 36400B  
CURRENT APPLICATION NUMBER: US/09/138,735  
CURRENT FILING DATE: 1998-08-24  
PRIOR APPLICATION NUMBER: US 08/480,917  
PRIOR FILING DATE: 1995-06-07  
PRIOR APPLICATION NUMBER: FR 94/10132  
PRIOR FILING DATE: 1994-08-12  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 5  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: primer  
US-09-138-735-5

Query Match 3.0%; Score 18; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 172 tcgggcactgacgcgcgcg 189  
|||||  
DB 1 tcgggcactgacgcgcgcg 18

RESULT 5  
US-09-138-735-8/c  
Sequence 8, Application US/09138735  
GENERAL INFORMATION:  
APPLICANT: PARANHOS-BACCALA, Glaucia  
APPLICANT: LESENECHAL, Mylene  
APPLICANT: JOLIVET, Michel  
TITLE OF INVENTION: TRYPANOSOMA CRUZI ANTIGEN, GENE ENCODING THEREFOR AND METHODS OF  
FILE REFERENCE: WPB 36400B  
CURRENT APPLICATION NUMBER: US/09/138,735  
CURRENT FILING DATE: 1998-08-24

PRIOR APPLICATION NUMBER: US 08/480,917  
PRIOR FILING DATE: 1995-06-07  
PRIOR APPLICATION NUMBER: FR 94/10132  
PRIOR FILING DATE: 1994-08-12  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 8  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: probe/primer  
US-09-138-735-8

Query Match 3.0%; Score 18; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 211 actctgcgcgtcgtcgtca 228  
|||||  
DB 18 ACTTCTGCCGCTGCTGCA 1

RESULT 6  
US-09-866-555-4980/C  
Sequence 4980, Application US/09866555  
GENERAL INFORMATION:  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Wang, Tonglong  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Algate, Paul A.  
APPLICANT: Jones, Robert  
APPLICANT: Klee, Jennifer  
TITLE OF INVENTION: LUNG TUMOR-ASSOCIATED SEQUENCES AND METHODS OF USE  
FILE REFERENCE: 210121.580  
CURRENT APPLICATION NUMBER: US/09/866,555  
CURRENT FILING DATE: 2001-05-25  
NUMBER OF SEQ ID NOS: 20487  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4980  
LENGTH: 261  
TYPE: DNA  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(261)  
OTHER INFORMATION: n = A,T,C or G  
US-09-866-555-4980

Query Match 3.0%; Score 18; DB 6; Length 261;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 gtagctgcgtcgtcgtcgt 61  
|||||  
DB 18 GTAGCTGCCTCTGCTG 1

RESULT 7  
US-09-863-524-3874  
Sequence 3874, Application US/09863524  
GENERAL INFORMATION:  
APPLICANT: Ito, Laura Y.  
APPLICANT: Gooding, Douglas H.  
APPLICANT: Sherman, Bradley K.  
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN ROOTS  
FILE REFERENCE: PI-0003 US  
CURRENT APPLICATION NUMBER: US/09/863,524  
CURRENT FILING DATE: 2001-05-22  
PRIOR APPLICATION NUMBER: 60/077,831  
PRIOR FILING DATE: 1998-03-13



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: NUMBER OF SEQ ID NOS: 6814
: SOFTWARE: PERL Program
: SEQ ID NO 3874
: LENGTH: 297
: TYPE: DNA
: ORGANISM: zea mays
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: Incyte ID No: 700047828H1
: OS-09-863-524-3874

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Query Match 3.0%; Score 18; DB 7; Length 297;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| Oy | 386 | cgccggccacgacgagtc | 403 |
|----|-----|--------------------|-----|
|    |     |                    |     |
| Db | 247 | cgccggccacgacgagtc | 264 |

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RESULT      8
US-09-764-891-1027/c
: Sequence 1027, Application US/09764891
: GENERAL INFORMATION:
:   APPLICANT: Rosen et al.
:   TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
:   FILE REFERENCE: PC006
:   CURRENT APPLICATION NUMBER: US/09/764,891
:   CURRENT FILING DATE: 2001-01-17
:   Prior application data removed - consult PALM or file wrapper
:   NUMBER OF SEQ ID NOS: 10231
:   SOFTWARE: PatentIn Ver. 2.0
:   SEQ ID NO 1027
:   LENGTH: 328
:   TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-764-891-1027

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|                       |                 |                     |           |             |
|-----------------------|-----------------|---------------------|-----------|-------------|
| Query Match           | 3.0%;           | Score 18;           | DB 6;     | Length 328; |
| Best Local Similarity | 100.0%;         | Pred. No. 18;       |           |             |
| Matches 18;           | Conservative 0; | Mismatches 0;       | Indels 0; | Gaps 0;     |
| OY                    | 211             | actctgcgcgtgctgca   | 228       |             |
|                       |                 |                     |           |             |
|                       |                 |                     |           |             |
|                       |                 |                     |           |             |
|                       |                 |                     |           |             |
| db                    | 251             | actctgcgcgcgtgctgca | 234       |             |

```

RESULT          9
US-09-540-213-5492
Sequence 5492, Application US/09540213
GENERAL INFORMATION:
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
APPLICANT: Mullaby, Sara J.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES OF LIVER AND PANCREAS
FILE REFERENCE: PD-1031 CIP
CURRENT APPLICATION NUMBER: US/09/540,213
CURRENT FILING DATE: 2000-03-31
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 53844
SEQ ID NO 5492
LENGTH: 348
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No: hu00532370
NAME/KEY: unsure

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; LOCATION: 4, 8, 304, 307
; OTHER INFORMATION: a, t, c, g, or other
US-09-540-213-5492

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|                       |         |               |       |               |
|-----------------------|---------|---------------|-------|---------------|
| Query Match           | 3.0%;   | Score 18;     | DB 7; | Length 348;   |
| Best Local Similarity | 100.0%; | Pred. No. 18; |       |               |
| Matches               | 18;     | Conservative  | 0;    | Mismatches 0; |
|                       |         |               |       | Indels 0;     |
|                       |         |               |       | Gaps 0;       |

```
QY      230 cccctgcatcacccctg 24
          |||||
Db      29  ccctgcatcacccctg 46
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RESULT 10
US-09-667-188A-4578/c
: Sequence 4578, Application US/09667188A
: GENERAL INFORMATION:
: APPLICANT: Andersen, Scott E.
: APPLICANT: Masucci, James D.
: TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
: TITLE OF INVENTION: Plants
: FILE REFERENCE: 38-21(51464)B
: CURRENT APPLICATION NUMBER: US/09/667,188A
: CURRENT FILING DATE: 2000-09-21
: PRIOR APPLICATION NUMBER: US 60/155,006
: PRIOR FILING DATE: 1999-09-22
: NUMBER OF SEQ ID NOS: 8135
: SEQ ID NO. 4578
: LENGTH: 371
: TYPE: DNA
: ORGANISM: Trifolium aestivum
: FEATURE:
: OTHER INFORMATION: Clone ID: LIB3281-014-P1-K1-E7
US-09-667-188A-4578

```

|                       |                |                    |          |            |
|-----------------------|----------------|--------------------|----------|------------|
| Query Match           | 3.0%           | Score 18           | DB 6     | Length 371 |
| Best Local Similarity | 100.0%         | Pred. No. 18       |          |            |
| Matches 18            | Conservative 0 | Mismatches 0       | Indels 0 | Gaps 0     |
| OY                    | 274            | cctcctgcgcgcgcgcga | 291      |            |
|                       |                |                    |          |            |
|                       |                |                    |          |            |
|                       |                |                    |          |            |
|                       |                |                    |          |            |
| DB                    | 153            | ccmctgcgcgcgcgcga  | 136      |            |

```

RESULT 11
US-09-864-761-52/c
; Sequence 52, Application US/09864761
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecmica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
;

```

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; OTHER INFORMATION: n = A,T,C or G
US-09-904-809-19378

Query Match          3.0%; Score 18; DB 7; Length 468;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 230 cccctgcatcacccctg 247
      |||||
DB 393 CCCCTGCATCACCCCTG 376

RESULT 12
US-09-904-809-19378/c
; Sequence 19378, Application US/09904809
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-757
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 09/234,611
; PRIOR FILING DATE: 1999-01-22
; NUMBER OF SEQ ID NOS: 21025
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19378
; LENGTH: 476
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(476)

```

```

; OTHER INFORMATION: n = A,T,C or G
US-09-904-809-19378

Query Match          3.0%; Score 18; DB 6; Length 476;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 gtagctgctcctgctg 61
      |||||
DB 384 GTAGCTGCTCCTGCTG 367

RESULT 13
US-09-909-627-11623/c
; Sequence 11623, Application US/09909627
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-766
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/277,227
; PRIOR FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 23680
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11623
; LENGTH: 476
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(476)
; OTHER INFORMATION: n = A,T,C or G
US-09-909-627-11623

Query Match          3.0%; Score 18; DB 6; Length 476;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 gtagctgctcctgctg 61
      |||||
DB 384 GTAGCTGCTCCTGCTG 367

RESULT 14
US-09-864-761-16893/c
; Sequence 16893, Application US/09864761
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667

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: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00664
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00669
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00665
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00668
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00663
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00662
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00661
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00670
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: US 60/234,687
: PRIOR FILING DATE: 2000-09-21
: PRIOR APPLICATION NUMBER: US 09/608,408
: PRIOR FILING DATE: 2000-06-30
: PRIOR APPLICATION NUMBER: US 09/774,203
: PRIOR FILING DATE: 2001-01-29
: NUMBER OF SEQ ID NOS: 49117
: SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
: SEQ ID NO 16893
: LENGTH: 478
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: MAP TO AC005921.3
: OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1
: OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
: OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.4
: OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
: OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
: OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.3
: OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
: OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 6.9
: OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
: OTHER INFORMATION: SWISSPROT HIT: P50555, EVALUATE 5.60e-01
: OTHER INFORMATION: EST_HUMAN HIT: BE74137.1, EVALUATE 0.00e+00
: OTHER INFORMATION: NT HIT: X99000.1, EVALUATE 3.00e-01
: US-09-864-761-16893
Query Match 3.0%; Score 18; DB 7; Length 478;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 230 cccctgcatacccccctg 247
Db 298 CCCCTGCATCACCCCTCG 281
RESULT 15
US-09-840-145-13709/c
: Sequence 13709, Application US/09840145
: GENERAL INFORMATION:
: APPLICANT: Adams, et. al.
: TITLE OF INVENTION: Human Genes, Sequences, and Expression Products
: FILE REFERENCE: POLAC1
: CURRENT APPLICATION NUMBER: US/09/840,145
: PRIOR FILING DATE: 2001-04-24
: PRIOR APPLICATION NUMBER: 08/276,163
: PRIOR FILING DATE: 1994-07-15
: NUMBER OF SEQ ID NOS: 15314
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 13709
: LENGTH: 506
: TYPE: DNA
: ORGANISM: Homo sapiens
```

```

: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (11)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (30)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (44)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (46)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (51)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (60)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (66)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (148)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (185)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (306)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (321)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (345)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (359)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (364)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (375)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (385)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (425)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (427)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (428)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (430)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (440)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (443)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (470)
: OTHER INFORMATION: n equals a,t,g, or c
```

```

NAME/KEY: misc.feature
LOCATION: (473)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc.feature
LOCATION: (476)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc.feature
LOCATION: (478)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc.feature
LOCATION: (489)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc.feature
LOCATION: (492)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc.feature
LOCATION: (494)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc.feature
LOCATION: (494)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc.feature
LOCATION: (501)
OTHER INFORMATION: n equals a,t,g, or c
IS-09-840-145-13709
```

|                          |         |                      |       |             |
|--------------------------|---------|----------------------|-------|-------------|
| Query Match              | 3.0%;   | Score 18;            | DB 7; | Length 506; |
| Best Local Similarity    | 100.0%; | Pred. No. 18;        |       |             |
| Matches 18; Conservative | 0;      | Mismatches           | 0;    | Gaps 0;     |
| Qy                       | 211     | actctgcgcgtcgtcgca   | 228   |             |
|                          |         |                      |       |             |
|                          |         |                      |       |             |
|                          |         |                      |       |             |
| Db                       | 243     | actctgcgcgcgtcgtcgca | 226   |             |

```

RESULT 16
US-60-312-544-4166/c
Sequence 4166, Application US/60312544
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Edgerton, Michael D
APPLICANT: Hinkle, Gregory J.
APPLICANT: Kovalic, David K.
APPLICANT: Liu, Jingdong
APPLICANT: Stein, Joshua
TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-10(52726)A
CURRENT APPLICATION NUMBER: US/60/312,544
CURRENT FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 10730
SEQ ID NO 4166
LENGTH: 1431
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: CDS
LOCATION: (2)..(778)
OTHER INFORMATION: Clone ID: LIB3205-113-E12_F11
US-60-312-544-4166

```

```
Query Match      3.0%; Score 18; DB 8; Length 1431;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

|    |     |                    |     |
|----|-----|--------------------|-----|
| OY | 386 | cgccgycacgacgagt   | 403 |
|    |     |                    |     |
| Db | 542 | CGCCGGCCACGACGAGGT | 525 |

RESULT 17  
PCT-US01-16450-789/c  
; Sequence 789, Application PC/TUS0116450  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.

```

1 TITLE OR INVENTION: Nucleic Acids, Proteins and Antibodies
2 FILE REFERENCE: PA131PCT
3 CURRENT APPLICATION NUMBER: PCT/US01/16450
4 CURRENT FILING DATE: 2001-06-01
5 PRIOR APPLICATION NUMBER: 60/205,515
6 PRIOR FILING DATE: 2000-05-19
7 NUMBER OF SEQ. ID NOS: 2820
8 SOFTWARE: Patentln Ver. 2.0
9 SEQ. ID NO 789
10 LENGTH: 1485
11 TYPE: DNA
12 ORGANISM: Homo sapiens
13 FEATURE:
14 NAME/KEY: SITE
15 LOCATION: (158)
16 OTHER INFORMATION: n equals a,t,g, or c
17 NAME/KEY: SITE
18 LOCATION: (749)
19 OTHER INFORMATION: n equals a,t,g, or c
20 PCT-US01-16450-789

```

|                       |                 |                     |           |              |
|-----------------------|-----------------|---------------------|-----------|--------------|
| Query Match           | 3.0%;           | Score 18;           | DB 1;     | Length 1485; |
| Best Local Similarity | 100.0%;         | Pred. No. 19;       |           |              |
| Matches 18;           | Conservative 0; | Mismatches 0;       | Indels 0; | Gaps 0;      |
| Oy                    | 44              | gttagctgctctcgtgctg | 61        |              |
|                       |                 |                     |           |              |
|                       |                 |                     |           |              |
|                       |                 |                     |           |              |
|                       |                 |                     |           |              |
| Db                    | 669             | gttagctgctctcgtgctg | 652       |              |

```

RESULT      18
US-09-836-472-1298/C
Sequence 1298, Application US/09836472
GENERAL INFORMATION:
APPLICANT: Geating, David P.
TITLE OF INVENTION: NOCLETIC ACID MOLECULES DERIVED FROM A
TITLE OF INVENTION: HUMAN FETAL LUNG LIBRARY
FILE REFERENCE: 1600.1033-002
CURRENT APPLICATION NUMBER: US/09/836,472
CURRENT FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: 60/090,245
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 09/338,663
PRIOR FILING DATE: 1999-06-22
NUMBER OF SEQ ID NOS: 1364
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1298
LENGTH: 2817
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(2817)
OTHER INFORMATION: n - A,T,C or G
US-09-836-472-1298

```

|                       |         |               |       |              |
|-----------------------|---------|---------------|-------|--------------|
| Query Match           | 3.0%;   | Score 18;     | DB 6; | Length 2817; |
| Best Local Similarity | 100.0%; | Pred. No. 19; |       |              |
| Matches               | 18;     | Conservative  | 0;    | Mismatches   |
|                       |         |               | 0;    | Indels       |
|                       |         |               |       | 0;           |
|                       |         |               |       | Gaps         |
|                       |         |               |       | 0;           |

QY 44 gtagctgcgtcctgctg 61  
 |||||  
 Db 1980 GTAGCTGCCGTCTGGCTG 1963

RESULT 19  
US-09-764-905-28829/c  
; Sequence 28829, Application US/09764905  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: PC004  
CURRENT FILING DATE: 2001-01-17  
PRIOR APPLICATION NUMBER: 60/179,065  
PRIOR FILING DATE: 2000-01-31  
PRIOR APPLICATION NUMBER: 60/180,628  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: 60/214,886  
PRIOR FILING DATE: 2000-06-28  
PRIOR APPLICATION NUMBER: 60/217,487  
PRIOR FILING DATE: 2000-07-11  
PRIOR APPLICATION NUMBER: 60/225,758  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/220,963  
PRIOR FILING DATE: 2000-07-26  
PRIOR APPLICATION NUMBER: 60/217,496  
PRIOR FILING DATE: 2000-07-11  
PRIOR APPLICATION NUMBER: 60/225,447  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/218,290  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: 60/225,757  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/226,868  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 60/216,647  
PRIOR FILING DATE: 2000-07-07  
PRIOR APPLICATION NUMBER: 60/225,267  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/216,880  
PRIOR FILING DATE: 2000-07-07  
PRIOR APPLICATION NUMBER: 60/225,270  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/251,869  
PRIOR FILING DATE: 2000-12-08  
PRIOR APPLICATION NUMBER: 60/235,834  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: 60/234,274  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: 60/234,223  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: 60/228,924  
PRIOR FILING DATE: 2000-08-30  
PRIOR APPLICATION NUMBER: 60/224,518  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/236,369  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/224,519  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/220,964  
PRIOR FILING DATE: 2000-07-26  
PRIOR APPLICATION NUMBER: 60/241,809  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/249,299  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/236,327  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/241,785  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/244,617  
PRIOR FILING DATE: 2000-11-01  
PRIOR APPLICATION NUMBER: 60/225,268  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/236,368  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/251,856  
PRIOR FILING DATE: 2000-12-08  
PRIOR APPLICATION NUMBER: 60/251,868  
PRIOR FILING DATE: 2000-12-08  
PRIOR APPLICATION NUMBER: 60/229,344  
PRIOR FILING DATE: 2000-09-01  
PRIOR APPLICATION NUMBER: 60/234,997

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PRIOR FILING DATE: 2000-09-25  
PRIOR APPLICATION NUMBER: 60/229,343  
PRIOR FILING DATE: 2000-09-01  
PRIOR APPLICATION NUMBER: 60/229,345  
PRIOR FILING DATE: 2000-09-01  
PRIOR APPLICATION NUMBER: 60/229,287  
PRIOR FILING DATE: 2000-09-01  
PRIOR APPLICATION NUMBER: 60/229,513  
PRIOR FILING DATE: 2000-09-05  
PRIOR APPLICATION NUMBER: 60/231,413  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: 60/229,509  
PRIOR FILING DATE: 2000-09-05  
PRIOR APPLICATION NUMBER: 60/236,367  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/237,039  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 60/237,038  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 60/236,370  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/236,802  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 60/237,037  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 60/237,040  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 60/240,960  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/239,935  
PRIOR FILING DATE: 2000-10-13  
PRIOR APPLICATION NUMBER: 60/239,937  
PRIOR FILING DATE: 2000-10-13  
PRIOR APPLICATION NUMBER: 60/241,787  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/246,474  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: 60/246,532  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: 60/249,216  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,210  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/226,681  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 60/225,759  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/225,213  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/227,182  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 60/225,214  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/235,836  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: 60/230,438  
PRIOR FILING DATE: 2000-09-06  
PRIOR APPLICATION NUMBER: 60/215,135  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: 60/225,266  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/249,218  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,208  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,213  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,212  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,207  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,245  
PRIOR FILING DATE: 2000-11-17

;; PRIOR APPLICATION NUMBER: 60/249,244  
;; PRIOR FILING DATE: 2000-11-17  
;; PRIOR APPLICATION NUMBER: 60/249,217  
;; PRIOR FILING DATE: 2000-11-17  
;; PRIOR APPLICATION NUMBER: 60/249,211  
;; PRIOR FILING DATE: 2000-11-17  
;; PRIOR APPLICATION NUMBER: 60/249,215  
;; PRIOR FILING DATE: 2000-11-17  
;; PRIOR APPLICATION NUMBER: 60/249,264  
;; PRIOR FILING DATE: 2000-11-17  
;; PRIOR APPLICATION NUMBER: 60/249,214  
;; PRIOR FILING DATE: 2000-11-17  
;; PRIOR APPLICATION NUMBER: 60/249,297  
;; PRIOR FILING DATE: 2000-11-17  
;; PRIOR APPLICATION NUMBER: 60/232,400  
;; PRIOR FILING DATE: 2000-09-14  
;; PRIOR APPLICATION NUMBER: 60/231,242  
;; PRIOR FILING DATE: 2000-09-08  
;; PRIOR APPLICATION NUMBER: 60/232,081  
;; PRIOR FILING DATE: 2000-09-08  
;; PRIOR APPLICATION NUMBER: 60/232,080  
;; PRIOR FILING DATE: 2000-09-08  
;; PRIOR APPLICATION NUMBER: 60/231,414  
;; PRIOR FILING DATE: 2000-09-08  
;; PRIOR APPLICATION NUMBER: 60/231,244  
;; PRIOR FILING DATE: 2000-09-08  
;; PRIOR APPLICATION NUMBER: 60/233,064  
;; PRIOR FILING DATE: 2000-09-14  
;; PRIOR APPLICATION NUMBER: 60/233,063  
;; PRIOR FILING DATE: 2000-09-14  
;; PRIOR APPLICATION NUMBER: 60/232,397  
;; PRIOR FILING DATE: 2000-09-14  
;; PRIOR APPLICATION NUMBER: 60/232,399  
;; PRIOR FILING DATE: 2000-09-14  
;; PRIOR APPLICATION NUMBER: 60/232,401  
;; PRIOR FILING DATE: 2000-09-14  
;; PRIOR APPLICATION NUMBER: 60/241,808  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/241,826  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/241,786  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/241,221  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/246,475  
;; PRIOR FILING DATE: 2000-11-08  
;; PRIOR APPLICATION NUMBER: 60/231,243  
;; PRIOR FILING DATE: 2000-09-08  
;; PRIOR APPLICATION NUMBER: 60/233,065  
;; PRIOR FILING DATE: 2000-09-14  
;; PRIOR APPLICATION NUMBER: 60/232,398  
;;  
Query Match 3.0%; Score 18; DB 7; Length 15270;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 227 catccctgcataccccc 244  
Db 11976 CATCCCTGCATCACCCC 11959  
;;  
RESULT 20  
US-09-764-905-40566/c  
;; Sequence 40566, Application US/09764905  
;; GENERAL INFORMATION:  
;; APPLICANT: Rosen et al.  
;; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
;; FILE REFERENCE: PC004  
;; CURRENT APPLICATION NUMBER: US/09/764,905  
;; PRIOR FILING DATE: 2001-01-17  
;; PRIOR APPLICATION NUMBER: 60/1179,065  
;; PRIOR FILING DATE: 2000-01-31  
;; PRIOR APPLICATION NUMBER: 60/180,628  
;;

;; PRIOR FILING DATE: 2000-02-04  
;; PRIOR APPLICATION NUMBER: 60/214,886  
;; PRIOR FILING DATE: 2000-06-28  
;; PRIOR APPLICATION NUMBER: 60/217,487  
;; PRIOR FILING DATE: 2000-07-11  
;; PRIOR APPLICATION NUMBER: 60/225,758  
;; PRIOR FILING DATE: 2000-08-14  
;; PRIOR APPLICATION NUMBER: 60/220,963  
;; PRIOR FILING DATE: 2000-07-26  
;; PRIOR APPLICATION NUMBER: 60/217,496  
;; PRIOR FILING DATE: 2000-07-11  
;; PRIOR APPLICATION NUMBER: 60/225,447  
;; PRIOR FILING DATE: 2000-08-14  
;; PRIOR APPLICATION NUMBER: 60/218,290  
;; PRIOR FILING DATE: 2000-07-11  
;; PRIOR APPLICATION NUMBER: 60/225,757  
;; PRIOR FILING DATE: 2000-08-14  
;; PRIOR APPLICATION NUMBER: 60/226,868  
;; PRIOR FILING DATE: 2000-08-22  
;; PRIOR APPLICATION NUMBER: 60/216,647  
;; PRIOR FILING DATE: 2000-07-07  
;; PRIOR APPLICATION NUMBER: 60/225,267  
;; PRIOR FILING DATE: 2000-08-14  
;; PRIOR APPLICATION NUMBER: 60/216,880  
;; PRIOR FILING DATE: 2000-07-07  
;; PRIOR APPLICATION NUMBER: 60/225,270  
;; PRIOR FILING DATE: 2000-08-14  
;; PRIOR APPLICATION NUMBER: 60/251,869  
;; PRIOR FILING DATE: 2000-12-08  
;; PRIOR APPLICATION NUMBER: 60/235,834  
;; PRIOR FILING DATE: 2000-09-27  
;; PRIOR APPLICATION NUMBER: 60/234,274  
;; PRIOR FILING DATE: 2000-09-21  
;; PRIOR APPLICATION NUMBER: 60/234,223  
;; PRIOR FILING DATE: 2000-09-21  
;; PRIOR APPLICATION NUMBER: 60/228,924  
;; PRIOR FILING DATE: 2000-08-30  
;; PRIOR APPLICATION NUMBER: 60/224,518  
;; PRIOR FILING DATE: 2000-08-14  
;; PRIOR APPLICATION NUMBER: 60/236,369  
;; PRIOR FILING DATE: 2000-09-29  
;; PRIOR APPLICATION NUMBER: 60/224,519  
;; PRIOR FILING DATE: 2000-08-14  
;; PRIOR APPLICATION NUMBER: 60/220,964  
;; PRIOR FILING DATE: 2000-07-26  
;; PRIOR APPLICATION NUMBER: 60/241,809  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/249,299  
;; PRIOR FILING DATE: 2000-11-17  
;; PRIOR APPLICATION NUMBER: 60/236,327  
;; PRIOR FILING DATE: 2000-09-29  
;; PRIOR APPLICATION NUMBER: 60/241,785  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/244,617  
;; PRIOR FILING DATE: 2000-11-01  
;; PRIOR APPLICATION NUMBER: 60/225,268  
;; PRIOR FILING DATE: 2000-08-14  
;; PRIOR APPLICATION NUMBER: 60/236,368  
;; PRIOR FILING DATE: 2000-09-29  
;; PRIOR APPLICATION NUMBER: 60/251,856  
;; PRIOR FILING DATE: 2000-12-08  
;; PRIOR APPLICATION NUMBER: 60/251,868  
;; PRIOR FILING DATE: 2000-12-08  
;; PRIOR APPLICATION NUMBER: 60/229,344  
;; PRIOR FILING DATE: 2000-09-01  
;; PRIOR APPLICATION NUMBER: 60/234,997  
;; PRIOR FILING DATE: 2000-09-25  
;; PRIOR APPLICATION NUMBER: 60/229,343  
;; PRIOR FILING DATE: 2000-09-01  
;; PRIOR APPLICATION NUMBER: 60/229,345  
;; PRIOR FILING DATE: 2000-09-01  
;; PRIOR APPLICATION NUMBER: 60/229,287  
;; PRIOR FILING DATE: 2000-09-01  
;;

PRIOR APPLICATION NUMBER: 60/229,513  
PRIOR FILING DATE: 2000-09-05  
PRIOR APPLICATION NUMBER: 60/231,413  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: 60/229,509  
PRIOR FILING DATE: 2000-09-05  
PRIOR APPLICATION NUMBER: 60/236,367  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/237,039  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 60/237,038  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 60/236,370  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/236,802  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 60/237,037  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 60/237,040  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 60/240,960  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/239,935  
PRIOR FILING DATE: 2000-10-13  
PRIOR APPLICATION NUMBER: 60/239,937  
PRIOR FILING DATE: 2000-10-13  
PRIOR APPLICATION NUMBER: 60/241,787  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/246,474  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: 60/246,532  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: 60/249,216  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,210  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/226,681  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 60/225,759  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/225,213  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/227,182  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 60/225,214  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/235,836  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: 60/230,438  
PRIOR FILING DATE: 2000-09-06  
PRIOR APPLICATION NUMBER: 60/215,135  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: 60/225,266  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/249,218  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,208  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,213  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,212  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,207  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,245  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,244  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,217  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,211  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,215

PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,264  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,214  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,297  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/232,400  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: 60/231,242  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: 60/232,081  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: 60/232,080  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: 60/231,414  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: 60/231,244  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: 60/233,064  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: 60/233,063  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: 60/232,397  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: 60/232,399  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: 60/241,826  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/241,786  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/241,221  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/246,475  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: 60/231,243  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: 60/233,065  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: 60/232,398

Query Match 3.0%; Score 18; DB 7; Length 15270;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 227 catccctgcatcacc 244  
Db 11976 CATCCCTGCATCACC 11959

RESULT 21  
US-09-803-736-1397/c  
Sequence 1397, Application US/09803736  
GENERAL INFORMATION:  
APPLICANT: Bush, David F.  
APPLICANT: Levin, Irene M.  
APPLICANT: Norris, Susan R.  
APPLICANT: Rounsley, Steven D.  
TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof.  
FILE REFERENCE: 38-10(15493)D  
CURRENT APPLICATION NUMBER: US/09/803,736  
PRIOR FILING DATE: 2001-03-12  
PRIOR APPLICATION NUMBER: US 09/534,859  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: identified by Attorney Docket number 04983.0206CPU501 38  
PRIOR FILING DATE: 2000-10-20  
NUMBER OF SEQ ID NOS: 1582  
SEQ ID NO 1397



LENGTH: 96424  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana.  
US-09-803-736-1397

Query Match 3.0%; Score 18; DB 6; Length 96424;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 202 accaatacgaactctgc 219  
|||||  
Db 81927 ACCAATACGACTCTGCC 81910

RESULT 22  
US-09-724-671-17298  
Sequence 17298, Application US/09724671  
GENERAL INFORMATION:  
APPLICANT: Watson, James D  
APPLICANT: Murison, James G  
TITLE OF INVENTION: polynucleotides, polypeptides expressed  
TITLE OF INVENTION: by the polynucleotides and methods for their use.  
FILE REFERENCE: 105002  
CURRENT APPLICATION NUMBER: US/09/724, 671  
CURRENT FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: U.S. No. 60/171,678  
PRIOR FILING DATE: 1999-12-23  
NUMBER OF SEQ ID NOS: 21907  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 17298  
LENGTH: 241  
TYPE: DNA  
ORGANISM: Mouse  
US-09-724-671-17298

Query Match 2.9%; Score 17; DB 7; Length 241;  
Best Local Similarity 100.0%; Pred. No. 62;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 113 aacagcagccagccaa 129  
|||||  
Db 98 aacagcagccagccaa 114

RESULT 23  
US-09-540-213-52685  
Sequence 52685, Application US/09540213  
GENERAL INFORMATION:  
APPLICANT: Seilhamer, Jeffrey J.  
APPLICANT: Delegeane, Angelo M.  
APPLICANT: Stuart, Susan G.  
APPLICANT: Stuve, Laura L.  
APPLICANT: Mullaly, Sara J.  
APPLICANT: Naughton, Rebecca E.  
TITLE OF INVENTION: POLYNUCLEOTIDES OF LIVER AND PANCREAS  
FILE REFERENCE: PD-1031 CIP  
CURRENT APPLICATION NUMBER: US/09/540, 213  
CURRENT FILING DATE: 2000-03-31  
Prior application data removed - consult PALM or file wrapper  
NUMBER OF SEQ ID NOS: 53844  
SEQ ID NO 52685  
LENGTH: 241  
TYPE: DNA  
ORGANISM: Rattus norvegicus  
FEATURE:  
NAME/KEY: misc\_feature  
OTHER INFORMATION: Incyte ID No: rat00171041  
US-09-540-213-52685

Query Match 2.9%; Score 17; DB 7; Length 241;

Best Local Similarity 100.0%; Pred. No. 62;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 113 aacagcagccagccaa 129  
|||||  
Db 71 aacagcagccagccaa 87

RESULT 24  
US-09-540-213-44587  
Sequence 44587, Application US/09540213  
GENERAL INFORMATION:  
APPLICANT: Seilhamer, Jeffrey J.  
APPLICANT: Delegeane, Angelo M.  
APPLICANT: Stuart, Susan G.  
APPLICANT: Stuve, Laura L.  
APPLICANT: Mullaly, Sara J.  
APPLICANT: Naughton, Rebecca E.  
TITLE OF INVENTION: POLYNUCLEOTIDES OF LIVER AND PANCREAS  
FILE REFERENCE: PD-1031 CIP  
CURRENT APPLICATION NUMBER: US/09/540, 213  
CURRENT FILING DATE: 2000-03-31  
Prior application data removed - consult PALM or file wrapper  
NUMBER OF SEQ ID NOS: 53844  
SEQ ID NO 44587  
LENGTH: 264  
TYPE: DNA  
ORGANISM: Rattus norvegicus  
FEATURE:  
NAME/KEY: misc\_feature  
OTHER INFORMATION: Incyte ID No: rat00163047  
US-09-540-213-44587

Query Match 2.9%; Score 17; DB 7; Length 264;  
Best Local Similarity 100.0%; Pred. No. 62;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 113 aacagcagccagccaa 129  
|||||  
Db 71 aacagcagccagccaa 87

RESULT 25  
US-09-540-213-33702  
Sequence 33702, Application US/09540213  
GENERAL INFORMATION:  
APPLICANT: Seilhamer, Jeffrey J.  
APPLICANT: Delegeane, Angelo M.  
APPLICANT: Stuart, Susan G.  
APPLICANT: Stuve, Laura L.  
APPLICANT: Mullaly, Sara J.  
APPLICANT: Naughton, Rebecca E.  
TITLE OF INVENTION: POLYNUCLEOTIDES OF LIVER AND PANCREAS  
FILE REFERENCE: PD-1031 CIP  
CURRENT APPLICATION NUMBER: US/09/540, 213  
CURRENT FILING DATE: 2000-03-31  
Prior application data removed - consult PALM or file wrapper  
NUMBER OF SEQ ID NOS: 53844  
SEQ ID NO 33702  
LENGTH: 300  
TYPE: DNA  
ORGANISM: Rattus norvegicus  
FEATURE:  
NAME/KEY: misc\_feature  
OTHER INFORMATION: Incyte ID No: rat00076798  
US-09-540-213-33702

Query Match 2.9%; Score 17; DB 7; Length 300;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 aacagcagccagccaa 129  
Db 76 aacagcagccagccaa 92

## RESULT 26

US-09-724-671-8427  
; Sequence 8427, Application US/09724671  
; GENERAL INFORMATION:  
; APPLICANT: Watson, James D  
; APPLICANT: Murison, James G  
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed  
; TITLE OF INVENTION: by the polynucleotides and methods for their use.  
; FILE REFERENCE: 105002  
; CURRENT APPLICATION NUMBER: US/09/724,671  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: U.S. No. 60/171,678  
; PRIOR FILING DATE: 1999-12-23  
; NUMBER OF SEQ ID NOS: 21907  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8427  
; LENGTH: 301  
; TYPE: DNA  
; ORGANISM: Mouse  
US-09-724-671-8427

Query Match 2.9%; Score 17; DB 7; Length 301;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 aacagcagccagccaa 129  
Db 98 aacagcagccagccaa 114

## RESULT 27

US-09-724-671-8448  
; Sequence 8448, Application US/09724671  
; GENERAL INFORMATION:  
; APPLICANT: Watson, James D  
; APPLICANT: Murison, James G  
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed  
; TITLE OF INVENTION: by the polynucleotides and methods for their use.  
; FILE REFERENCE: 105002  
; CURRENT APPLICATION NUMBER: US/09/724,671  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: U.S. No. 60/171,678  
; PRIOR FILING DATE: 1999-12-23  
; NUMBER OF SEQ ID NOS: 21907  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8448  
; LENGTH: 303  
; TYPE: DNA  
; ORGANISM: Mouse  
US-09-724-671-8448

Query Match 2.9%; Score 17; DB 7; Length 303;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 aacagcagccagccaa 129  
Db 98 aacagcagccagccaa 114

## RESULT 28

US-09-863-524-3604/C  
; Sequence 3604, Application US/09863524  
; GENERAL INFORMATION:  
; APPLICANT: Ito, Laura Y.  
; APPLICANT: Gooding, Douglas H.

; APPLICANT: Sherman, Bradley K.  
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN ROOTS  
; FILE REFERENCE: PL-0003 US  
; CURRENT APPLICATION NUMBER: US/09/863,524  
; CURRENT FILING DATE: 2001-05-22  
; PRIOR APPLICATION NUMBER: 60/077,831  
; PRIOR FILING DATE: 1998-03-13  
; NUMBER OF SEQ ID NOS: 6814  
; SOFTWARE: PERL Program  
; SEQ ID NO 3604  
; LENGTH: 322  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Incyte ID No: 700047418H1  
; NAME/KEY: unsure  
; LOCATION: 203, 238, 261, 276  
; OTHER INFORMATION: a, t, c, g, or other  
US-09-863-524-3604

Query Match 2.9%; Score 17; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 gtactggcagcgcgca 155  
Db 231 gtactggcagcgcgca 215

## RESULT 29

US-09-724-671-5748  
; Sequence 5748, Application US/09724671  
; GENERAL INFORMATION:  
; APPLICANT: Watson, James D  
; APPLICANT: Murison, James G  
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed  
; TITLE OF INVENTION: by the polynucleotides and methods for their use.  
; FILE REFERENCE: 105002  
; CURRENT APPLICATION NUMBER: US/09/724,671  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: U.S. No. 60/171,678  
; PRIOR FILING DATE: 1999-12-23  
; NUMBER OF SEQ ID NOS: 21907  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5748  
; LENGTH: 353  
; TYPE: DNA  
; ORGANISM: Mouse  
US-09-724-671-5748

Query Match 2.9%; Score 17; DB 7; Length 353;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 aacagcagccagccaa 129  
Db 98 aacagcagccagccaa 114

## RESULT 30

US-09-724-671-4945  
; Sequence 4945, Application US/09724671  
; GENERAL INFORMATION:  
; APPLICANT: Watson, James D  
; APPLICANT: Murison, James G  
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed  
; TITLE OF INVENTION: by the polynucleotides and methods for their use.  
; FILE REFERENCE: 105002  
; CURRENT APPLICATION NUMBER: US/09/724,671  
; CURRENT FILING DATE: 2000-11-28

PRIOR APPLICATION NUMBER: U.S. No. 60/171,678  
PRIOR FILING DATE: 1999-12-23  
NUMBER OF SEQ ID NOS: 21907  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4945  
LENGTH: 396  
TYPE: DNA  
ORGANISM: Mouse  
US-09-724-671-4945

Query Match 2.9%; Score 17; DB 7; Length 396;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 113 aacagcagccagcgccaa 129  
|||||  
DB 98 aacagcagccagcgccaa 114

## RESULT 31

US-09-804-730-15348  
Sequence 15348, Application US/09804730  
GENERAL INFORMATION:  
APPLICANT: Andersen, Scott E.  
APPLICANT: Hammond-Kosack, Kim  
APPLICANT: Masucci, James D.  
APPLICANT: Urban, Martin  
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
FILE REFERENCE: 38-21(51838)B  
CURRENT APPLICATION NUMBER: US/09/804,730  
CURRENT FILING DATE: 2001-03-13  
PRIOR APPLICATION NUMBER: US 60/189,657  
PRIOR FILING DATE: 2000-03-15  
NUMBER OF SEQ ID NOS: 22828  
SEQ ID NO 15348  
LENGTH: 398  
TYPE: DNA  
ORGANISM: Trifolium aestivum  
OTHER INFORMATION: Clone ID: LIB3399-028-P1-K1-B7  
US-09-804-730-15348

Query Match 2.9%; Score 17; DB 6; Length 398;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 386 cgcgcgcagcagcagcagc 402  
|||||  
DB 270 cgcgcgcagcagcagcagc 286

## RESULT 32

US-09-904-703-4316  
Sequence 4316, Application US/09904703  
GENERAL INFORMATION:  
APPLICANT: Hyseq, Inc.  
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
FILE REFERENCE: 20411-758CON1  
CURRENT APPLICATION NUMBER: US/09/904,703  
CURRENT FILING DATE: 2001-07-12  
PRIOR APPLICATION NUMBER: 09/210,298  
PRIOR FILING DATE: 1998-12-09  
NUMBER OF SEQ ID NOS: 17812  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 4316  
LENGTH: 402  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-904-703-4316

Query Match 2.9%; Score 17; DB 6; Length 402;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 113 aacagcagccagcgccaa 129  
|||||  
DB 73 aacagcagccagcgccaa 89

## RESULT 33

US-09-866-555-6918/c  
Sequence 6918, Application US/09866555  
GENERAL INFORMATION:  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Wang, Tongtong  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Algate, Paul A.  
APPLICANT: Jones, Robert  
APPLICANT: Klee, Jennifer  
TITLE OF INVENTION: LUNG TUMOR-ASSOCIATED SEQUENCES AND METHODS OF USE  
FILE REFERENCE: 210121.580  
CURRENT APPLICATION NUMBER: US/09/866,555  
CURRENT FILING DATE: 2001-05-25  
NUMBER OF SEQ ID NOS: 20487  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6918  
LENGTH: 404  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-866-555-6918

Query Match 2.9%; Score 17; DB 6; Length 404;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 352 aatgtaccccaaggag 368  
|||||  
DB 326 AATGTACCCCAAGGAG 310

## RESULT 34

US-09-692-257A-6664/c  
Sequence 6664, Application US/09692257A  
GENERAL INFORMATION:  
APPLICANT: Miller, Phillip W.  
APPLICANT: Peng, Ming  
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
FILE REFERENCE: 38-21(15771)B  
CURRENT APPLICATION NUMBER: US/09/692,257A  
CURRENT FILING DATE: 2000-10-19  
PRIOR APPLICATION NUMBER: US 60/162,747  
PRIOR FILING DATE: 1999-10-28  
NUMBER OF SEQ ID NOS: 14882  
SEQ ID NO 6664  
LENGTH: 419  
TYPE: DNA  
ORGANISM: Zea mays  
FEATURE:  
OTHER INFORMATION: Clone ID: LIB3137-020-Q1-K1-B5  
US-09-692-257A-6664

Query Match 2.9%; Score 17; DB 7; Length 419;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 274 cctctgcgcgcgcgcgc 290  
|||||  
DB 284 CCTCTGCCGCGCGCGC 268

```
RESULT 35
; US-09-804-730-8033
; Sequence 8033, Application US/09804730
; GENERAL INFORMATION:
; APPLICANT: Andersen, Scott E.
; APPLICANT: Hammond, Kosack, Kim
; APPLICANT: Masucci, James D.
; APPLICANT: Urban, Martin
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(51838)B
; CURRENT APPLICATION NUMBER: US/09/804,730
; CURRENT FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: US 60/189,657
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 22828
; SEQ ID NO 8033
; LENGTH: 426
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: (1)..(426)
; LOCATION: (1)..(426)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB351-013-P1-K1-A4
US-09-804-730-8033
```

```
Query Match 2.9%; Score 17; DB 6; Length 426;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 386 cgcgcgcacacgagcagg 402
|||||
Db 117 cgcgcgcacacgagcagg 133
```

```
RESULT 36
; US-09-904-809-4385/C
; Sequence 4385, Application US/09904809
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-757
; CURRENT APPLICATION NUMBER: US/09/904,809
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 09/234,611
; PRIOR FILING DATE: 1999-01-22
; NUMBER OF SEQ ID NOS: 21025
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4385
; LENGTH: 430
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (1)..(430)
; OTHER INFORMATION: n = A,T,C or G
US-09-904-809-4385
```

```
Query Match 2.9%; Score 17; DB 6; Length 430;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 515 cctcgtctccacagcc 531
|||||
Db 173 cctcgtctccacagcc 157
```

```
RESULT 37
```

```
US-09-881-797-3357/C
; Sequence 3357, Application US/09881797
; GENERAL INFORMATION:
; APPLICANT: Tim Keith
; TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO RESPIRATORY DISEASES AND OBESITY
; FILE REFERENCE: H0M01-04
; CURRENT APPLICATION NUMBER: US/09/881,797
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/211,749
; PRIOR FILING DATE: 2000-06-14
; NUMBER OF SEQ ID NOS: 4687
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3357
; LENGTH: 439
; TYPE: DNA
; ORGANISM: Human
US-09-881-797-3357
```

```
Query Match 2.9%; Score 17; DB 7; Length 439;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 546 agcgaagaagaagcct 562
|||||
Db 157 AGGAGAGAGAAAGCGCT 141
```

```
RESULT 38
; US-09-724-671-4408
; Sequence 4408, Application US/09724671
; GENERAL INFORMATION:
; APPLICANT: Watson, James D
; APPLICANT: Murison, James G
; TITLE OF INVENTION: polynucleotides, polypeptides expressed
; TITLE OF INVENTION: by the polynucleotides and methods for their use.
; FILE REFERENCE: 105002
; CURRENT APPLICATION NUMBER: US/09/724,671
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 60/171,678
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 21907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4408
; LENGTH: 444
; TYPE: DNA
; ORGANISM: Mouse
US-09-724-671-4408
```

```
Query Match 2.9%; Score 17; DB 7; Length 444;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 113 aacagcagcagccaa 129
|||||
Db 98 aacagcagcagccaa 114
```

```
RESULT 39
; US-09-758-463-219
; Sequence 219, Application US/09758463
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PM011
; CURRENT APPLICATION NUMBER: US/09/758,463
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
```

NUMBER OF SEQ ID NOS: 1304  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 219  
LENGTH: 468  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (390)  
OTHER INFORMATION: n equals a,t,g, or c  
US-09-758-463-219

Query Match 2.9%; Score 17; DB 6; Length 468;  
Best Local Similarity 100.0%; Pred. No. 64;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 113 aacagcagcagcgccaa 129  
|||||  
Db 242 aacagcagcagcgccaa 258

RESULT 40  
US-09-881-797-3356/c  
Sequence 3356, Application US/09881797  
GENERAL INFORMATION:  
APPLICANT: Tim Keith  
TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES  
FILE REFERENCE: HOM01-04  
CURRENT APPLICATION NUMBER: US/09/881,797  
CURRENT FILING DATE: 2001-06-14  
PRIORITY FILING DATE: 2000-06-14  
PRIORITY FILING DATE: 2000-06-14  
NUMBER OF SEQ ID NOS: 4687  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 3356  
LENGTH: 474  
TYPE: DNA  
ORGANISM: Human  
US-09-881-797-3356

Query Match 2.9%; Score 17; DB 7; Length 474;  
Best Local Similarity 100.0%; Pred. No. 64;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 546 aggaagaagaagcct 562  
|||||  
Db 190 AGGAGAGAGAAAGCCT 174

RESULT 41  
US-60-253-652-24408/c  
Sequence 24408, Application US/60253652  
GENERAL INFORMATION:  
APPLICANT: Grigor, Murray R  
TITLE OF INVENTION: Compositions Isolated from bovine  
FILE REFERENCE: 1055P2  
CURRENT APPLICATION NUMBER: US/60/253,652  
CURRENT FILING DATE: 2000-11-28  
NUMBER OF SEQ ID NOS: 29954  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 24408  
LENGTH: 481  
TYPE: DNA  
ORGANISM: Bovine  
US-60-253-652-24408

Query Match 2.9%; Score 17; DB 8; Length 481;

Best Local Similarity 100.0%; Pred. No. 64;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 483 atgtgtgcagctata 499  
|||||  
Db 447 ATTGTTGCAGCTATA 431

RESULT 42  
US-09-823-241-6683  
Sequence 6683, Application US/09823241  
GENERAL INFORMATION:  
APPLICANT: Gearling, David P.  
APPLICANT: Holtzman, Douglas A.  
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES  
TITLE OF INVENTION: THEREFOR  
FILE REFERENCE: 1600.2075-001  
CURRENT APPLICATION NUMBER: US/09/823,241  
CURRENT FILING DATE: 2001-03-30  
PRIORITY FILING DATE: 2000-03-30  
PRIORITY FILING DATE: 2000-03-30  
NUMBER OF SEQ ID NOS: 10028  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 6683  
LENGTH: 492  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(492)  
OTHER INFORMATION: n = A,T,C or G  
US-09-823-241-6683

Query Match 2.9%; Score 17; DB 6; Length 492;  
Best Local Similarity 100.0%; Pred. No. 64;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 113 aacagcagcagcgccaa 129  
|||||  
Db 78 aacagcagcagcgccaa 94

RESULT 43  
US-09-850-147-15830  
Sequence 15830, Application US/09850147  
GENERAL INFORMATION:  
APPLICANT: Andersen, Scott E.  
APPLICANT: Edgerton, Michael D  
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
FILE REFERENCE: 38-21(51914)B  
CURRENT APPLICATION NUMBER: US/09/850,147  
CURRENT FILING DATE: 2001-05-08  
PRIORITY FILING DATE: 2000-05-08  
PRIORITY FILING DATE: 2000-05-08  
PRIORITY FILING DATE: 2000-09-05  
PRIORITY FILING DATE: 2000-09-05  
PRIORITY FILING DATE: 2000-09-05  
PRIORITY FILING DATE: 2000-10-10  
NUMBER OF SEQ ID NOS: 18014  
SEQ ID NO 15830  
LENGTH: 500  
TYPE: DNA  
ORGANISM: Sorghum bicolor  
OTHER INFORMATION: Clone ID: LIB3481-018-P1-K1-A10  
US-09-850-147-15830

Query Match 2.9%; Score 17; DB 7; Length 500;  
Best Local Similarity 100.0%; Pred. No. 64;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 248 tttaagcagccagccaa 264  
|||||  
Db 82 tttaagcagccagccaa 98

RESULT 44  
US-09-834-366-4311

; Sequence 4311, Application US/09834366  
; GENERAL INFORMATION:  
; APPLICANT: Benjamin, Stephane  
; APPLICANT: Tanaka, Hiroaki  
; APPLICANT: Dumas Maline Edwards, Jean Baptiste  
; APPLICANT: Jobert, Severin  
; APPLICANT: Giordano, Jean-Yves  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: 81 US2 REG  
; CURRENT APPLICATION NUMBER: US/09/834,366  
; CURRENT FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: US 60/197,873  
; PRIOR FILING DATE: 2000-04-18  
; NUMBER OF SEQ ID NOS: 52153  
; SOFTWARE: Patent.pm  
; SEQ ID NO 4311  
; LENGTH: 501  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 121..501  
US-09-834-366-4311

Query Match  
Best Local Similarity 2.9%; Score 17; DB 7; Length 501;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 aacagcagccagccaa 129  
|||||  
Db 126 aacagcagccagccaa 142

RESULT 45

US-09-758-463-239  
; Sequence 239, Application US/09758463  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antipodides  
; FILE REFERENCE: PM011  
; CURRENT APPLICATION NUMBER: US/09/758,463  
; CURRENT FILING DATE: 2001-01-11  
; PRIOR APPLICATION NUMBER: 60/179,065  
; PRIOR FILING DATE: 2000-01-31  
; PRIOR APPLICATION NUMBER: 60/180,628  
; PRIOR FILING DATE: 2000-02-04  
; NUMBER OF SEQ ID NOS: 1304  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 239  
; LENGTH: 514  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-758-463-239

Query Match  
Best Local Similarity 2.9%; Score 17; DB 6; Length 514;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 aacagcagccagccaa 129  
|||||  
Db 137 aacagcagccagccaa 153

RESULT 46

US-09-821-837-4107  
; Sequence 4107, Application US/09821837  
; GENERAL INFORMATION:  
; APPLICANT: Gearing, David P.  
; APPLICANT: Holtzman, Douglas A.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES  
; TITLE OF INVENTION: THEREFOR  
; FILE REFERENCE: 1600.2076-001  
; CURRENT APPLICATION NUMBER: US/09/821,837  
; CURRENT FILING DATE: 2001-03-29  
; PRIOR APPLICATION NUMBER: US 60/193,481  
; PRIOR FILING DATE: 2000-03-29  
; NUMBER OF SEQ ID NOS: 9928  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4107  
; LENGTH: 562  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(562)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-821-837-4107

Query Match  
Best Local Similarity 2.9%; Score 17; DB 7; Length 562;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 265 gcaagcagcgcctcctgc 281  
|||||  
Db 34 gcaagcagcgcctcctgc 50

RESULT 47

US-09-823-327-3606  
; Sequence 3606, Application US/09823327  
; GENERAL INFORMATION:  
; APPLICANT: Richardson, Jennifer  
; APPLICANT: Macbeth, Kyle J.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES  
; TITLE OF INVENTION: THEREFOR  
; FILE REFERENCE: 1600.2083-001  
; CURRENT APPLICATION NUMBER: US/09/823,327  
; CURRENT FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: US 60/193,433  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 9746  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3606  
; LENGTH: 643  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(643)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-823-327-3606

Query Match  
Best Local Similarity 2.9%; Score 17; DB 7; Length 643;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 aacagcagccagccaa 129  
|||||  
Db 84 aacagcagccagccaa 100

RESULT 48

US-09-623-746A-60  
; Sequence 60, Application US/09623746A  
; GENERAL INFORMATION:

```
; APPLICANT: SPECHT, THOMAS
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHWITT, ARMIN
; APPLICANT: PILARSKY, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM PROSTATE TISSUE
; FILE REFERENCE: ALBRE 10
; CURRENT APPLICATION NUMBER: US/09/623,746A
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: PCT/DE99/00722
; PRIOR FILING DATE: 1999-03-09
; NUMBER OF SEQ ID NOS: 297
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 697
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-623-746A-60
```

```
Query Match          2.9%; Score 17; DB 6; Length 697;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 113 aacagcagccagcgccaa 129
    |||
DB 110 aacagcagccagcgccaa 126
```

```
RESULT 49
PCT-US01-08631-9801/c
; Sequence 9801, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 9801
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (129)..(689)
; OTHER INFORMATION: 29% homologous to Santalum album proline rich
; OTHER INFORMATION: protein, accession number AF020261, Smith-Waterman Score=112.
PCT-US01-08631-9801
```

```
Query Match          2.9%; Score 17; DB 1; Length 771;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 257 cagccaagcagcgccg 273
    |||
DB 602 CAGCCAAGCAGCGCCG 586
```

```
RESULT 50
PCT-US01-08631-9802/c
; Sequence 9802, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049
```

```
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 9802
; LENGTH: 781
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (8)..(493)
; OTHER INFORMATION: 30% homologous to Homo sapiens Human PRO1305 (UN0671) amino
; OTHER INFORMATION: acid sequence SEQ ID NO:153, accession number Y93386, Smith-Wate
; OTHER INFORMATION: Score=110.
PCT-US01-08631-9802
```

```
Query Match          2.9%; Score 17; DB 1; Length 781;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 257 cagccaagcagcgccg 273
    |||
DB 557 CAGCCAAGCAGCGCCG 541
```

```
Search completed: September 21, 2001, 13:33:10
Job time: 551 sec
```



---

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 21, 2001, 13:59:40 : Search time 15806.4 Seconds  
(without alignments)  
581.273 Million cell updates/sec

Title: US-09-138-735-1\_COPY\_1232\_1825  
Perfect score: 594  
Sequence: 1 caggtacagcgtacagcgtc.....aaacgagctccgtgagcata 594

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 1344157 seqs, 7733874588 residues

Word size: 0

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database:

GenEmbl:  
1: gb\_ba1:\*  
2: gb\_ba2:\*  
3: gb\_ba3:\*  
4: gb\_in1:\*  
5: gb\_in2:\*  
6: gb\_in3:\*  
7: gb\_om:\*  
8: gb\_ov:\*  
9: gb\_pat1:\*  
10: gb\_pat2:\*  
11: gb\_ph:\*  
12: gb\_pl1:\*  
13: gb\_pl2:\*  
14: gb\_pl3:\*  
15: gb\_pl4:\*  
16: gb\_pl5:\*  
17: em\_ba2:\*  
18: em\_fun:\*  
19: em\_htgo\_hum:\*  
20: em\_htgo\_inv:\*  
21: em\_htgo\_rod:\*  
22: em\_htg\_hum1:\*  
23: em\_htg\_hum2:\*  
24: em\_htg\_hum3:\*  
25: em\_htg\_hum4:\*  
26: em\_htg\_hum5:\*  
27: em\_htg\_hum6:\*  
28: em\_htg\_hum7:\*  
29: em\_htg\_hum8:\*  
30: em\_htg\_inv1:\*  
31: em\_htg\_inv2:\*  
32: em\_htg\_other:\*  
33: em\_htg\_rod:\*  
34: em\_hum1:\*  
35: em\_hum2:\*  
36: em\_hum3:\*  
37: em\_hum4:\*  
38: em\_hum5:\*  
39: em\_hum6:\*  
40: em\_hum7:\*  
41: em\_in:\*  
42: em\_om:\*  
43: em\_or:\*

Oligo Search

5+

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 594   | 100.0       | 3402   | 9     | AR047920    |
| 2          | 492   | 82.8        | 3402   | 9     | A48910      |
| 3          | 492   | 82.8        | 3402   | 96    | TCU24190    |
| 4          | 22    | 3.7         | 22     | 9     | A48918      |
| 5          | 22    | 3.7         | 22     | 9     | AR047927    |
| 6          | 22    | 3.7         | 331801 | 3     | NMA42491    |
| 7          | 20    | 3.4         | 72056  | 62    | AC011183    |
| 8          | 20    | 3.4         | 91470  | 12    | AC011438    |

AR047920 Sequence  
A48910 Sequence 1  
TCU24190 Trypanosoma  
A48918 Sequence 9  
AR047927 Sequence  
A162755 Neisseria  
AC011183 Homo sapi  
AC011438 Genomic s

|     |    |     |        |    |             |                            |
|-----|----|-----|--------|----|-------------|----------------------------|
| 9   | 20 | 3.4 | 177816 | 65 | AC017643    | AC017643 Drosophila        |
| 10  | 20 | 3.4 | 194897 | 4  | AC007697    | AC007697 Drosophila        |
| 11  | 20 | 3.4 | 262395 | 5  | AE003802    | AE003802 Drosophila        |
| 12  | 19 | 3.2 | 1152   | 14 | D89210      | D89210 Schistosoma         |
| 13  | 19 | 3.2 | 1279   | 94 | AF273691    | AF273691 Mus musculus      |
| 14  | 19 | 3.2 | 10128  | 1  | AE005021    | AE005021 Halobacter        |
| 15  | 19 | 3.2 | 11873  | 9  | AR083116    | AR083116 Sequence          |
| 16  | 19 | 3.2 | 11878  | 9  | AR083115    | AR083115 Sequence          |
| 17  | 19 | 3.2 | 11883  | 9  | AR083114    | AR083114 Sequence          |
| 18  | 19 | 3.2 | 36493  | 15 | SPBC2122    | SPBC2122 S. pombe          |
| 19  | 19 | 3.2 | 82033  | 94 | AC068903    | AC068903 Mus musculus      |
| 20  | 19 | 3.2 | 95292  | 94 | AC068952    | AC068952 Mus musculus      |
| 21  | 19 | 3.2 | 110000 | 79 | AL54832_1   | Continuation (2 of         |
| 22  | 19 | 3.2 | 111071 | 68 | AC024591    | AC024591 Homo sapi         |
| 23  | 19 | 3.2 | 128562 | 66 | AC020962    | AC020962 Mus musculus      |
| 24  | 19 | 3.2 | 130734 | 94 | AC073882    | AC073882 Mus musculus      |
| 25  | 19 | 3.2 | 131888 | 93 | HSJ1057D4   | AL121777 Human DNA         |
| 26  | 19 | 3.2 | 147009 | 76 | AC084179    | AC084179 Homo sapi         |
| 27  | 19 | 3.2 | 156599 | 76 | AC083840    | AC083840 Homo sapi         |
| 28  | 19 | 3.2 | 161549 | 64 | AC015815    | AC015815 Homo sapi         |
| 29  | 19 | 3.2 | 170431 | 61 | AC009108    | AC009108 Homo sapi         |
| 30  | 19 | 3.2 | 175249 | 63 | AC013343    | AC013343 Homo sapi         |
| 31  | 19 | 3.2 | 179844 | 73 | AP002501    | AP002501 Homo sapi         |
| 32  | 19 | 3.2 | 180717 | 73 | AC068169    | AC068169 Homo sapi         |
| 33  | 19 | 3.2 | 181853 | 68 | AC024597    | AC024597 Homo sapi         |
| 34  | 19 | 3.2 | 185892 | 78 | AC090652    | AC090652 Mus musculus      |
| 35  | 19 | 3.2 | 191257 | 74 | AC069560    | AC069560 Mus musculus      |
| 36  | 19 | 3.2 | 194575 | 81 | AL512653    | AL512653 Homo sapi         |
| 37  | 19 | 3.2 | 198453 | 62 | AC011359    | AC011359 Homo sapi         |
| 38  | 19 | 3.2 | 200860 | 81 | AL445211    | AL445211 Homo sapi         |
| 39  | 19 | 3.2 | 225141 | 85 | AC004615    | AC004615 Homo sapi         |
| 40  | 19 | 3.2 | 236050 | 79 | AL354813    | AL354813 Homo sapi         |
| 41  | 18 | 3.0 | 18     | 9  | A48917      | A48917 Sequence 5          |
| 42  | 18 | 3.0 | 18     | 9  | A48917      | A48917 Sequence 8          |
| 43  | 18 | 3.0 | 18     | 9  | AR047923    | AR047923 Sequence          |
| 44  | 18 | 3.0 | 18     | 9  | AR047926    | AR047926 Sequence          |
| 45  | 18 | 3.0 | 1389   | 53 | AU049339    | AU049339 Rattus norvegicus |
| 46  | 18 | 3.0 | 1589   | 10 | AX086831    | AX086831 Sequence          |
| 47  | 18 | 3.0 | 1589   | 93 | HSM801826   | AL116858 Homo sapi         |
| 48  | 18 | 3.0 | 2520   | 9  | AR051480    | AR051480 Sequence          |
| 49  | 18 | 3.0 | 2520   | 9  | AR072620    | AR072620 Sequence          |
| 50  | 18 | 3.0 | 2520   | 9  | AR073165    | AR073165 Sequence          |
| 51  | 18 | 3.0 | 2723   | 89 | AK026431    | AK026431 Homo sapi         |
| 52  | 18 | 3.0 | 9450   | 59 | HPCCK09E1   | D63821 Hepatitis C         |
| 53  | 18 | 3.0 | 10863  | 1  | AE005678    | AE005678 Calicivirus       |
| 54  | 18 | 3.0 | 11031  | 1  | AE004648    | AE004648 Pseudomonas       |
| 55  | 18 | 3.0 | 14704  | 1  | AE001970    | AE001970 Deinococcus       |
| 56  | 18 | 3.0 | 38000  | 61 | AC010079    | AC010079 Leishmania        |
| 57  | 18 | 3.0 | 42000  | 77 | AC087836    | AC087836 Leishmania        |
| 58  | 18 | 3.0 | 58733  | 2  | AF217189    | AF217189 Sorangium         |
| 59  | 18 | 3.0 | 68750  | 2  | AF210842    | AF210843 Sorangium         |
| 60  | 18 | 3.0 | 80515  | 87 | AC011992    | AC011992 Homo sapi         |
| 61  | 18 | 3.0 | 96424  | 14 | ATT22P11    | AL162971 Arabidopsis       |
| 62  | 18 | 3.0 | 97749  | 85 | AC004906    | AC004906 Homo sapi         |
| 63  | 18 | 3.0 | 110000 | 84 | LMFCHR32_03 | Continuation (4 of         |
| 64  | 18 | 3.0 | 113345 | 88 | AF109076    | AF109076 Homo sapi         |
| 65  | 18 | 3.0 | 115429 | 81 | AL500525    | AL500525 Homo sapi         |
| 66  | 18 | 3.0 | 115925 | 75 | AC074128    | AC074128 Homo sapi         |
| 67  | 18 | 3.0 | 135303 | 73 | AC068257    | AC068257 Homo sapi         |
| 68  | 18 | 3.0 | 137506 | 85 | AC004824    | AC004824 Homo sapi         |
| 69  | 18 | 3.0 | 144067 | 78 | AL138798    | AL138798 Homo sapi         |
| 70  | 18 | 3.0 | 154461 | 69 | AC025711    | AC025711 Homo sapi         |
| 71  | 18 | 3.0 | 154788 | 66 | AC021498    | AC021498 Homo sapi         |
| 72  | 18 | 3.0 | 157349 | 78 | AF145206    | AF145206 Homo sapi         |
| 73  | 18 | 3.0 | 157981 | 85 | AC005184    | AC005184 Homo sapi         |
| 74  | 18 | 3.0 | 158427 | 79 | AL355516    | AL355516 Homo sapi         |
| 75  | 18 | 3.0 | 162454 | 79 | AL158169    | AL158169 Homo sapi         |
| 76  | 18 | 3.0 | 164679 | 86 | AC005921    | AC005921 Homo sapi         |
| 77  | 18 | 3.0 | 169195 | 67 | AC023165    | AC023165 Homo sapi         |
| 78  | 18 | 3.0 | 173081 | 78 | AL137001    | AL137001 Homo sapi         |
| 79  | 18 | 3.0 | 177424 | 61 | AC009832    | AC009832 Homo sapi         |
| 80  | 18 | 3.0 | 177720 | 69 | AC025680    | AC025680 Homo sapi         |
| 81  | 18 | 3.0 | 180863 | 76 | AC079809    | AC079809 Homo sapi         |
| 82  | 18 | 3.0 | 183235 | 66 | AC020714    | AC020714 Homo sapi         |
| 83  | 18 | 3.0 | 207221 | 62 | AC012564    | AC012564 Homo sapi         |
| 84  | 18 | 3.0 | 217730 | 77 | AC084823    | AC084823 Mus musculus      |
| 85  | 18 | 3.0 | 218553 | 76 | AC079940    | AC079940 Mus musculus      |
| 86  | 18 | 3.0 | 224376 | 61 | AC010538    | AC010538 Homo sapi         |
| 87  | 18 | 3.0 | 326419 | 76 | AC079635    | AC079635 Mus musculus      |
| 88  | 17 | 2.9 | 198    | 58 | AF065721    | AF065721 Stealit           |
| 89  | 17 | 2.9 | 339    | 93 | HSN052E17   | HSN0523 H. sapiens         |
| 90  | 17 | 2.9 | 376    | 53 | AU026316    | AU026316 Rattus norvegicus |
| 91  | 17 | 2.9 | 383    | 76 | AC080428    | AC080428 Giardia           |
| 92  | 17 | 2.9 | 400    | 58 | AF174900    | AF174900 HIV-1 iso         |
| 93  | 17 | 2.9 | 400    | 58 | AF174963    | AF174963 HIV-1 iso         |
| 94  | 17 | 2.9 | 661    | 8  | AF243428    | AF243428 Oncorhynchus      |
| 95  | 17 | 2.9 | 663    | 88 | AF001597    | AF001597 Homo sapi         |
| 96  | 17 | 2.9 | 697    | 9  | AX017873    | AX017873 Sequence          |
| 97  | 17 | 2.9 | 804    | 88 | AF110775    | AF110775 Homo sapi         |
| 98  | 17 | 2.9 | 839    | 93 | HSN250393   | HSN250393 Giardia          |
| 99  | 17 | 2.9 | 915    | 77 | AC085350    | AC085350 Giardia           |
| 100 | 17 | 2.9 | 920    | 71 | AC034857    | AC034857 Giardia           |
| 101 | 17 | 2.9 | 925    | 53 | CNS074H6    | AL428800 clone BAO         |
| 102 | 17 | 2.9 | 945    | 7  | BOVCS08     | L08798 Bos taurus          |
| 103 | 17 | 2.9 | 977    | 94 | MM0250394   | AL250394 Mus musculus      |
| 104 | 17 | 2.9 | 990    | 53 | CNS0722C    | AL426862 clone BAO         |
| 105 | 17 | 2.9 | 1009   | 71 | AC029282    | AC029282 Giardia           |
| 106 | 17 | 2.9 | 1046   | 89 | AF161497    | AF161497 Homo sapi         |
| 107 | 17 | 2.9 | 1047   | 53 | CNS07B1H    | AL437919 T7 end of         |
| 108 | 17 | 2.9 | 1062   | 94 | BC004726    | BC004726 Mus musculus      |
| 109 | 17 | 2.9 | 1063   | 5  | AF316150    | AF316150 Trypanosoma       |
| 110 | 17 | 2.9 | 1151   | 53 | CNS06TMT    | AL414747 T3 end of         |
| 111 | 17 | 2.9 | 1181   | 97 | HUMHMT      | L29376 Homo sapien         |
| 112 | 17 | 2.9 | 1449   | 1  | AF075168    | AF075168 Brucella          |
| 113 | 17 | 2.9 | 1454   | 2  | BSF299998   | Z99998 Uncultured          |
| 114 | 17 | 2.9 | 1671   | 53 | AF309358    | AF309358 Hordeum           |
| 115 | 17 | 2.9 | 1675   | 3  | RS06694     | AF309358 Hordeum           |
| 116 | 17 | 2.9 | 2002   | 14 | CRU03632    | U70290 S. macrospora       |
| 117 | 17 | 2.9 | 2242   | 15 | SMYUBA      | U63320 S. macrospora       |
| 118 | 17 | 2.9 | 2251   | 97 | HSU63336    | U63336 Human MHC           |
| 119 | 17 | 2.9 | 2298   | 94 | AF177346    | AF177346 Mus musculus      |
| 120 | 17 | 2.9 | 2585   | 58 | AF247522    | AF247522 HIV-1 iso         |
| 121 | 17 | 2.9 | 2984   | 91 | BC002482    | BC002482 Homo sapi         |
| 122 | 17 | 2.9 | 3337   | 10 | I23337      | I23337 Sequence 1          |
| 123 | 17 | 2.9 | 3348   | 2  | D83672      | D83672 Streptomyces        |
| 124 | 17 | 2.9 | 3453   | 3  | MTU43540    | U43540-Mycobacterium       |
| 125 | 17 | 2.9 | 4501   | 85 | AB056760    | AB056760 Macaca            |
| 126 | 17 | 2.9 | 4545   | 94 | AB030448S1  | AB030448 Mus musculus      |
| 127 | 17 | 2.9 | 4601   | 3  | PAU67315    | U67315 Pseudomonas         |
| 128 | 17 | 2.9 | 4624   | 88 | AF064104    | AF064104 Homo sapi         |
| 129 | 17 | 2.9 | 4823   | 89 | AK001661    | AK001661 Homo sapi         |
| 130 | 17 | 2.9 | 4960   | 88 | AF064105    | AF064105 Homo sapi         |
| 131 | 17 | 2.9 | 5186   | 3  | SADNATF2    | X87940 S. aureus           |
| 132 | 17 | 2.9 | 5851   | 94 | AF152533S1  | AF152533 Mus musculus      |
| 133 | 17 | 2.9 | 6074   | 94 | MUSP3VPRI   | AF098866 Mus sp.           |
| 134 | 17 | 2.9 | 6167   | 85 | AB023148    | AB023148 Homo sapi         |
| 135 | 17 | 2.9 | 6867   | 7  | BOVCOX7AL   | L09603 Bovine cyto         |
| 136 | 17 | 2.9 | 9083   | 58 | AF193253    | AF193253 HIV-1 sub         |
| 137 | 17 | 2.9 | 10599  | 1  | AE000939    | AE000939 Methanobac        |
| 138 | 17 | 2.9 | 11421  | 1  | AE004505    | AE004505 Pseudomonas       |
| 139 | 17 | 2.9 | 11672  | 2  | ECOPHN      | D90227 Escherichia         |
| 140 | 17 | 2.9 | 11908  | 1  | AE005822    | AE005822 Caulobacter       |
| 141 | 17 | 2.9 | 12213  | 1  | AE004441    | AE004441 Pseudomonas       |
| 142 | 17 | 2.9 | 12857  | 1  | AE005375    | AE005375 Escherichia       |
| 143 | 17 | 2.9 | 15552  | 1  | AE004049    | AE004049 Xylella           |
| 144 | 17 | 2.9 | 15611  | 2  | ECOPHMO     | J05260 E. coli             |
| 145 | 17 | 2.9 | 20102  | 1  | AE000482    | AE003212 Streptomyces      |
| 146 | 17 | 2.9 | 20906  | 3  | SC9B2       | AE000482 Escherichia       |
| 147 | 17 | 2.9 | 27887  | 3  | SC9E50      | AL163672 Streptomyces      |
| 148 | 17 | 2.9 | 27887  | 4  | AE002700    | AE002700 Drosophila        |
| 149 | 17 | 2.9 | 28719  | 85 | AB023052    | AB023052 Homo sapi         |
| 150 | 17 | 2.9 | 29139  | 65 | AC020057    | AC020057 Drosophila        |
| 151 | 17 | 2.9 | 33451  | 12 | AC007293    | AC007293 Arabidopsis       |
| 152 | 17 | 2.9 | 33490  | 6  | CEZK20      | Z69894 Caenorhabditis      |
| 153 | 17 | 2.9 | 33758  | 6  | CEW79       | Z69894 Caenorhabditis      |
| 154 | 17 | 2.9 | 35525  | 77 | AC087068    | AC087068 Leishmania        |

|     |    |     |        |    |              |                     |     |    |     |        |    |           |                     |
|-----|----|-----|--------|----|--------------|---------------------|-----|----|-----|--------|----|-----------|---------------------|
| 155 | 17 | 2.9 | 36849  | 3  | SC1C3        | AL023702 Streptomy  | 228 | 17 | 2.9 | 155645 | 66 | AC021153  | AC021153 Homo sapi  |
| 156 | 17 | 2.9 | 37056  | 85 | AC004700     | AC004700 Homo sapi  | 229 | 17 | 2.9 | 155813 | 65 | AC019350  | AC019350 Homo sapi  |
| 157 | 17 | 2.9 | 38024  | 6  | CELF52B10    | U41990 Caenorhabdi  | 230 | 17 | 2.9 | 156241 | 80 | AL358034  | AL358034 Homo sapi  |
| 158 | 17 | 2.9 | 39207  | 3  | SC4G1        | AL391039 Streptomy  | 231 | 17 | 2.9 | 156557 | 63 | AC015545  | AC015545 Homo sapi  |
| 159 | 17 | 2.9 | 39436  | 85 | AB000879     | AB000879 Homo sapi  | 232 | 17 | 2.9 | 157189 | 4  | AC008307  | AC008307 Drosophill |
| 160 | 17 | 2.9 | 40121  | 3  | MSGY414A     | AD000007 Mycobacte  | 233 | 17 | 2.9 | 158447 | 75 | AC079071  | AC079071 Homo sapi  |
| 161 | 17 | 2.9 | 40673  | 6  | LMFL377      | AL136326 Leishmani  | 234 | 17 | 2.9 | 158458 | 86 | AC007395  | AC007395 Homo sapi  |
| 162 | 17 | 2.9 | 40881  | 85 | AC004679     | AC004679 Homo sapi  | 235 | 17 | 2.9 | 158646 | 79 | AL354708  | AL354708 Homo sapi  |
| 163 | 17 | 2.9 | 42467  | 6  | CELF26F12    | U53373 Caenorhabdi  | 236 | 17 | 2.9 | 159452 | 63 | AC015746  | AC015746 Homo sapi  |
| 164 | 17 | 2.9 | 42584  | 89 | AF215839     | AF215839 Homo sapi  | 237 | 17 | 2.9 | 160972 | 4  | AC007723  | AC007723 Drosophill |
| 165 | 17 | 2.9 | 43401  | 3  | MY13E12      | Z95390 Mycobacteri  | 238 | 17 | 2.9 | 161087 | 65 | AC018850  | AC018850 Homo sapi  |
| 166 | 17 | 2.9 | 43430  | 3  | MYCY16B7     | Z81331 Mycobacteri  | 239 | 17 | 2.9 | 162014 | 74 | AC074323  | AC074323 Homo sapi  |
| 167 | 17 | 2.9 | 43600  | 85 | AC004209     | AC004209 Homo sapi  | 240 | 17 | 2.9 | 162691 | 95 | AC003061  | AC003061 Mouse Chr  |
| 168 | 17 | 2.9 | 44710  | 85 | AC004184     | AC004184 Homo sapi  | 241 | 17 | 2.9 | 162853 | 13 | AP003285  | AP003285 Oryza sat  |
| 169 | 17 | 2.9 | 45087  | 82 | AL590645     | AL590645 Homo sapi  | 242 | 17 | 2.9 | 163570 | 77 | AC016910  | AC016910 Homo sapi  |
| 170 | 17 | 2.9 | 46344  | 90 | AL356497     | AL356497 Human DNA  | 243 | 17 | 2.9 | 163578 | 84 | AC073657  | AC073657 Homo sapi  |
| 171 | 17 | 2.9 | 51082  | 78 | AC090454     | AC090454 Homo sapi  | 244 | 17 | 2.9 | 163836 | 88 | AC073917  | AC073917 Homo sapi  |
| 172 | 17 | 2.9 | 57399  | 91 | AP000433     | AP000433 Homo sapi  | 245 | 17 | 2.9 | 164034 | 87 | AC011489  | AC011489 Homo sapi  |
| 173 | 17 | 2.9 | 57597  | 77 | AC090035     | AC090035 Homo sapi  | 246 | 17 | 2.9 | 164408 | 83 | CNS01DRF  | AL117190 Homo sapi  |
| 174 | 17 | 2.9 | 65174  | 69 | AC025214     | AC025214 Homo sapi  | 247 | 17 | 2.9 | 165405 | 61 | AC009420  | AC009420 Homo sapi  |
| 175 | 17 | 2.9 | 66066  | 70 | AC026566     | AC026566 Homo sapi  | 248 | 17 | 2.9 | 165817 | 60 | AC007935  | AC007935 Homo sapi  |
| 176 | 17 | 2.9 | 66686  | 77 | AC087757     | AC087757 Homo sapi  | 249 | 17 | 2.9 | 166107 | 68 | AC024427  | AC024427 Homo sapi  |
| 177 | 17 | 2.9 | 67392  | 65 | AC018284     | AC018284 Drosophill | 250 | 17 | 2.9 | 167237 | 66 | AC021609  | AC021609 Homo sapi  |
| 178 | 17 | 2.9 | 74371  | 85 | AC005369     | AC005369 Homo sapi  | 251 | 17 | 2.9 | 167310 | 73 | AC068972  | AC068972 Homo sapi  |
| 179 | 17 | 2.9 | 80099  | 13 | AP002040     | AP002040 Arabidops  | 252 | 17 | 2.9 | 167590 | 80 | AL356221  | AL356221 Homo sapi  |
| 180 | 17 | 2.9 | 82604  | 91 | AL500522     | AL500522 Human DNA  | 253 | 17 | 2.9 | 169241 | 72 | AL445987  | AL445987 Homo sapi  |
| 181 | 17 | 2.9 | 84957  | 12 | AC006200     | AC006200 Arabidops  | 254 | 17 | 2.9 | 169256 | 86 | AC048358  | AC048358 Homo sapi  |
| 182 | 17 | 2.9 | 85657  | 12 | AC069473     | AC069473 Arabidops  | 255 | 17 | 2.9 | 170030 | 86 | AC005829  | AC005829 Homo sapi  |
| 183 | 17 | 2.9 | 86135  | 90 | AL159169     | AL159169 Human DNA  | 256 | 17 | 2.9 | 170324 | 4  | AC007805  | AC007805 Drosophill |
| 184 | 17 | 2.9 | 88296  | 88 | AC027328     | AC027328 Homo sapi  | 257 | 17 | 2.9 | 170457 | 76 | AC083944  | AC083944 Homo sapi  |
| 185 | 17 | 2.9 | 88614  | 70 | AC026865     | AC026865 Homo sapi  | 258 | 17 | 2.9 | 170711 | 71 | AC032020  | AC032020 Homo sapi  |
| 186 | 17 | 2.9 | 88784  | 63 | AC012997     | AC012997 Drosophill | 259 | 17 | 2.9 | 170854 | 83 | AP002383  | AP002383 Homo sapi  |
| 187 | 17 | 2.9 | 90767  | 78 | H0510A06     | AL442104 Oryza sat  | 260 | 17 | 2.9 | 170856 | 73 | AC068160  | AC068160 Homo sapi  |
| 188 | 17 | 2.9 | 94641  | 84 | AF257499     | AF257499 Homo sapi  | 261 | 17 | 2.9 | 170891 | 60 | AL502118  | AL502118 Homo sapi  |
| 189 | 17 | 2.9 | 100000 | 91 | AP000506     | AP000506 Homo sapi  | 262 | 17 | 2.9 | 171539 | 81 | AL512788  | AL512788 Homo sapi  |
| 190 | 17 | 2.9 | 100000 | 91 | AP000513     | AP000513 Homo sapi  | 263 | 17 | 2.9 | 171775 | 70 | AC027015  | AC027015 Homo sapi  |
| 191 | 17 | 2.9 | 107150 | 60 | AC008839     | AC008839 Homo sapi  | 264 | 17 | 2.9 | 171790 | 62 | AC011106  | AC011106 Homo sapi  |
| 192 | 17 | 2.9 | 107152 | 88 | AC020930     | AC020930 Homo sapi  | 265 | 17 | 2.9 | 172004 | 86 | AC008482  | AC008482 Homo sapi  |
| 193 | 17 | 2.9 | 109626 | 87 | AC008727     | AC008727 Homo sapi  | 266 | 17 | 2.9 | 172312 | 86 | AL359822  | AL359822 Homo sapi  |
| 194 | 17 | 2.9 | 109626 | 87 | AC010346     | AC010346 Homo sapi  | 267 | 17 | 2.9 | 172650 | 62 | AC011042  | AC011042 Homo sapi  |
| 195 | 17 | 2.9 | 110000 | 84 | LMFLCHR5_03  | Continuation (4 of  | 268 | 17 | 2.9 | 173235 | 68 | AC023756  | AC023756 Homo sapi  |
| 196 | 17 | 2.9 | 110000 | 84 | LMFLCHR5_03  | Continuation (4 of  | 269 | 17 | 2.9 | 173254 | 68 | AC012057  | AC012057 Homo sapi  |
| 197 | 17 | 2.9 | 110000 | 84 | LMFLCHR36_09 | Continuation (10 o  | 270 | 17 | 2.9 | 173425 | 66 | AC021482  | AC021482 Homo sapi  |
| 198 | 17 | 2.9 | 110000 | 84 | LMFLCHR36_11 | Continuation (12 o  | 271 | 17 | 2.9 | 174517 | 77 | AC087831  | AC087831 Homo sapi  |
| 199 | 17 | 2.9 | 110603 | 84 | LMFLCHR36_12 | Continuation (13 o  | 272 | 17 | 2.9 | 174831 | 72 | AC060809  | AC060809 Homo sapi  |
| 200 | 17 | 2.9 | 110603 | 93 | HS3421D16    | AL109940 Human DNA  | 273 | 17 | 2.9 | 174852 | 61 | AC010195  | AC010195 Homo sapi  |
| 201 | 17 | 2.9 | 113320 | 61 | AC010662     | AC010662 Drosophill | 274 | 17 | 2.9 | 176300 | 71 | AC027708  | AC027708 Homo sapi  |
| 202 | 17 | 2.9 | 122258 | 80 | AL356427     | AL356427 Homo sapi  | 275 | 17 | 2.9 | 177654 | 69 | AC025988  | AC025988 Homo sapi  |
| 203 | 17 | 2.9 | 123085 | 90 | AL157406     | AL157406 Human DNA  | 276 | 17 | 2.9 | 177656 | 76 | AC079911  | AC079911 Mus muscu  |
| 204 | 17 | 2.9 | 126152 | 92 | HS433M19     | Z95703 Human DNA    | 277 | 17 | 2.9 | 177826 | 84 | AC016852  | AC016852 Homo sapi  |
| 205 | 17 | 2.9 | 132275 | 72 | AC048388     | AC048388 Homo sapi  | 278 | 17 | 2.9 | 178395 | 81 | AL512664  | AL512664 Homo sapi  |
| 206 | 17 | 2.9 | 133751 | 92 | HS1131C10    | AL121931 Human DNA  | 279 | 17 | 2.9 | 178518 | 69 | AC025332  | AC025332 Homo sapi  |
| 207 | 17 | 2.9 | 137928 | 78 | AC090419     | AC090419 Homo sapi  | 280 | 17 | 2.9 | 179471 | 75 | AC078868  | AC078868 Homo sapi  |
| 208 | 17 | 2.9 | 138141 | 65 | AC018433     | AC018433 Homo sapi  | 281 | 17 | 2.9 | 182718 | 64 | AC017095  | AC017095 Homo sapi  |
| 209 | 17 | 2.9 | 139505 | 93 | HSJ591C20    | AL118506 Human DNA  | 282 | 17 | 2.9 | 183251 | 63 | AC013555  | AC013555 Homo sapi  |
| 210 | 17 | 2.9 | 143759 | 88 | AC073532     | AC073532 Homo sapi  | 283 | 17 | 2.9 | 184165 | 60 | AC008763  | AC008763 Homo sapi  |
| 211 | 17 | 2.9 | 145642 | 71 | AC027805     | AC027805 Homo sapi  | 284 | 17 | 2.9 | 184651 | 81 | AL450317  | AL450317 Mus muscu  |
| 212 | 17 | 2.9 | 146018 | 65 | AC018404     | AC018404 Homo sapi  | 285 | 17 | 2.9 | 185260 | 64 | AC016065  | AC016065 Homo sapi  |
| 213 | 17 | 2.9 | 146393 | 70 | AC026791     | AC026791 Homo sapi  | 286 | 17 | 2.9 | 185551 | 93 | HSJ171K16 | AL121881 Human DNA  |
| 214 | 17 | 2.9 | 148960 | 85 | AB000882     | AB000882 Homo sapi  | 287 | 17 | 2.9 | 185948 | 87 | AC022370  | AC022370 Homo sapi  |
| 215 | 17 | 2.9 | 149143 | 62 | AC011591     | AC011591 Homo sapi  | 288 | 17 | 2.9 | 186102 | 83 | AP001983  | AP001983 Homo sapi  |
| 216 | 17 | 2.9 | 150250 | 70 | AC027573     | AC027573 Homo sapi  | 289 | 17 | 2.9 | 187965 | 64 | AC017010  | AC017010 Homo sapi  |
| 217 | 17 | 2.9 | 151289 | 83 | AP003228     | AP003228 Oryza sat  | 290 | 17 | 2.9 | 188463 | 74 | AC073413  | AC073413 Homo sapi  |
| 218 | 17 | 2.9 | 151496 | 83 | AP003312     | AP003312 Oryza sat  | 291 | 17 | 2.9 | 188526 | 62 | AC012342  | AC012342 Homo sapi  |
| 219 | 17 | 2.9 | 151497 | 71 | AC027809     | AC027809 Homo sapi  | 292 | 17 | 2.9 | 188713 | 88 | AC024167  | AC024167 Homo sapi  |
| 220 | 17 | 2.9 | 152159 | 70 | AC027334     | AC027334 Homo sapi  | 293 | 17 | 2.9 | 188755 | 87 | AC013562  | AC013562 Homo sapi  |
| 221 | 17 | 2.9 | 152513 | 83 | AP003207     | AP003207 Oryza sat  | 294 | 17 | 2.9 | 188812 | 63 | AC013419  | AC013419 Homo sapi  |
| 222 | 17 | 2.9 | 152517 | 87 | AC009468     | AC009468 Homo sapi  | 295 | 17 | 2.9 | 189333 | 76 | AC079445  | AC079445 Mus muscu  |
| 223 | 17 | 2.9 | 154685 | 86 | AC007214     | AC007214 Pan trogl  | 296 | 17 | 2.9 | 189786 | 73 | AC068015  | AC068015 Homo sapi  |
| 224 | 17 | 2.9 | 154745 | 61 | AC010860     | AC010860 Homo sapi  | 297 | 17 | 2.9 | 190386 | 75 | AC074216  | AC074216 Homo sapi  |
| 225 | 17 | 2.9 | 155068 | 70 | AC027307     | AC027307 Homo sapi  | 298 | 17 | 2.9 | 190844 | 75 | AC073990  | AC073990 Homo sapi  |
| 226 | 17 | 2.9 | 155238 | 84 | HS66C13      | AL354047 Homo sapi  | 299 | 17 | 2.9 | 191111 | 86 | AC007458  | AC007458 Homo sapi  |
| 227 | 17 | 2.9 | 155399 | 69 | AC025663     | AC025663 Homo sapi  | 300 | 17 | 2.9 | 192431 | 67 | AC022059  | AC022059 Homo sapi  |

|       |    |     |        |    |            |     |    |     |     |    |            |                    |
|-------|----|-----|--------|----|------------|-----|----|-----|-----|----|------------|--------------------|
| C 301 | 17 | 2.9 | 192868 | 88 | AC023484   | 374 | 16 | 2.7 | 343 | 59 | HIV1S31756 | L13574 Human Immun |
| C 302 | 17 | 2.9 | 193098 | 89 | AL137140   | 375 | 16 | 2.7 | 343 | 59 | HIV1S31757 | L13575 Human Immun |
| C 303 | 17 | 2.9 | 193426 | 73 | AC067942   | 376 | 16 | 2.7 | 343 | 59 | HIV1S37R1  | L13525 Human Immun |
| C 304 | 17 | 2.9 | 193505 | 79 | AL139818   | 377 | 16 | 2.7 | 343 | 59 | HIV1S37R10 | L13534 Human Immun |
| C 305 | 17 | 2.9 | 193816 | 69 | AC025874   | 378 | 16 | 2.7 | 343 | 59 | HIV1S37R11 | L13533 Human Immun |
| C 306 | 17 | 2.9 | 194151 | 66 | AC021185   | 379 | 16 | 2.7 | 343 | 59 | HIV1S37R12 | L13536 Human Immun |
| C 307 | 17 | 2.9 | 195310 | 68 | AC024189   | 380 | 16 | 2.7 | 343 | 59 | HIV1S37R2  | L13526 Human Immun |
| C 308 | 17 | 2.9 | 195466 | 71 | AC032024   | 381 | 16 | 2.7 | 343 | 59 | HIV1S37R3  | L13527 Human Immun |
| C 309 | 17 | 2.9 | 195472 | 65 | AC018398   | 382 | 16 | 2.7 | 343 | 59 | HIV1S37R4  | L13528 Human Immun |
| C 310 | 17 | 2.9 | 195556 | 65 | AC018382   | 383 | 16 | 2.7 | 343 | 59 | HIV1S37R5  | L13529 Human Immun |
| C 311 | 17 | 2.9 | 197871 | 73 | AC068053   | 384 | 16 | 2.7 | 343 | 59 | HIV1S37R6  | L13530 Human Immun |
| C 312 | 17 | 2.9 | 198388 | 74 | AC073426   | 385 | 16 | 2.7 | 343 | 59 | HIV1S37R7  | L13531 Human Immun |
| C 313 | 17 | 2.9 | 198677 | 1  | AE001863   | 386 | 16 | 2.7 | 343 | 59 | HIV1S37R8  | L13532 Human Immun |
| C 314 | 17 | 2.9 | 199314 | 61 | AC009097   | 387 | 16 | 2.7 | 343 | 59 | HIV1S37R9  | L13533 Human Immun |
| C 315 | 17 | 2.9 | 199853 | 75 | AC073785   | 388 | 16 | 2.7 | 343 | 59 | HIV1B05G1  | L36011 Human Immun |
| C 316 | 17 | 2.9 | 200033 | 93 | HSR251973  | 389 | 16 | 2.7 | 343 | 59 | HIV1B05G2  | L36012 Human Immun |
| C 317 | 17 | 2.9 | 200033 | 69 | AC025105   | 390 | 16 | 2.7 | 344 | 58 | AF028581   | AF028581 HIV-1 Iso |
| C 318 | 17 | 2.9 | 201660 | 60 | AC009036   | 391 | 16 | 2.7 | 354 | 58 | AF224030   | AF224030 HIV-1 C25 |
| C 319 | 17 | 2.9 | 201846 | 72 | AC055797   | 392 | 16 | 2.7 | 354 | 58 | AF020207   | AF020207 Rattus no |
| C 320 | 17 | 2.9 | 209034 | 75 | AC073789   | 393 | 16 | 2.7 | 356 | 58 | AF050932   | AF050932 HIV-1 Iso |
| C 321 | 17 | 2.9 | 212209 | 68 | AC024651   | 394 | 16 | 2.7 | 357 | 58 | AF191457   | AF191457 HIV-1 Iso |
| C 322 | 17 | 2.9 | 217115 | 68 | AC007305   | 395 | 16 | 2.7 | 360 | 58 | AF073390   | AF073390 HIV-1 Iso |
| C 323 | 17 | 2.9 | 220995 | 61 | AC010687   | 396 | 16 | 2.7 | 360 | 58 | AF224046   | AF224046 HIV-1 C26 |
| C 324 | 17 | 2.9 | 221913 | 67 | AC022129   | 397 | 16 | 2.7 | 368 | 58 | AF017866   | AF017866 HIV-1 Pat |
| C 325 | 17 | 2.9 | 223000 | 6  | LMFCHRA4   | 398 | 16 | 2.7 | 372 | 58 | AF050938   | AF050938 HIV-1 Iso |
| C 326 | 17 | 2.9 | 226483 | 5  | AE003693   | 399 | 16 | 2.7 | 372 | 58 | AF020208   | AF020208 Rattus no |
| C 327 | 17 | 2.9 | 228859 | 66 | AC021141   | 400 | 16 | 2.7 | 375 | 58 | AF050937   | AF050937 HIV-1 Iso |
| C 328 | 17 | 2.9 | 229122 | 5  | AE003700   | 401 | 16 | 2.7 | 379 | 58 | AF050939   | AF050939 HIV-1 Iso |
| C 329 | 17 | 2.9 | 229252 | 81 | AL390732   | 402 | 16 | 2.7 | 380 | 58 | AF050935   | AF050935 HIV-1 Iso |
| C 330 | 17 | 2.9 | 230651 | 74 | AC073535   | 403 | 16 | 2.7 | 385 | 58 | AF073402   | AF073402 HIV-1 Iso |
| C 331 | 17 | 2.9 | 233752 | 74 | AC073583   | 404 | 16 | 2.7 | 386 | 58 | AF028584   | AF028584 HIV-1 Iso |
| C 332 | 17 | 2.9 | 240285 | 60 | AC008939   | 405 | 16 | 2.7 | 386 | 58 | AF028587   | AF028587 HIV-1 Iso |
| C 333 | 17 | 2.9 | 240825 | 10 | AX087869   | 406 | 16 | 2.7 | 388 | 58 | AF014238   | AF014238 HIV-1 Pat |
| C 334 | 17 | 2.9 | 258825 | 75 | AC073771   | 407 | 16 | 2.7 | 388 | 58 | AF014239   | AF014239 HIV-1 Pat |
| C 335 | 17 | 2.9 | 259421 | 74 | AC073689   | 408 | 16 | 2.7 | 388 | 58 | AF014240   | AF014240 HIV-1 Pat |
| C 336 | 17 | 2.9 | 286758 | 86 | AC006449   | 409 | 16 | 2.7 | 388 | 58 | AF014344   | AF014344 HIV-1 Pat |
| C 337 | 17 | 2.9 | 291136 | 2  | AP002556   | 410 | 16 | 2.7 | 388 | 58 | AF014345   | AF014345 HIV-1 Pat |
| C 338 | 17 | 2.9 | 294308 | 4  | AE003595   | 411 | 16 | 2.7 | 388 | 58 | AF014358   | AF014358 HIV-1 Pat |
| C 339 | 17 | 2.9 | 303250 | 2  | AP001518   | 412 | 16 | 2.7 | 390 | 58 | AF015406   | AF015406 HIV-1 Pat |
| C 340 | 17 | 2.9 | 310360 | 75 | AC074172   | 413 | 16 | 2.7 | 390 | 58 | AF062050   | AF062050 HIV-1 Iso |
| C 341 | 17 | 2.9 | 310565 | 83 | CEX62P5    | 414 | 16 | 2.7 | 391 | 58 | AF014194   | AF014194 HIV-1 Pat |
| C 342 | 17 | 2.9 | 338534 | 2  | ECOMW93    | 415 | 16 | 2.7 | 391 | 58 | AF014199   | AF014199 HIV-1 Pat |
| C 343 | 17 | 2.9 | 339485 | 13 | AP172282   | 416 | 16 | 2.7 | 391 | 58 | AF014202   | AF014202 HIV-1 Pat |
| C 344 | 17 | 2.9 | 340000 | 91 | AP001675   | 417 | 16 | 2.7 | 391 | 58 | AF014216   | AF014216 HIV-1 Pat |
| C 345 | 16 | 2.7 | 41     | 10 | E08211     | 418 | 16 | 2.7 | 391 | 58 | AF014225   | AF014225 HIV-1 Pat |
| C 346 | 16 | 2.7 | 222    | 10 | E08211     | 419 | 16 | 2.7 | 391 | 58 | AF014228   | AF014228 HIV-1 Pat |
| C 347 | 16 | 2.7 | 222    | 14 | OSTROSL1A  | 420 | 16 | 2.7 | 391 | 58 | AF014233   | AF014233 HIV-1 Pat |
| C 348 | 16 | 2.7 | 224    | 14 | ROMLPTS2   | 421 | 16 | 2.7 | 391 | 58 | AF050899   | AF050899 HIV-1 mat |
| C 349 | 16 | 2.7 | 224    | 14 | ROMLPTS2   | 422 | 16 | 2.7 | 391 | 58 | AF050900   | AF050900 HIV-1 mat |
| C 350 | 16 | 2.7 | 224    | 14 | ROMLPTS2   | 423 | 16 | 2.7 | 391 | 58 | AF050927   | AF050927 HIV-1 Iso |
| C 351 | 16 | 2.7 | 224    | 14 | ROMLPTS2   | 424 | 16 | 2.7 | 391 | 58 | AF050928   | AF050928 HIV-1 Iso |
| C 352 | 16 | 2.7 | 224    | 14 | ROMLPTS2   | 425 | 16 | 2.7 | 391 | 58 | AF050929   | AF050929 HIV-1 Iso |
| C 353 | 16 | 2.7 | 224    | 14 | ROMLPTS2   | 426 | 16 | 2.7 | 391 | 58 | AF050931   | AF050931 HIV-1 Iso |
| C 354 | 16 | 2.7 | 225    | 14 | CGRACITS2  | 427 | 16 | 2.7 | 391 | 58 | AF050936   | AF050936 HIV-1 Iso |
| C 355 | 16 | 2.7 | 225    | 14 | CGRACITS2  | 428 | 16 | 2.7 | 391 | 58 | AF050942   | AF050942 HIV-1 Iso |
| C 356 | 16 | 2.7 | 225    | 14 | ROMLPTS2   | 429 | 16 | 2.7 | 391 | 58 | AF050944   | AF050944 HIV-1 Iso |
| C 357 | 16 | 2.7 | 225    | 14 | ROMLPTS2   | 430 | 16 | 2.7 | 391 | 58 | AF050946   | AF050946 HIV-1 Iso |
| C 358 | 16 | 2.7 | 225    | 14 | ROMLPTS2   | 431 | 16 | 2.7 | 391 | 58 | AF050951   | AF050951 HIV-1 Iso |
| C 359 | 16 | 2.7 | 225    | 14 | ROMLPTS2   | 432 | 16 | 2.7 | 391 | 58 | AF050952   | AF050952 HIV-1 Iso |
| C 360 | 16 | 2.7 | 225    | 14 | ROMLPTS2   | 433 | 16 | 2.7 | 391 | 58 | AF050953   | AF050953 HIV-1 Iso |
| C 361 | 16 | 2.7 | 225    | 14 | ROMLPTS2   | 434 | 16 | 2.7 | 391 | 58 | AF050959   | AF050959 HIV-1 Iso |
| C 362 | 16 | 2.7 | 225    | 14 | ROMLPTS2   | 435 | 16 | 2.7 | 391 | 58 | AF050960   | AF050960 HIV-1 Iso |
| C 363 | 16 | 2.7 | 225    | 14 | ROMLPTS2   | 436 | 16 | 2.7 | 391 | 58 | AF051008   | AF051008 HIV-1 Iso |
| C 364 | 16 | 2.7 | 293    | 54 | G04984     | 437 | 16 | 2.7 | 391 | 58 | AF051009   | AF051009 HIV-1 Iso |
| C 365 | 16 | 2.7 | 334    | 9  | AX000736   | 438 | 16 | 2.7 | 391 | 58 | AF051010   | AF051010 HIV-1 Iso |
| C 366 | 16 | 2.7 | 336    | 59 | HIV1EKG4   | 439 | 16 | 2.7 | 391 | 58 | AF051012   | AF051012 HIV-1 Iso |
| C 367 | 16 | 2.7 | 341    | 58 | AF028579   | 440 | 16 | 2.7 | 391 | 58 | AF051013   | AF051013 HIV-1 Iso |
| C 368 | 16 | 2.7 | 343    | 58 | AF028578   | 441 | 16 | 2.7 | 391 | 58 | AF051014   | AF051014 HIV-1 Iso |
| C 369 | 16 | 2.7 | 343    | 59 | HIV1S317S1 | 442 | 16 | 2.7 | 391 | 58 | AF051016   | AF051016 HIV-1 Iso |
| C 370 | 16 | 2.7 | 343    | 59 | HIV1S317S2 | 443 | 16 | 2.7 | 391 | 58 | AF051019   | AF051019 HIV-1 Iso |
| C 371 | 16 | 2.7 | 343    | 59 | HIV1S317S3 | 444 | 16 | 2.7 | 391 | 58 | AF051022   | AF051022 HIV-1 Iso |
| C 372 | 16 | 2.7 | 343    | 59 | HIV1S317S4 | 445 | 16 | 2.7 | 391 | 58 | AF051024   | AF051024 HIV-1 Iso |
| C 373 | 16 | 2.7 | 343    | 59 | HIV1S317S5 | 446 | 16 | 2.7 | 391 | 58 | AF051027   | AF051027 HIV-1 Iso |

|     |    |     |     |    |            |                     |     |    |     |      |    |           |                          |
|-----|----|-----|-----|----|------------|---------------------|-----|----|-----|------|----|-----------|--------------------------|
| 447 | 16 | 2.7 | 391 | 58 | AF051030   | AF051030 HIV-1 iso  | 520 | 16 | 2.7 | 626  | 13 | AF202406  | AF202406 Roscoe h        |
| 448 | 16 | 2.7 | 393 | 94 | AF020209   | AF020209 Rattus no  | 521 | 16 | 2.7 | 627  | 13 | AF202376  | AF202376 Hedychium       |
| 449 | 16 | 2.7 | 394 | 58 | AF014269   | AF014269 HIV-1 pat  | 522 | 16 | 2.7 | 627  | 13 | AF202380  | AF202380 Hedychium       |
| 450 | 16 | 2.7 | 396 | 58 | AF084766   | AF084766 HIV-1 pat  | 523 | 16 | 2.7 | 627  | 13 | AF202381  | AF202381 Hedychium       |
| 451 | 16 | 2.7 | 396 | 58 | AF084767   | AF084767 HIV-1 pat  | 524 | 16 | 2.7 | 627  | 13 | AF202382  | AF202382 Hedychium       |
| 452 | 16 | 2.7 | 396 | 58 | AF084768   | AF084768 HIV-1 pat  | 525 | 16 | 2.7 | 627  | 13 | AF202393  | AF202393 Hedychium       |
| 453 | 16 | 2.7 | 396 | 58 | AF084769   | AF084769 HIV-1 pat  | 526 | 16 | 2.7 | 627  | 13 | AF202394  | AF202394 Hedychium       |
| 454 | 16 | 2.7 | 396 | 58 | AF084770   | AF084770 HIV-1 pat  | 527 | 16 | 2.7 | 627  | 13 | AF202397  | AF202397 Hedychium       |
| 455 | 16 | 2.7 | 396 | 58 | AF084771   | AF084771 HIV-1 pat  | 528 | 16 | 2.7 | 628  | 13 | AF202377  | AF202377 Hedychium       |
| 456 | 16 | 2.7 | 396 | 58 | AF084772   | AF084772 HIV-1 pat  | 529 | 16 | 2.7 | 628  | 13 | AF202378  | AF202378 Hedychium       |
| 457 | 16 | 2.7 | 396 | 58 | AF084773   | AF084773 HIV-1 pat  | 530 | 16 | 2.7 | 628  | 13 | AF202383  | AF202383 Hedychium       |
| 458 | 16 | 2.7 | 396 | 58 | AF084774   | AF084774 HIV-1 pat  | 531 | 16 | 2.7 | 628  | 13 | AF202384  | AF202384 Hedychium       |
| 459 | 16 | 2.7 | 396 | 58 | AF084775   | AF084775 HIV-1 pat  | 532 | 16 | 2.7 | 628  | 13 | AF202389  | AF202389 Hedychium       |
| 460 | 16 | 2.7 | 396 | 58 | AF084776   | AF084776 HIV-1 pat  | 533 | 16 | 2.7 | 628  | 13 | AF202390  | AF202390 Hedychium       |
| 461 | 16 | 2.7 | 396 | 58 | AF084777   | AF084777 HIV-1 pat  | 534 | 16 | 2.7 | 628  | 13 | AF202391  | AF202391 Hedychium       |
| 462 | 16 | 2.7 | 396 | 59 | HIV1DUMC   | Z79559 Human Immun  | 535 | 16 | 2.7 | 628  | 13 | AF202392  | AF202392 Hedychium       |
| 463 | 16 | 2.7 | 396 | 59 | HIV1DUMK   | Z79558 Human Immun  | 536 | 16 | 2.7 | 628  | 13 | AF202396  | AF202396 Hedychium       |
| 464 | 16 | 2.7 | 397 | 58 | AF014195   | AF014195 HIV-1 pat  | 537 | 16 | 2.7 | 629  | 13 | AF202379  | AF202379 Hedychium       |
| 465 | 16 | 2.7 | 399 | 58 | AF174897   | AF174897 HIV-1 iso  | 538 | 16 | 2.7 | 629  | 13 | AF202402  | AF202402 Hedychium       |
| 466 | 16 | 2.7 | 399 | 58 | AF174898   | AF174898 HIV-1 iso  | 539 | 16 | 2.7 | 631  | 13 | AF202401  | AF202401 Hedychium       |
| 467 | 16 | 2.7 | 399 | 58 | AF174899   | AF174899 HIV-1 iso  | 540 | 16 | 2.7 | 651  | 97 | HUM0288BF | D85542 Human CPG 1       |
| 468 | 16 | 2.7 | 400 | 58 | AF014222   | AF014222 HIV-1 pat  | 541 | 16 | 2.7 | 729  | 58 | AF071291  | AF071291 HIV-1 iso       |
| 469 | 16 | 2.7 | 400 | 58 | AF174851   | AF174851 HIV-1 iso  | 542 | 16 | 2.7 | 729  | 58 | AF071300  | AF071300 HIV-1 iso       |
| 470 | 16 | 2.7 | 400 | 58 | AF174895   | AF174895 HIV-1 iso  | 543 | 16 | 2.7 | 729  | 58 | AF196682  | AF196682 HIV-1 iso       |
| 471 | 16 | 2.7 | 400 | 58 | AF174896   | AF174896 HIV-1 iso  | 544 | 16 | 2.7 | 738  | 58 | AF071302  | AF071302 HIV-1 iso       |
| 472 | 16 | 2.7 | 400 | 58 | AF174902   | AF174902 HIV-1 iso  | 545 | 16 | 2.7 | 738  | 58 | AF071308  | AF071308 HIV-1 iso       |
| 473 | 16 | 2.7 | 400 | 58 | AF174962   | AF174962 HIV-1 iso  | 546 | 16 | 2.7 | 759  | 96 | TVA250739 | AI250739 Trypanoso       |
| 474 | 16 | 2.7 | 400 | 58 | AF174964   | AF174964 HIV-1 iso  | 547 | 16 | 2.7 | 774  | 9  | A70164    | A70164 Sequence 25       |
| 475 | 16 | 2.7 | 400 | 58 | AF174965   | AF174965 HIV-1 iso  | 548 | 16 | 2.7 | 774  | 14 | MAZ93103  | Z93103 M.acuminata       |
| 476 | 16 | 2.7 | 400 | 58 | AF174966   | AF174966 HIV-1 iso  | 549 | 16 | 2.7 | 790  | 53 | CNS07270  | AL425866 clone BA0       |
| 477 | 16 | 2.7 | 400 | 58 | AF174967   | AF174967 HIV-1 iso  | 550 | 16 | 2.7 | 843  | 93 | CNS072WV  | AL426776 clone BA0       |
| 478 | 16 | 2.7 | 400 | 58 | AF174968   | AF174968 HIV-1 iso  | 551 | 16 | 2.7 | 869  | 91 | BC005052  | BC005052 Homo sapi       |
| 479 | 16 | 2.7 | 400 | 58 | AF174969   | AF174969 HIV-1 iso  | 552 | 16 | 2.7 | 871  | 97 | HUMH1SAG  | ME07522 Human histo      |
| 480 | 16 | 2.7 | 400 | 58 | AF174970   | AF174970 HIV-1 iso  | 553 | 16 | 2.7 | 886  | 53 | CNS07502E | AL430428 clone BA0       |
| 481 | 16 | 2.7 | 400 | 58 | AF174971   | AF174971 HIV-1 iso  | 554 | 16 | 2.7 | 892  | 72 | AC052426  | AC052426 clone BA0       |
| 482 | 16 | 2.7 | 401 | 58 | AF028583   | AF028583 HIV-1 iso  | 555 | 16 | 2.7 | 910  | 75 | AC075071  | AC075071 Giardia i       |
| 483 | 16 | 2.7 | 401 | 58 | AF073401   | AF073401 HIV-1 iso  | 556 | 16 | 2.7 | 926  | 53 | CNS07308  | AL426897 clone BA0       |
| 484 | 16 | 2.7 | 406 | 58 | AF073400   | AF073400 HIV-1 iso  | 557 | 16 | 2.7 | 952  | 76 | AC083683  | AL403306 clone Giardia i |
| 485 | 16 | 2.7 | 409 | 58 | AF014214   | AF014214 HIV-1 pat  | 558 | 16 | 2.7 | 966  | 53 | CNS07630  | AL430906 clone XBA       |
| 486 | 16 | 2.7 | 411 | 94 | AF020210   | AF020210 Rattus no  | 559 | 16 | 2.7 | 990  | 10 | AX089467  | AX089467 Sequence        |
| 487 | 16 | 2.7 | 412 | 58 | AF014335   | AF014335 HIV-1 pat  | 560 | 16 | 2.7 | 999  | 74 | AC070320  | AC070320 Giardia i       |
| 488 | 16 | 2.7 | 414 | 4  | AB040074   | AB040074 Hydra mag  | 561 | 16 | 2.7 | 1022 | 76 | AC080628  | AC080628 Giardia i       |
| 489 | 16 | 2.7 | 414 | 58 | AF028577   | AF028577 HIV-1 iso  | 562 | 16 | 2.7 | 1040 | 72 | AC060129  | AC060129 Giardia i       |
| 490 | 16 | 2.7 | 420 | 58 | AF028580   | AF028580 HIV-1 iso  | 563 | 16 | 2.7 | 1061 | 53 | CNS0738M  | AL427196 clone BA0       |
| 491 | 16 | 2.7 | 448 | 58 | AF073403   | AF073403 HIV-1 iso  | 564 | 16 | 2.7 | 1150 | 7  | OC077896  | U77896 Oryctolagus       |
| 492 | 16 | 2.7 | 454 | 58 | AF028586   | AF028586 HIV-1 iso  | 565 | 16 | 2.7 | 1247 | 85 | AB051152  | AB051152 Macaca fa       |
| 493 | 16 | 2.7 | 480 | 14 | CNS01BXR   | AL114823 Botrytis   | 566 | 16 | 2.7 | 1292 | 3  | DB085123  | DB085123 Unidentifite    |
| 494 | 16 | 2.7 | 492 | 3  | SCSCYGEN   | XJ7833 S.cyanogenu  | 567 | 16 | 2.7 | 1299 | 5  | AF017268  | AF017268 Toxoplas        |
| 495 | 16 | 2.7 | 492 | 3  | SGSGHE     | XJ7837 S.glaucosce  | 568 | 16 | 2.7 | 1314 | 9  | AF072866  | AR072866 Sequence        |
| 496 | 16 | 2.7 | 492 | 3  | SGSGHE     | S63672 trichophyall | 569 | 16 | 2.7 | 1314 | 10 | E14942    | E14942 Aspergillus       |
| 497 | 16 | 2.7 | 504 | 97 | HUMYO86H04 | AF075094 Homo sapi  | 570 | 16 | 2.7 | 1314 | 10 | E14955    | E14955 Aspergillus       |
| 498 | 16 | 2.7 | 523 | 9  | A93100     | A93100 Sequence 4   | 571 | 16 | 2.7 | 1314 | 10 | E27570    | E27570 Thermotabi        |
| 499 | 16 | 2.7 | 559 | 14 | RP0388304  | AJ388304 Roscoe p   | 572 | 16 | 2.7 | 1314 | 13 | ATFA0A    | ATFA0A Human immu        |
| 500 | 16 | 2.7 | 559 | 14 | RP0388304  | AJ388304 Roscoe p   | 573 | 16 | 2.7 | 1381 | 94 | AF273690  | AF273690 Mus muscu       |
| 501 | 16 | 2.7 | 561 | 14 | CSP388301  | AJ388301 Cauliteya  | 574 | 16 | 2.7 | 1417 | 96 | TG064517  | U64517 Toxoplasma        |
| 502 | 16 | 2.7 | 562 | 14 | HMU388297  | AJ388297 Hedychium  | 575 | 16 | 2.7 | 1419 | 89 | AF287302  | AF287302 Homo sapi       |
| 503 | 16 | 2.7 | 563 | 14 | CGR388299  | AJ388299 Cauliteya  | 576 | 16 | 2.7 | 1455 | 97 | IR1845189 | AL350057 Homo sapi       |
| 504 | 16 | 2.7 | 565 | 14 | HET388296  | AJ388296 Hedychium  | 577 | 16 | 2.7 | 1468 | 3  | TTASNS    | XJ1008 T.thermophi       |
| 505 | 16 | 2.7 | 574 | 54 | HS421120S  | AL035140 H.sapiens  | 578 | 16 | 2.7 | 1468 | 89 | AF119879  | AF119879 Homo sapi       |
| 506 | 16 | 2.7 | 602 | 5  | AF320100   | AF320100 Dendronep  | 579 | 16 | 2.7 | 1477 | 59 | HIVY1205  | L11785 Human immu        |
| 507 | 16 | 2.7 | 603 | 5  | AF320102   | AF320102 Dendronep  | 580 | 16 | 2.7 | 1513 | 10 | AX082314  | AX082314 Sequence        |
| 508 | 16 | 2.7 | 603 | 5  | AF320103   | AF320103 Dendronep  | 581 | 16 | 2.7 | 1519 | 94 | AF273689  | AF273689 Mus muscu       |
| 509 | 16 | 2.7 | 604 | 5  | AF320098   | AF320098 Dendronep  | 582 | 16 | 2.7 | 1525 | 94 | AB005049  | AB005049 Cavia por       |
| 510 | 16 | 2.7 | 604 | 5  | AF320101   | AF320101 Dendronep  | 583 | 16 | 2.7 | 1581 | 94 | AF134488  | AF134488 Cavia por       |
| 511 | 16 | 2.7 | 608 | 54 | C39591     | G39591 Zedira       | 584 | 16 | 2.7 | 1600 | 3  | RCAN1FQ   | M23323 Rhododactyl       |
| 512 | 16 | 2.7 | 610 | 5  | AF320099   | AF320099 Dendronep  | 585 | 16 | 2.7 | 1669 | 94 | AF273686  | AF273686 Mus muscu       |
| 513 | 16 | 2.7 | 612 | 13 | AF202374   | AF202374 Hedychium  | 586 | 16 | 2.7 | 1669 | 94 | AF273687  | AF273687 Mus muscu       |
| 514 | 16 | 2.7 | 621 | 13 | AF202403   | AF202403 Hedychium  | 587 | 16 | 2.7 | 1699 | 3  | SABLA     | X13597 Streptomyce       |
| 515 | 16 | 2.7 | 621 | 13 | AF202405   | AF202405 Pommeresc  | 588 | 16 | 2.7 | 1723 | 94 | AF273688  | AF273688 Mus muscu       |
| 516 | 16 | 2.7 | 623 | 13 | AF202419   | AF202419 Cauliteya  | 589 | 16 | 2.7 | 1788 | 93 | HSHP512   | X12433 Human phsi-       |
| 517 | 16 | 2.7 | 626 | 13 | AF202385   | AF202385 Hedychium  | 590 | 16 | 2.7 | 1790 | 12 | AF181826  | AF181826 Magnaport       |
| 518 | 16 | 2.7 | 626 | 13 | AF202388   | AF202388 Hedychium  | 591 | 16 | 2.7 | 1803 | 10 | AX090436  | AX090436 Sequence        |
| 519 | 16 | 2.7 | 626 | 13 | AF202395   | AF202395 Hedychium  | 592 | 16 | 2.7 | 1839 | 12 | AB045892  | AB045892 Neptenhes       |

|       |    |     |      |    |            |       |    |     |       |    |            |                     |
|-------|----|-----|------|----|------------|-------|----|-----|-------|----|------------|---------------------|
| C 593 | 16 | 2.7 | 1864 | 9  | AR0761171  | c 666 | 16 | 2.7 | 3892  | 6  | DERE2PE    | X69311 D. erecta re |
| C 594 | 16 | 2.7 | 1864 | 9  | AR076862   | c 667 | 16 | 2.7 | 3919  | 3  | KPU00985   | U00985 Klebsiella   |
| C 595 | 16 | 2.7 | 1864 | 12 | AF036949   | c 668 | 16 | 2.7 | 3952  | 3  | PSEDGD     | J05822 P. cepacia 2 |
| C 596 | 16 | 2.7 | 1900 | 94 | AF287300   | c 669 | 16 | 2.7 | 3960  | 8  | CHKCMF     | D28596 Chicken gen  |
| C 597 | 16 | 2.7 | 1907 | 10 | AX086887   | c 670 | 16 | 2.7 | 3984  | 6  | DMREF2POL  | X16993 Drosophila   |
| C 598 | 16 | 2.7 | 1984 | 4  | AB012617   | c 671 | 16 | 2.7 | 4088  | 94 | MUSB3RP    | J04036 Mus musculus |
| C 599 | 16 | 2.7 | 2025 | 3  | REU41754   | c 672 | 16 | 2.7 | 4261  | 1  | AB016241   | AB016241 Streptomy  |
| C 600 | 16 | 2.7 | 2053 | 9  | AX048734   | c 673 | 16 | 2.7 | 4265  | 1  | AB028210   | AB028210 Streptomy  |
| C 601 | 16 | 2.7 | 2065 | 88 | AF049459   | c 674 | 16 | 2.7 | 4494  | 13 | AF335465   | AF335465 Aspergill  |
| C 602 | 16 | 2.7 | 2140 | 97 | HU07NPBA   | c 675 | 16 | 2.7 | 4523  | 3  | PFL1233    | Y12368 P. fluoresce |
| C 603 | 16 | 2.7 | 2163 | 94 | BC004039   | c 676 | 16 | 2.7 | 4569  | 7  | RABAALG    | M93344 Rabbit acid  |
| C 604 | 16 | 2.7 | 2184 | 94 | AF132727   | c 677 | 16 | 2.7 | 4648  | 63 | AC014057   | AC014057 Drosophi   |
| C 605 | 16 | 2.7 | 2192 | 15 | SCYN253W   | c 678 | 16 | 2.7 | 4736  | 13 | AF205944   | AF205944 Blasticoc  |
| C 606 | 16 | 2.7 | 2214 | 9  | AR039357   | c 679 | 16 | 2.7 | 4746  | 1  | AF034831   | AF034831 Ritzobium  |
| C 607 | 16 | 2.7 | 2214 | 10 | E15639     | c 680 | 16 | 2.7 | 4756  | 97 | HUMPTPS    | D37781 Human mRN    |
| C 608 | 16 | 2.7 | 2255 | 6  | DMREFPNN   | c 681 | 16 | 2.7 | 4887  | 5  | AF331187   | AF331187 Drosophi   |
| C 609 | 16 | 2.7 | 2271 | 96 | TRBEPCK    | c 682 | 16 | 2.7 | 4972  | 5  | MAMAMIM    | X79927 M. ammoniaph |
| C 610 | 16 | 2.7 | 2324 | 88 | AF148713   | c 683 | 16 | 2.7 | 5084  | 3  | SGSTRFMB   | X62567 S. griseus s |
| C 611 | 16 | 2.7 | 2329 | 88 | AF049460   | c 684 | 16 | 2.7 | 5117  | 9  | ARI09903   | ARI09903 Sequence   |
| C 612 | 16 | 2.7 | 2332 | 3  | STMHRDB    | c 685 | 16 | 2.7 | 5117  | 97 | HS010986   | HS010986 Human deni |
| C 613 | 16 | 2.7 | 2332 | 8  | GBGEN      | c 686 | 16 | 2.7 | 5282  | 97 | HSY13034   | Y13034 Homo saplen  |
| C 614 | 16 | 2.7 | 2363 | 10 | AX089466   | c 687 | 16 | 2.7 | 5591  | 94 | MMSKELINA  | AF32644 Ralstonia   |
| C 615 | 16 | 2.7 | 2394 | 6  | DMREFP02   | c 688 | 16 | 2.7 | 5596  | 1  | AF026544   | AF026544 Ralstonia  |
| C 616 | 16 | 2.7 | 2394 | 88 | AF061795   | c 689 | 16 | 2.7 | 5596  | 94 | MNM012072  | MNM012072 Mus muscu |
| C 617 | 16 | 2.7 | 2416 | 91 | BC000770   | c 690 | 16 | 2.7 | 5645  | 94 | AF064748   | AF064748 Mus muscu  |
| C 618 | 16 | 2.7 | 2449 | 85 | AB006965   | c 691 | 16 | 2.7 | 5774  | 2  | ASAJ187    | AJ000187 Arthrobac  |
| C 619 | 16 | 2.7 | 2452 | 94 | AF273685   | c 692 | 16 | 2.7 | 6213  | 7  | BTU02285   | U02285 Bos taurus   |
| C 620 | 16 | 2.7 | 2472 | 89 | AF151685   | c 693 | 16 | 2.7 | 6396  | 7  | BTU02285   | J01448 E. coli malB |
| C 621 | 16 | 2.7 | 2493 | 88 | AF000430   | c 694 | 16 | 2.7 | 6545  | 2  | ECOMALB    | AC014309 Drosophi   |
| C 622 | 16 | 2.7 | 2512 | 58 | XU68724    | c 695 | 16 | 2.7 | 7581  | 63 | AC014309   | AC014309 Drosophi   |
| C 623 | 16 | 2.7 | 2544 | 58 | AF037263   | c 696 | 16 | 2.7 | 8200  | 3  | STNMACYR   | L27063 Streptomyce  |
| C 624 | 16 | 2.7 | 2545 | 59 | SLI011838  | c 697 | 16 | 2.7 | 9323  | 2  | AF237894S1 | AF237894 Streptomy  |
| C 625 | 16 | 2.7 | 2610 | 9  | AX023369   | c 698 | 16 | 2.7 | 9551  | 9  | AR076233   | AR076233 Sequence   |
| C 626 | 16 | 2.7 | 2612 | 94 | AF273684   | c 699 | 16 | 2.7 | 9551  | 10 | I39845     | I39845 Sequence 93  |
| C 627 | 16 | 2.7 | 2661 | 15 | TRAGLUCS   | c 700 | 16 | 2.7 | 9551  | 97 | HUMT8RYAL  | L09190 Human trich  |
| C 628 | 16 | 2.7 | 2673 | 14 | PAM133148  | c 701 | 16 | 2.7 | 9910  | 1  | AE006387   | AE006387 Lactococc  |
| C 629 | 16 | 2.7 | 2684 | 6  | DMU23926   | c 702 | 16 | 2.7 | 10021 | 1  | AE002537   | AE002537 Neisseria  |
| C 630 | 16 | 2.7 | 2689 | 1  | AF128272   | c 703 | 16 | 2.7 | 10114 | 3  | U32812     | U32812 Haemophilus  |
| C 631 | 16 | 2.7 | 2691 | 6  | DMU23923   | c 704 | 16 | 2.7 | 10130 | 1  | AE002085   | AE002085 Deinococc  |
| C 632 | 16 | 2.7 | 2691 | 6  | DMU23927   | c 705 | 16 | 2.7 | 10307 | 1  | AE004366   | AE004366 Vibrio ch  |
| C 633 | 16 | 2.7 | 2691 | 6  | DMU23933   | c 706 | 16 | 2.7 | 10338 | 1  | AE006005   | AE006005 Caulobact  |
| C 634 | 16 | 2.7 | 2707 | 6  | DSU23930   | c 707 | 16 | 2.7 | 10392 | 1  | AE004399   | AE004399 Vibrio ch  |
| C 635 | 16 | 2.7 | 2708 | 6  | DMU23928   | c 708 | 16 | 2.7 | 10437 | 5  | AF310159   | AF310159 Drosophi   |
| C 636 | 16 | 2.7 | 2708 | 6  | DMU23931   | c 709 | 16 | 2.7 | 10458 | 1  | AE002440   | AE002440 Neisseria  |
| C 637 | 16 | 2.7 | 2708 | 6  | DMU23932   | c 710 | 16 | 2.7 | 10905 | 1  | AE001881   | AE001881 Deinococc  |
| C 638 | 16 | 2.7 | 2709 | 6  | DMU23929   | c 711 | 16 | 2.7 | 10529 | 1  | AE005636   | AE005636 Escherich  |
| C 639 | 16 | 2.7 | 2719 | 6  | DMU23924   | c 712 | 16 | 2.7 | 10619 | 1  | AE005683   | AE005683 Caulobact  |
| C 640 | 16 | 2.7 | 2720 | 6  | DMU23925   | c 713 | 16 | 2.7 | 10807 | 1  | AE002451   | AE002451 Neisseria  |
| C 641 | 16 | 2.7 | 2772 | 89 | AK002127   | c 714 | 16 | 2.7 | 11108 | 63 | AC015358   | AC015358 Drosophi   |
| C 642 | 16 | 2.7 | 2776 | 91 | BC004237   | c 715 | 16 | 2.7 | 11137 | 63 | AC014837   | AC014837 Drosophi   |
| C 643 | 16 | 2.7 | 2823 | 2  | ECOHSD     | c 716 | 16 | 2.7 | 11158 | 1  | AE004682   | AE004682 Pseudomon  |
| C 644 | 16 | 2.7 | 2916 | 8  | CHRCMPOPLF | c 717 | 16 | 2.7 | 11414 | 1  | AE005666   | AE005666 Escherich  |
| C 645 | 16 | 2.7 | 2932 | 93 | HSMB01716  | c 718 | 16 | 2.7 | 11553 | 1  | AE002026   | AE002026 Deinococc  |
| C 646 | 16 | 2.7 | 3045 | 9  | A96458     | c 719 | 16 | 2.7 | 11579 | 1  | AE004565   | AE004565 Pseudomon  |
| C 647 | 16 | 2.7 | 3045 | 9  | A96458     | c 720 | 16 | 2.7 | 11613 | 1  | AE005650   | AE005650 Escherich  |
| C 648 | 16 | 2.7 | 3055 | 94 | AF273683   | c 721 | 16 | 2.7 | 11725 | 13 | AF180355   | AF180355 Brassica   |
| C 649 | 16 | 2.7 | 3216 | 3  | SCU51332   | c 722 | 16 | 2.7 | 12088 | 1  | AE000489   | AE000489 Escherich  |
| C 650 | 16 | 2.7 | 3226 | 91 | BC000136   | c 723 | 16 | 2.7 | 13000 | 2  | BSTYRABCD  | Y15234 Bacillus su  |
| C 651 | 16 | 2.7 | 3233 | 6  | RNND4P     | c 724 | 16 | 2.7 | 13364 | 7  | AF171666   | AF171666 Bos tauru  |
| C 652 | 16 | 2.7 | 3331 | 95 | DM6074     | c 725 | 16 | 2.7 | 13579 | 1  | AE005061   | AE005061 Halobacte  |
| C 653 | 16 | 2.7 | 3331 | 9  | AR093958   | c 726 | 16 | 2.7 | 13632 | 1  | AF135170   | AF135170 Yersinia   |
| C 654 | 16 | 2.7 | 3331 | 9  | AR093959   | c 727 | 16 | 2.7 | 14021 | 1  | AE005820   | AE005820 Caulobact  |
| C 655 | 16 | 2.7 | 3331 | 10 | E15640     | c 728 | 16 | 2.7 | 14372 | 63 | AC012930   | AC012930 Drosophi   |
| C 656 | 16 | 2.7 | 3381 | 8  | S63276     | c 729 | 16 | 2.7 | 14674 | 1  | AE000476   | AE000476 Escherich  |
| C 657 | 16 | 2.7 | 3444 | 6  | CHKMYLCC   | c 730 | 16 | 2.7 | 14720 | 1  | AE005056   | AE005056 Halobacte  |
| C 658 | 16 | 2.7 | 3453 | 6  | DMU76378   | c 731 | 16 | 2.7 | 15052 | 1  | AF055579   | AF055579 Streptomy  |
| C 659 | 16 | 2.7 | 3492 | 3  | RCSOR      | c 732 | 16 | 2.7 | 15294 | 1  | AE000753   | AE000753 Aquifex a  |
| C 660 | 16 | 2.7 | 3500 | 3  | SERORF1    | c 733 | 16 | 2.7 | 15898 | 2  | AX024393   | AX024393 Sequence   |
| C 661 | 16 | 2.7 | 3600 | 14 | NEUFJDA    | c 734 | 16 | 2.7 | 15898 | 9  | AX024286   | AX024286 Sequence   |
| C 662 | 16 | 2.7 | 3621 | 85 | AB033116   | c 735 | 16 | 2.7 | 15999 | 15 | SPAC142    | SPAC142 S. pombe c  |
| C 663 | 16 | 2.7 | 3682 | 89 | AK001713   | c 736 | 16 | 2.7 | 16034 | 1  | AE001057   | AE001057 Archaeogl  |
| C 664 | 16 | 2.7 | 3747 | 14 | BEPAT1     | c 737 | 16 | 2.7 | 16310 | 93 | HSTNFBX    | Z15026 Homo saplen  |
| C 665 | 16 | 2.7 | 3845 | 94 | AF019043   | c 738 | 16 | 2.7 | 16890 | 12 | AC007133   | AC007133 Arbidops   |



|     |    |     |       |    |            |                     |     |    |     |        |    |           |                      |
|-----|----|-----|-------|----|------------|---------------------|-----|----|-----|--------|----|-----------|----------------------|
| 739 | 16 | 2.7 | 17063 | 85 | AB031007   | AB031007 Homo sapi  | 812 | 16 | 2.7 | 52797  | 11 | AF068845  | AF068845 Mycobacte   |
| 740 | 16 | 2.7 | 17286 | 91 | D49493     | D49493 Human gene   | 813 | 16 | 2.7 | 55700  | 65 | AC017867  | AC017867 Drosophill  |
| 741 | 16 | 2.7 | 18221 | 64 | AC017207   | AC017207 Drosophill | 814 | 16 | 2.7 | 55699  | 60 | AC008776  | AC008776 Homo sapi   |
| 742 | 16 | 2.7 | 18510 | 65 | AC017804   | AC017804 Drosophill | 815 | 16 | 2.7 | 57214  | 65 | AC019870  | AC019870 Homo sapi   |
| 743 | 16 | 2.7 | 20400 | 13 | AF271736S1 | AF271736 Englena g  | 816 | 16 | 2.7 | 57306  | 4  | AC005416  | AC005416 Drosophill  |
| 744 | 16 | 2.7 | 20413 | 85 | AC004631   | AC004631 Homo sapi  | 817 | 16 | 2.7 | 57906  | 14 | NCB7219   | NCB7219 Neurospor    |
| 745 | 16 | 2.7 | 20823 | 85 | CELT24H7   | U28940 Caenorhabdi  | 818 | 16 | 2.7 | 58220  | 78 | AC091188  | AC091188 Homo sapi   |
| 746 | 16 | 2.7 | 21040 | 13 | AF271738S2 | AF271739 Englena g  | 819 | 16 | 2.7 | 59264  | 75 | AC018278  | AC018278 Homo sapi   |
| 747 | 16 | 2.7 | 21721 | 9  | AX000057   | AX000057 Sequence   | 820 | 16 | 2.7 | 59747  | 89 | AF119117  | AF119117 Homo sapi   |
| 748 | 16 | 2.7 | 22789 | 3  | SC2A11     | AL031184 Streptomy  | 821 | 16 | 2.7 | 60040  | 4  | AC005128  | AC005128 Drosophill  |
| 749 | 16 | 2.7 | 22898 | 6  | CELF35A5   | U46675 Caenorhabdi  | 822 | 16 | 2.7 | 60966  | 85 | AC003030  | AC003030 Homo sapi   |
| 750 | 16 | 2.7 | 22976 | 9  | AX000035   | AX000035 Sequence   | 823 | 16 | 2.7 | 61133  | 86 | AC005838  | AC005838 Homo sapi   |
| 751 | 16 | 2.7 | 23187 | 10 | AX100598   | AX100598 Sequence   | 824 | 16 | 2.7 | 61845  | 78 | AC0090837 | AC0090837 Homo sapi  |
| 752 | 16 | 2.7 | 23222 | 3  | SCGH18     | AL359572 Streptomy  | 825 | 16 | 2.7 | 63397  | 63 | AC014103  | AC014103 Drosophill  |
| 753 | 16 | 2.7 | 23952 | 6  | CEP29D10   | Z75952 Caenorhabdi  | 826 | 16 | 2.7 | 63997  | 90 | AL353604  | AL353604 Human DNA   |
| 754 | 16 | 2.7 | 24700 | 3  | SC68       | AL033654 Streptomy  | 827 | 16 | 2.7 | 64120  | 63 | AC014287  | AC014287 Drosophill  |
| 755 | 16 | 2.7 | 25359 | 6  | CEFO2D10   | Z67990 Caenorhabdi  | 828 | 16 | 2.7 | 65318  | 77 | AC084339  | AC084339 Homo sapi   |
| 756 | 16 | 2.7 | 25459 | 3  | SGA06985   | AJ006985 Streptomy  | 829 | 16 | 2.7 | 65591  | 67 | AC023031  | AC023031 Homo sapi   |
| 757 | 16 | 2.7 | 25657 | 63 | AC014155   | AC014155 Streptomy  | 830 | 16 | 2.7 | 67392  | 65 | AC018284  | AC018284 Drosophill  |
| 758 | 16 | 2.7 | 27300 | 3  | SCD39      | AL392146 Streptomy  | 831 | 16 | 2.7 | 67823  | 70 | AC026579  | AC026579 Homo sapi   |
| 759 | 16 | 2.7 | 27887 | 3  | SCE50      | AL163672 Streptomy  | 832 | 16 | 2.7 | 68334  | 61 | AC010563  | AC010563 Drosophill  |
| 760 | 16 | 2.7 | 28519 | 93 | HSJ563E14  | AL117379 Human DNA  | 833 | 16 | 2.7 | 68418  | 65 | AC018090  | AC018090 Drosophill  |
| 761 | 16 | 2.7 | 29552 | 6  | CELF45F2   | U64845 Caenorhabdi  | 834 | 16 | 2.7 | 68626  | 60 | AC006168  | AC006168 Drosophill  |
| 762 | 16 | 2.7 | 31392 | 6  | LMFL5852   | AL499614 Leishmani  | 835 | 16 | 2.7 | 68986  | 78 | AC091053  | AC091053 Homo sapi   |
| 763 | 16 | 2.7 | 31720 | 93 | HSJ196E3   | Z68277 Human DNA s  | 836 | 16 | 2.7 | 68986  | 78 | AC091053  | AC091053 Homo sapi   |
| 764 | 16 | 2.7 | 32424 | 6  | CEZK131    | Z83245 Caenorhabdi  | 837 | 16 | 2.7 | 69274  | 75 | AC084228  | AC084228 Homo sapi   |
| 765 | 16 | 2.7 | 32610 | 65 | AC019840   | AC019840 Drosophill | 838 | 16 | 2.7 | 71512  | 94 | AF234171  | AF234171 Mus muscu   |
| 766 | 16 | 2.7 | 33016 | 14 | SCCHXIVL   | X96722 S.cerevisia  | 839 | 16 | 2.7 | 71707  | 65 | AC018210  | AC018210 Drosophill  |
| 767 | 16 | 2.7 | 33500 | 61 | AC011016   | AC011016 Leishmani  | 840 | 16 | 2.7 | 72593  | 66 | AC021519  | AC021519 Homo sapi   |
| 768 | 16 | 2.7 | 33818 | 3  | MTCY78     | Z77165 Mycobacteri  | 841 | 16 | 2.7 | 73907  | 65 | AC018257  | AC018257 Drosophill  |
| 769 | 16 | 2.7 | 34074 | 3  | SCE81      | AL133171 Streptomy  | 842 | 16 | 2.7 | 75588  | 90 | AL356742  | AL356742 Human DNA   |
| 770 | 16 | 2.7 | 34220 | 63 | AC014160   | AC014160 Drosophill | 843 | 16 | 2.7 | 76179  | 63 | AC012976  | AC012976 Homo sapi   |
| 771 | 16 | 2.7 | 34644 | 1  | AF080235   | AP080235 Streptomy  | 844 | 16 | 2.7 | 76693  | 93 | HSJ475B7  | HSJ475B7 Homo sapi   |
| 772 | 16 | 2.7 | 35042 | 6  | LMFL3665   | AL359775 Leishmani  | 845 | 16 | 2.7 | 76748  | 65 | AC000400  | AC000400 Genomic s   |
| 773 | 16 | 2.7 | 35437 | 3  | SCF43A     | AL096837 Streptomy  | 846 | 16 | 2.7 | 80167  | 65 | AC020038  | AC020038 Drosophill  |
| 774 | 16 | 2.7 | 35722 | 63 | AC015427   | AC015427 Drosophill | 847 | 16 | 2.7 | 80327  | 72 | AC055889  | AC055889 Homo sapi   |
| 775 | 16 | 2.7 | 35922 | 85 | AC000045   | AC000045 Homo sapi  | 848 | 16 | 2.7 | 81662  | 12 | AB008265  | AB008265 Arabidops   |
| 776 | 16 | 2.7 | 36148 | 60 | AC002321   | AC002321 Homo sapi  | 849 | 16 | 2.7 | 83059  | 91 | AP001435  | AP001435 Homo sapi   |
| 777 | 16 | 2.7 | 37730 | 3  | SCE9       | AL049841 Streptomy  | 850 | 16 | 2.7 | 84056  | 91 | AC002121  | AC002121 Genomic s   |
| 778 | 16 | 2.7 | 37799 | 6  | CELC05E11  | U53338 Caenorhabdi  | 851 | 16 | 2.7 | 84702  | 12 | AB018114  | AB018114 Arabidops   |
| 779 | 16 | 2.7 | 37840 | 85 | AC018301   | AC018301 Drosophill | 852 | 16 | 2.7 | 85095  | 4  | AC004573  | AC004573 Drosophill  |
| 780 | 16 | 2.7 | 38000 | 67 | AC008974   | AC008974 Homo sapi  | 853 | 16 | 2.7 | 85138  | 89 | AL137224  | AL137224 Human DNA   |
| 781 | 16 | 2.7 | 38177 | 6  | LMFL5213   | AL583332 Leishmani  | 854 | 16 | 2.7 | 85165  | 14 | NC99H12   | NC99H12 Neurospor    |
| 782 | 16 | 2.7 | 38702 | 4  | AC018661   | AC018661 Leishmani  | 855 | 16 | 2.7 | 85402  | 92 | HS31B8    | HS31B8 Homo sapi     |
| 783 | 16 | 2.7 | 38785 | 92 | HS695020B  | AL049853 Human DNA  | 856 | 16 | 2.7 | 85490  | 67 | AC022957  | AC022957 Homo sapi   |
| 784 | 16 | 2.7 | 39329 | 85 | AC004091   | AC004091 Human Cos  | 857 | 16 | 2.7 | 87210  | 12 | AB011485  | AB011485 Arabidops   |
| 785 | 16 | 2.7 | 39741 | 3  | SC8E7      | AL591338 Streptomy  | 858 | 16 | 2.7 | 87925  | 85 | AC005318  | AC005318 Homo sapi   |
| 786 | 16 | 2.7 | 39796 | 97 | AX037570   | AX037570 Sequence   | 859 | 16 | 2.7 | 88307  | 92 | AC009982  | AC009982 Drosophill  |
| 787 | 16 | 2.7 | 40007 | 3  | HSU35G3    | Z93848 Human DNA s  | 860 | 16 | 2.7 | 89301  | 30 | HS34B20   | HS34B20 Homo sapi    |
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## ALIGNMENTS

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ACCESSION AR047920  
VERSION AR047920.1 GI:5970263

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 3402)  
AUTHORS Paranhos-Baccala,G., Lesenechal,M. and Jolivet,M.  
TITLE Trypanosoma cruzi antigen, gene encoding therefor and methods of  
detecting and treating chagas disease  
JOURNAL Patent: US 5820864-A I 13-OCT-1998;  
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DEFINITION Sequence 9 from Patent WO9605312.
ACCESSION A48918
VERSION A48918.1 GI:2302577
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Paranhos-Baccala,G., Lesenechal,M. and Jolivet,M.
TITLE NOVEL TRYPANOSOMA CRUZI ANTIGEN, AND GENE CODING THEREFOR, THEIR APPLICATION TO THE DETECTION OF CHAGAS' DISEASE
JOURNAL BIO MERIEUX (FR)
COMMENT Other publication CA 2173957 960222
Other publication AU 3169195 960307
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DEFINITION Sequence 9 from patent US 5820864.
ACCESSION AR047927
VERSION AR047927.1 GI:5970270
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Paranhos-Baccala,G., Lesenechal,M. and Jolivet,M.
TITLE Trypanosoma cruzi antigen, gene encoding therefor and methods of detecting and treating chagas disease
JOURNAL Patent: US 5820864-A 9 13-OCT-1998;
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 ORGANISM Neisseria meningitidis Z2491.  
 Bacteria; Proteobacteria; beta subdivision; Neisseriaceae;  
 Neisseria.  
 REFERENCE 1 (bases 1 to 331801)  
 AUTHORS Parkhill,J., Achtman,M., James,K.D., Bentley,S.D., Churcher,C., Klee,S.R., Morelli,G., Basham,D., Brown,D., Chillingworth,T., Davies,R.M., Davis,P., Devlin,K., Felwell,T., Hamlin,N., Holtrop,S., Jagels,K., Leather,S., Moule,S., Mungall,K., Quail,M.A., Rajandream,M.A., Rutherford,K.M., Simmonds,M., Skellon,J., Whitehead,S., Spratt,B.G. and Barrell,B.G.  
 TITLE Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491  
 JOURNAL Nature 404 (6777), 502-506 (2000)  
 MEDLINE 20222556  
 REFERENCE 2 (bases 1 to 331801)  
 AUTHORS Parkhill,J.  
 TITLE Direct Submission  
 JOURNAL Submitted (30-MAR-2000) Submitted on behalf of the Neisseria sequencing team, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk

COMMENTS  
 Notes: Details of N. meningitidis sequencing at the Sanger Centre are available on the World Wide Web.  
 (URL, [http://www.sanger.ac.uk/Projects/N\\_meningitidis/](http://www.sanger.ac.uk/Projects/N_meningitidis/)).  
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 /note="NMA1045, clpA, probable ATP-dependent protease ATP-binding protein, len: 759 aa; similar to many e.g. SW:CLPA.ECOLI (EMBL:M31045), clpA, Escherichia coli ATP-dependent Clp protease ATP-binding subunit (738 aa), fasta scores: E(): 0.56.2% identity in 762 aa overlap. Similar to NMA1683, fasta scores: E(): 0.37.2% identity in 844 aa overlap. Contains Pfam match to entry PF00495 clpA\_B, Chaperonin clpA/B, PS00870 Chaperonins clpA/B signature 1, PS00871 Chaperonins clpA/B signature 2 and two PS00017 ATP/GTP-binding site motif A (P-loop)"  
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Shinn, P., Brooks, S., Buehler, E., Chao, O., Johnson-Hopson, C.,



TITLE  
JOURNML  
REFERENCE  
AUTHORS

Unpublished  
2 (bases 1 to 91470)  
Ecker,J.R.

Direct Submission  
Submitted (07-OCT-1999) Arabidopsis thaliana Genome Center,  
Department of Biology, University of Pennsylvania, 38th Street and  
Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA  
3 (bases 1 to 91470)  
Ecker,J.R.

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Submitted (09-NOV-1999) Arabidopsis thaliana Genome Center,  
Department of Biology, University of Pennsylvania, 38th Street and  
Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA  
4 (bases 1 to 91470)  
Chao,Q., Brooks,S., Buehler,E., Johnson-Hopson,C., Khan,S., Kim,C.,  
Shinn,P., Altafi,H., Bel,B., Chin,C., Chlou.J., Choi,E., Conn,L.,  
Conway,A., Gonzalez,A., Hansen,N., Howling,B., Koo,T., Lam,B.,  
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Nguyen,M., Palm,C., Pham,P., Sakano,H., Schwartz,J., Southwick,A.,  
Thaverl,A., Toriumi,M., Vaysberg,M., Yu,G., Davis,R.,  
Federspiel,N., Theologis,A. and Ecker,J.

Direct Submission  
Submitted (15-DEC-1999) Arabidopsis thaliana Genome Center,  
Department of Biology, University of Pennsylvania, 38th and  
Hamilton Walk, Philadelphia, PA 19104-6018, USA  
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Cheuk,R., Brooks,S., Buehler,E., Chao,Q., Johnson-Hopson,C.,  
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Direct Submission  
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Department of Biology, University of Pennsylvania, 38th and  
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Department of Biology, University of Pennsylvania, 38th and  
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COMMENT  
FEATURES  
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TITLE  
JOURNML  
REFERENCE  
AUTHORS

Unpublished  
2 (bases 1 to 91470)  
Ecker,J.R.

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OY 212 cttctgcgtcgtcgtcgtc 231  
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 Db 42747 CTTCTGCCGTCGTCATCC 42728

RESULT 9  
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 LOCUS Drosophila melanogaster, \*\*\* SEQUENCING IN PROGRESS \*\*\*, in ordered  
 DEFINITION pieces.  
 AC017643  
 AC017643.1 GI:6554354  
 HTG; HTGS\_PHRASE2.  
 SOURCE fruit fly.  
 ORGANISM Drosophila melanogaster  
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 1 (bases 1 to 177816)  
 Adams, M. and Venter, J. C.  
 Direct Submission  
 Submitted (10-DEC-1999) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD, USA  
 This sequence was identified as CDM:10211585 by the submitter.  
 For more information on this record e-mail to fly@celera.com.  
 \* NOTE: This is a 'working draft' sequence.  
 \* This sequence will be replaced

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Query Match 3.4%; Score 20; DB 65; Length 177816;  
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 AC007697  
 AC007697.5 GI:13270541  
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 KEYWORDS fruit fly.  
 SOURCE Drosophila melanogaster  
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 1 (bases 1 to 194897)  
 Celniker, S. E., Adams, M. D., Krommiller, B., Tyler, D., Wan, K. H.,  
 Holt, R. A., Evans, C. A., Gocayne, J. D., Amanatides, P. G., Brandon, R. C.,  
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 Sequencing of Drosophila chromosome 2R, region 54D4-54E7  
 Unpublished  
 2 (bases 1 to 194897)  
 Celniker, S. E., Agbayani, A., Arcaina, T. T., Baxter, E., Blazek, R. G.,  
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 Doyle, C. M., Fartan, D. E., Galle, R., George, R. A., Harris, N. L.,  
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 Rubin, G. M.  
 Direct Submission  
 Submitted (02-JUN-1999) Drosophila Genome Center, Lawrence Berkeley  
 Laboratory, MS 64-121, Berkeley, CA 94720, USA  
 On Mar 10, 2001 this sequence version replaced gi:15670564.  
 Sequence submitted by:  
 Berkeley Drosophila Genome Project  
 Lawrence Berkeley National Laboratory, MS 64-121  
 Berkeley, CA 94720  
 This sequence was assembled using end sequences from a whole genome  
 shotgun and from subclones of this BAC and its neighboring clones.  
 For further information about this sequence, including its location  
 and relationship to other sequences, please visit our sequence  
 archive web site (<http://www.fruitfly.org/sequence/>) or send email  
 to [bdgpf@fruitfly.berkeley.edu](mailto:bdgpf@fruitfly.berkeley.edu)  
 Location/Qualifiers

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ORIGIN

Query Match      3.4%; Score 20; DB 4; Length 194897;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION      of 52, complete sequence.
ACCESSION      AE003802 AE002787
KEYWORDS
VERSION      AE003802.2 GI:10727480
SOURCE      HTG.
ORGANISM      fruit fly.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephyridiidea; Drosophilidae; Drosophila.
1 (bases 1 to 262395)
Adams,M.D., Celniker,S.E., Holt,R.A., Evans,C.A., Gocayne,J.D.,
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| TITLE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | JOURNAL | MEDLINE                      | REFERENCE             | AUTHORS                                                           | JOURNAL                 | COMMENT                                                 | FEATURES                                                   |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------|------------------------------|-----------------------|-------------------------------------------------------------------|-------------------------|---------------------------------------------------------|------------------------------------------------------------|
| Zhong,F.N., Zhong,W., Zhou,X., Zhu,S., Zhu,X., Smith,H.O., Gibbs,R.A., Myers,E.W., Rubin,G.M. and Venter,J.C.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | Science | 287 (5461), 2185-2193 (2000) | 2 (bases 1 to 262395) | Adams,M.D., Celniker,S.E., Gibbs,R.A., Rubin,G.M. and Venter,C.J. | Submitted (21-MAR-2000) | Celera Genomics, 45 West Gude Drive, Rockville, MD, USA | On Oct 9, 2000, this sequence version replaced gi:7302706. |
| Location/Qualifiers                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |         |                              |                       |                                                                   |                         |                                                         |                                                            |
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 50 ggcctcgtcgtacatgctc 69
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DB 140906 GCGTCTGCTGCTACATGTCG 140925

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RESULT 12
D89210/c D89210 1152 bp mRNA PLN 13-MAR-1998
LOCUS Schizosaccharomyces pombe mRNA, partial cds, clone: SY 1164.
DEFINITION D89210
ACCESSION D89210
VERSION D89210.1 GI:1749627
KEYWORDS
SOURCE Schizosaccharomyces pombe (strain:PR745) cDNA to mRNA,
clone:lib:library of H. Nojima clone:SY1164.
ORGANISM Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
1 (bases 1 to 1152)
Yoshioaka,S.
Direct Submission
Submitted (15-NOV-1996) to the DDBJ/EMBL/GenBank databases. Sachio
Yoshioaka, Tsukita Cell Axis Project ERATO JST, Kyoto Research Park;
17 Chidouji Minamimachi, Shimokyo-ku, Kyoto, Kyoto 600, Japan
(E-mail: syoshi@cell.tsukita.jst.go.jp, Tel:+81-75-315-7913,
Fax:+81-75-315-6420)
2 (sites)
REFERENCE Yoshioaka,S., Kato,K., Nakai,K., Okayama,H. and Nojima,H.
AUTHORS Identification of open reading frames in Schizosaccharomyces pombe
TITLE cDNAs
JOURNAL DNA Res. 4 (6), 363-369 (1997)
MEDLINE 98162722
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|                                                                                                                                                                                                                                                                             |                                                                                                                                                                                                                                                                                                                                                                                                   |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| RESULT                                                                                                                                                                                                                                                                      | 13                                                                                                                                                                                                                                                                                                                                                                                                |
| LOCUS                                                                                                                                                                                                                                                                       | AF273691                                                                                                                                                                                                                                                                                                                                                                                          |
| DEFINITION                                                                                                                                                                                                                                                                  | Mus musculus ribosome receptor isoform mRNA, complete cds,                                                                                                                                                                                                                                                                                                                                        |
| ACCESSION                                                                                                                                                                                                                                                                   | AF273691                                                                                                                                                                                                                                                                                                                                                                                          |
| VERSION                                                                                                                                                                                                                                                                     | AF273691.1                                                                                                                                                                                                                                                                                                                                                                                        |
| KEYWORDS                                                                                                                                                                                                                                                                    | GI:13094692                                                                                                                                                                                                                                                                                                                                                                                       |
| SOURCE                                                                                                                                                                                                                                                                      | 'house mouse.'                                                                                                                                                                                                                                                                                                                                                                                    |
| ORGANISM                                                                                                                                                                                                                                                                    | Mus musculus<br>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;<br>Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.                                                                                                                                                                                                                                                    |
| REFERENCE                                                                                                                                                                                                                                                                   | 1 (bases 1 to 1279)                                                                                                                                                                                                                                                                                                                                                                               |
| AUTHORS                                                                                                                                                                                                                                                                     | Kim,Y.-J., Lee,M.-C., Kim,S. and Chun,J.-Y.                                                                                                                                                                                                                                                                                                                                                       |
| TITLE                                                                                                                                                                                                                                                                       | Identification and characterization of multiple isoforms of a mouse<br>ribosome receptor                                                                                                                                                                                                                                                                                                          |
| JOURNAL                                                                                                                                                                                                                                                                     | Gene 261 (2), 337-344 (2000)                                                                                                                                                                                                                                                                                                                                                                      |
| PUBMED                                                                                                                                                                                                                                                                      | 11167022                                                                                                                                                                                                                                                                                                                                                                                          |
| REFERENCE                                                                                                                                                                                                                                                                   | 2 (bases 1 to 1279)                                                                                                                                                                                                                                                                                                                                                                               |
| AUTHORS                                                                                                                                                                                                                                                                     | Kim,Y.-J., Lee,M.-C., Kim,S. and Chun,J.-Y.                                                                                                                                                                                                                                                                                                                                                       |
| TITLE                                                                                                                                                                                                                                                                       | Direct Submission                                                                                                                                                                                                                                                                                                                                                                                 |
| JOURNAL                                                                                                                                                                                                                                                                     | Submitted (01-JUN-2000) Kumho Life and Environmental Science<br>Laboratory, 572 Sangam-Dong, Kwangsan-Gu, Kwangju 506-712, Korea                                                                                                                                                                                                                                                                  |
| FEATURES                                                                                                                                                                                                                                                                    | Location/Qualifiers                                                                                                                                                                                                                                                                                                                                                                               |
| source                                                                                                                                                                                                                                                                      | 1..1279                                                                                                                                                                                                                                                                                                                                                                                           |
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| BASE COUNT                                                                                                                                                                                                                                                                  | 357 a 309 c 346 g 267 t                                                                                                                                                                                                                                                                                                                                                                           |
| ORIGIN                                                                                                                                                                                                                                                                      |                                                                                                                                                                                                                                                                                                                                                                                                   |
| Query Match                                                                                                                                                                                                                                                                 | 3.2%; Score 19; DB 94; Length 1279;                                                                                                                                                                                                                                                                                                                                                               |
| Best Local Similarity                                                                                                                                                                                                                                                       | 100.0%; Pred. No. 68;                                                                                                                                                                                                                                                                                                                                                                             |
| Matches                                                                                                                                                                                                                                                                     | 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                                                                                                                                                                                                                                                                                                                                               |
| Oy                                                                                                                                                                                                                                                                          | 115 cagcagccgacgcacaaaaa 133<br>                                                                                                                                                                                                                                                                                                                                                                  |
| Db                                                                                                                                                                                                                                                                          | 791 CAGCAGCCAGCGCAAAAAA 809                                                                                                                                                                                                                                                                                                                                                                       |
| RESULT                                                                                                                                                                                                                                                                      | 14                                                                                                                                                                                                                                                                                                                                                                                                |
| LOCUS                                                                                                                                                                                                                                                                       | AE005021/c                                                                                                                                                                                                                                                                                                                                                                                        |
| DEFINITION                                                                                                                                                                                                                                                                  | AE005021 10128 bp DNA BCT 12-FEB-2001                                                                                                                                                                                                                                                                                                                                                             |
| ACCESSION                                                                                                                                                                                                                                                                   | Halobacterium sp. NNC-1 section 52 of 170 of the complete genome.<br>AE005021 AE004437                                                                                                                                                                                                                                                                                                            |
| VERSION                                                                                                                                                                                                                                                                     | AE005021.1                                                                                                                                                                                                                                                                                                                                                                                        |
| KEYWORDS                                                                                                                                                                                                                                                                    | GI:10580357                                                                                                                                                                                                                                                                                                                                                                                       |
| SOURCE                                                                                                                                                                                                                                                                      | 'Halobacterium sp. NRC-1.<br>Halobacterium sp. NRC-1<br>Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;<br>Halobacterium.'                                                                                                                                                                                                                                                             |
| ORGANISM                                                                                                                                                                                                                                                                    |                                                                                                                                                                                                                                                                                                                                                                                                   |
| REFERENCE                                                                                                                                                                                                                                                                   | 1 (bases 1 to 10128)                                                                                                                                                                                                                                                                                                                                                                              |
| AUTHORS                                                                                                                                                                                                                                                                     | Ng,W.V., Kennedy,S.P., Mahairas,G.G., Bergquist,B., Pan,M.,<br>Shukla,H.D., Wasky,S.R., Balliga,N., Thorsson,V., Sbrogna,J.,<br>Swartzell,S., Leir,D., Hall,J., Dahl,T.A., Weili,R., Goo,Y.A.,<br>Leithausen,B., Keller,K., Cruz,R., Danson,M.J., Hough,D.W.,<br>Maddocks,D.G., Jablonski,P.E., Krebs,M.P., Angevine,C.M., Dale,H.,<br>Isenberger,T.A., Peck,R.F., Pohlschrod,M., Spudisich,J.L., |

| TITLE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | JOURNAL                             | PUBMED  | REFERENCE          | AUTHORS |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------|---------|--------------------|---------|
| Jung, K.-H., Alam, M., Freitas, T., Hou, S., Daniels, C.J., Dennis, P.P., Omer, A.D., Ehardt, H., Lowe, T.M., Liang, P., Riley, M., Hood, L. and Dassarma, S.                                                                                                                                                                                                                                                                                                                                                                                                               | Proc. Natl. Acad. Sci. USA          | 97 (42) | 12176-12181 (2000) |         |
| 2 (bases 1 to 10128)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |                                     |         |                    |         |
| Ng, W.-Y., Kennedy, S.P., Mahatras, G.G., Berquist, B., Pan, M., Shukla, H.D., Lasky, S.R., Balliga, N., Thorsson, V., Shrogha, J., Swartzell, S., Weir, D., Hall, J., Dahl, T.A., Weltl, R., Goo, Y.A., Leitnauer, S.B., Keller, K., Cruz, R., Danson, M.J., Hough, D.W., Maddocks, D.G., Jablonski, P.E., Krebs, M.P., Angewine, C.M., Dale, H., Isenberger, T.A., Peck, R.F., Pohlschod, M., Spudis, J.L., Jung, K.-H., Alam, M., Freitas, T., Hou, S., Daniels, C.J., Dennis, P.P., Omer, A.D., Ehardt, H., Lowe, T.M., Liang, P., Riley, M., Hood, L. and Dassarma, S. | Direct Submission                   |         |                    |         |
| Submitted (14-JUL-2000)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | Institute for Systems Biology       | 4225    |                    |         |
| Roosevelt Way NE, Seattle, WA 98105, USA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |                                     |         |                    |         |
| Location/Qualifiers                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                     |         |                    |         |
| 1. 10128                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | /organism="Halobacterium sp. NRC-1" |         |                    |         |
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| SDAEVDAASGTGTRMPDQGEDDLAAVAQPRFAAGALCETDEQDGLADLAA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |                                     |         |                    |         |
| VSERTSAGLDDADADDTLTSLVAIDSLSDEGVADAQEMDLSVRKLRREGTYEWA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |                                     |         |                    |         |
| DKHNDPEPTALKQWQKQNVEMTILICMEHLDEEYVARDGSPNLTALKAIVGETSGESQV                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |                                     |         |                    |         |
| GOLARRDKPAIEVQKIGVEDGLEHIEEYVARDGSPNLTALKAIVGETSGESQV                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |                                     |         |                    |         |
| VAQDLRADVRSQAARALGLIGDTRAIAPLVDIIESDSEFTVRSASAAALVQIGTE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |                                     |         |                    |         |
| ALEAAEYVADRRYVEQETRAVTAALDRDAADASTGSA"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |                                     |         |                    |         |
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| LIVGAGFVASAVRGLITATVDTGHEHTEGVOTTLAATLAAAGLVAGVEQIVTGAA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |                                     |         |                    |         |
| GLVAVLVSTIEYEDLLVLDALAMGVQAGAVAPALAGAPKALFGMGALVLPAP                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |                                     |         |                    |         |
| RFVWRA"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |                                     |         |                    |         |
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| WQNVDEGGNISPQATTEVTLVPGEYTYICIRHEGAGMGKLVVD"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                     |         |                    |         |

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AGYDEVGVPSOVVSEPPSHSGAAGSOAAPTTASHVYVYCCAAVADASTVCAVA  
FALAREVGHDPDVTYAGAVADGVPEPPADYRAAEVTRPGVGTATDAAAGLAIS  
TLVHAFSGDGEAGAFGLAELGDPEDPAARRLASAVLADATADAPCAADAVHHA  
LRPRATPDGMATVEGYADVLNAYMAAPGAGVALGVDRTAVLAMQAHAPSHA  
AVRAASLARRRGVADVPTAVPTARLRLDRATEPVALAVGTETALATTADANA  
VLPSVGTERRAAVTTLDSSDADAVIEFVGGGL"  
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HDSQIGIKRDEGVCTPPDYKLAIGCKVYTELLEHDAPELPEDPRNLEAVRL  
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/product="tRNA-Ala"  
6115. .6186  
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YTLKLDLLPADVVSMLVNETRGTVASTELAEGLSLADLAPWTTAAVPEBPGND  
SAVMTAEQSYRSPVLNDEPVALDEPVALDEPVALDEPVALDEPVALDEPVALDE  
ILNTGDEPVLDSNRFDAALTDLSIAVRNRTTATTVTSNGRYALSAAPHTDMVY  
TSVDTGEAFVADTVGQTVVAVLVAVSLAIVGIALGRHVTPKLRNRADIEEG  
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ADAVDQILIAOERMSDIDGILEFTDIAEONTMALNANIIEARADKDGDFAVANE  
VKDAEEETKQAAADIESEIOAVOAEETBEVADIRATSEHIDDGVSTKRRAAADIEDY  
DAIDANGIOETSDATDEQDADQOSVARRVDVADIOSHYTERADQVSAAEQSSAS  
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/note="yufN"  
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ETQAVTLAASSNPAYDLVCCVGFQADSLGESAAPQOEIVPTADASVASYVE  
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TASDIDVLAAYIGDFEVEAARTAAAMVADGADIVYHAAGAGVYLOAAQANGRA  
IGVSDQSRSNPRYADVLIAMVNRITDPVADTLEATIDGDLPGDVPYSLGLANNGVS  
VQVCTGCPAIPRTVTDALGCTREALVAGDITVTERPQSGGGGV"  
BASE COUNT 1353 a 3628 c 3425 g 1722 t  
ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 46;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 386 ggcgcgcacgcagcagcgc 404  
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DB 574 CCGCGCCACGACGAGGTC 556  
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RESULT 15  
AR083116 11873 bp DNA PAT 01-SEP-2000  
LOCUS AR083116  
DEFINITION Sequence 32 from patent US 5976803.  
ACCESSION AR083116  
VERSION AR083116.1 GI:10009906  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 11873)  
AUTHORS Meek,K.D.  
TITLE Genetic test for equine severe combined immunodeficiency disease  
JOURNALS Patent: US 5976803-A 32 02-NOV-1999;  
FEATURES Location/Qualifiers  
source 1..11873  
/organism="unknown"  
BASE COUNT 3585 a 2320 c 2669 g 3299 t  
ORIGIN  
Query Match 3.2%; Score 19; DB 9; Length 11873;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 211 acttcgcgcgtcgtcat 229  
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DB 6446 ACTTCTGCCGCTGTCAT 6428



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2337..5567
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CDS
2337..5567
/note="SPBC262.02"
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phosphate phosphatase (1107 aa), fasta scores: opt: 1630,
E():0, (39.0% identity in 1100 aa)"
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SKVCVSCVQVSGSIPIFMEOGQMGOKIDIPSEATRAFEKHFTSLIEEGPH
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FODKROETIDLLGLRIDQHPVILYDPIHEVYHNLKRENESEKNNKIFVAVN
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LNGCSTGPGVYVLRSGOIVGTALMIFKESCLDPIKNECTVKKTLGCVSGKQAY
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KKILFEELYNQROEVDAQSOTSYTLIDIASGAPNLPHLPANGVDIKIQPSSE
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GVPRNPITPVNPPPPPKRSSASQSRGDLASSPEBSISMKLV"
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6364..6378))
/gene="SPBC262.03c"
/note="SPBC262.03c, len:101, SIMILARITY:Saccharomyces
cerevisiae, S6B2_YEAST, protein transport protein sec61
beta 2 subunit., (88 aa), fasta scores: opt: 242,
E():2.1e-09, (46.3% identity in 82 aa)"
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beta 2 subunit-like"
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/db_xref="SPTREMBL:O43002"
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6050..6055
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6246..6251
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misc_feature
6314..6324
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CDS
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E():7.5e-17, (44.0% identity in 141 aa)
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/translation="MLRALGSRLLVAPRAVRSFQSLRPPREFTHKSKTPINS
PKLSSAGPVNOAIKANGVICSQOIPVANGVIEGTGDDYRQCLNIOEVLDEAGSS
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8092..8097
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8135..8149
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10752..10797,10835..11043,11090..11116))
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/note="SPBC262.06c, len:676, SIMILARITY:Drosophila
melanogaster, Q24253, beta-adaptin drosophila 1., (921
aa), fasta scores: opt: 1724, E():0, (45.2% identity in
3.2%; Score 19; DB 15; Length 36493;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 233 ctgcatcacccctgttc 251
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Db 27668 CTGCATCACCCCTGTTC 27686
RESULT 19
AC068903/c 82033 bp DNA 20-SEP-2000
LOCUS AC068903/c
DEFINITION Mus musculus chromosome 2 clone ct7-196d19 strain 129/Sv ES cell
line C77, complete sequence.
ACCESSION AC068903
VERSION AC068903.11 GI:9837949
KEYWORDS HTC.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 82033)
AUTHORS Shaull,S., Rahhal,R., Yao,Z., Richieth,K. and Roe,B.A.
TITLE Mus musculus Chromosome 2 BAC Clone ct7b-196d19
JOURNALS Unpublished
REFERENCE 2 (bases 1 to 82033)
AUTHORS Shaull,S., Rahhal,R., Yao,Z., Richieth,K. and Roe,B.A.
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TITLE Direct Submission  
JOURNAL Submitted (11-MAY-2000) Department Of Chemistry And Biochemistry,  
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,  
OK 73019, USA  
REFERENCE 3 (bases 1 to 82033)  
AUTHORS Shaull,S., Rahhal,R., Yao,Z., Rithidech,K. and Roe,B.A.  
JOURNAL Direct Submission  
Submitted (20-SEP-2000) Department Of Chemistry And Biochemistry,  
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,  
OK 73019, USA  
COMMENT On Aug 17, 2000 this sequence version replaced g1:9797790.  
FEATURES  
source location/Qualifiers  
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/organism="Mus musculus"  
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/db\_xref="taxon:10090"  
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/clone="ct7-196d19"  
/clone\_1lb="Caltech CITB-BAC library"  
BASE COUNT 23822 a 16503 c 15652 g 26056 t  
ORIGIN

Query Match 3.2%; Score 19; DB 94; Length 82033;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 537 gaaccacagagagaagaa 555  
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DB 61880 GAACCAACAGAGAGAA 61862

RESULT 20  
AC068952 95292 bp DNA ROD 18-AUG-2000  
LOCUS Mus musculus chromosome 2 clone ct7-254f1 strain 129/Sv ES cell  
DEFINITION line Cj7, complete sequence.  
ACCESSION AC068952  
VERSION AC068952.10 GI:9845112  
KEYWORDS HTG.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 95292)  
AUTHORS Shaull,S., Rahhal,R., Yao,Z., Rithidech,K. and Roe,B.A.  
JOURNAL Mus musculus Chromosome 2 BAC Clone cltb-254f1  
TITLE Unpublished  
AUTHORS 2 (bases 1 to 95292)  
JOURNAL Shaull,S., Rahhal,R., Yao,Z., Rithidech,K. and Roe,B.A.  
TITLE Direct Submission  
Submitted (13-MAY-2000) Department Of Chemistry And Biochemistry,  
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,  
OK 73019, USA  
REFERENCE 3 (bases 1 to 95292)  
AUTHORS Shaull,S., Rahhal,R., Yao,Z., Rithidech,K. and Roe,B.A.  
JOURNAL Direct Submission  
Submitted (18-AUG-2000) Department Of Chemistry And Biochemistry,  
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,  
OK 73019, USA  
COMMENT On Aug 18, 2000 this sequence version replaced g1:9795634.  
FEATURES  
source location/Qualifiers  
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BASE COUNT 28084 a 18825 c 18104 g 30279 t  
ORIGIN

Query Match 3.2%; Score 19; DB 94; Length 95292;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 537 gaaccacagagagaagaa 555  
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DB 76659 GAACCAACAGAGAGAA 76641

RESULT 21  
AL354832.1  
WPCOMMENT  
Sequence split into 4 fragments LOCUS AL354832 Accession AL354832  
Fragment Name Begin End  
AL354832\_0 1 110000  
AL354832.1 100001 210000  
AL354832.2 200001 310000  
AL354832\_3 300001 372955  
Continuation (2 of 4) of AL354832 from base 100001 (AL354832 Homo sapiens chromosome

Query Match 3.2%; Score 19; DB 79; Length 110000;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 215 ctgcgcgtgctgcatcccc 233  
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DB 66912 CTGCCGCTGCTGCATCCCC 66930

RESULT 22  
AC024591 111071 bp DNA HTG 18-JUL-2000  
LOCUS Homo sapiens chromosome 16 clone RP11-511G21, WORKING DRAFT  
DEFINITION SEQUENCE, 13 ordered pieces.  
ACCESSION AC024591  
VERSION AC024591.3 GI:9256450  
KEYWORDS HTG; HTGS\_PHASE2; HTGS\_DRAFT.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 111071)  
AUTHORS DOE Joint Genome Institute.  
TITLE Sequencing of Human Chromosome 16  
JOURNAL Unpublished  
AUTHORS 2 (bases 1 to 111071)  
JOURNAL DOE Joint Genome Institute.  
TITLE Direct Submission  
Submitted (29-FEB-2000) Production Sequencing Facility, DOE Joint  
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
On Jul 18, 2000 this sequence version replaced g1:7705016.  
-----Genome Center  
Center: Joint Genome Institute  
Center Code: JGI  
Web site: http://www.jgi.doe.gov  
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Project Information  
Center Project Name: 602754  
Center clone name: RPCI-11\_511G21  
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Summary Statistics  
Consensus quality: 104021 bases at least Q40  
Consensus quality: 108348 bases at least Q30  
Consensus quality: 109319 bases at least Q20  
Estimated insert size: 118930; agarose-fp estimation  
Estimated insert size: 110521; sum-of-contigs estimation  
Quality coverage: 8.44 in Q20 bases; agarose-fp estimation  
Quality coverage: 9.08 in Q20 bases; sum-of-contigs estimation.  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 13 contigs. Gaps between the contigs  
\* are represented as runs of N. The order of the pieces  
\* is believed to be correct as given, however the sizes



\* of the gps between them are based on estimates that have  
\* provided by the submittor.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.

|   |        |         |                              |
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| * | 1      | 3999:   | contig of 3999 bp in length  |
| * | 4000   | 4099:   | gap of unknown length        |
| * | 4100   | 6224:   | contig of 2125 bp in length  |
| * | 6225   | 6324:   | gap of unknown length        |
| * | 6325   | 14602:  | contig of 8278 bp in length  |
| * | 14603  | 14702:  | gap of unknown length        |
| * | 14703  | 54285:  | contig of 39543 bp in length |
| * | 54246  | 54345:  | gap of unknown length        |
| * | 54346  | 58599:  | contig of 4224 bp in length  |
| * | 58570  | 58669:  | gap of unknown length        |
| * | 58670  | 59480:  | contig of 811 bp in length   |
| * | 59481  | 59580:  | gap of unknown length        |
| * | 59581  | 60683:  | contig of 1103 bp in length  |
| * | 60684  | 60783:  | gap of unknown length        |
| * | 60784  | 62950:  | contig of 2167 bp in length  |
| * | 62951  | 63050:  | gap of unknown length        |
| * | 63051  | 64092:  | contig of 1042 bp in length  |
| * | 64093  | 64192:  | gap of unknown length        |
| * | 64193  | 85067:  | contig of 20875 bp in length |
| * | 85068  | 85167:  | gap of unknown length        |
| * | 85168  | 91149:  | contig of 5982 bp in length  |
| * | 91150  | 91249:  | gap of unknown length        |
| * | 91250  | 108236: | contig of 16987 bp in length |
| * | 108237 | 108336: | gap of unknown length        |
| * | 108337 | 111071: | contig of 2735 bp in length. |

| FEATURES   | location                             | Qualifiers                    |
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| SOURCE     | 1. 111071                            |                               |
|            | /organism="Homo sapiens"             |                               |
|            | /db_xref="taxon:9606"                |                               |
|            | /chromosome="16"                     |                               |
|            | /clone="RP11-511c21"                 |                               |
| BASE COUNT | /clone_1b="PC1 human BAC library 11" |                               |
| ORIGIN     | a 27517                              | c 28256 g 26944 t 1202 others |

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| Query Match           | 3.2%;   | Score 19;     | DB 68; | length 111071; |
| Best Local Similarity | 100.0%; | Pred. No. 29; |        |                |
| Matches               | 19;     | Conservative  | 0;     | Mismatches     |
|                       |         |               | 0;     | Indels         |
|                       |         |               |        | Gaps           |
|                       |         |               |        | 0;             |

QY      280 gccgcgcgcatcgcgtg    298  
         |||||  
Db 19460 GCCGCGGCATCGCCTG 19442

|            |                               |     |             |  |
|------------|-------------------------------|-----|-------------|--|
| RESULT     | 23                            |     |             |  |
| LOCUS      | AC020962                      |     |             |  |
| DEFINITION | AC020962 128562 bp DNA        | HTG | 10-FEB-2000 |  |
| ACCESSION  | AC020962                      |     |             |  |
| VERSION    | AC020962.1                    |     |             |  |
| KEYWORDS   | HTG; HTGS_PHASE1; HTGS_DRAFT. |     |             |  |
| SOURCE     | house mouse.                  |     |             |  |
| ORGANISM   | Mus musculus                  |     |             |  |

|           |                                                                                                                                      |
|-----------|--------------------------------------------------------------------------------------------------------------------------------------|
| REFERENCE | 1 (bases 1 to 128562)                                                                                                                |
| AUTHORS   | DOE Joint Genome Institute.                                                                                                          |
| TITLE     | Sequencing of Mouse                                                                                                                  |
| JOURNAL   | Unpublished                                                                                                                          |
| REFERENCE | 2 (bases 1 to 128562)                                                                                                                |
| AUTHORS   | DOE Joint Genome Institute.                                                                                                          |
| TITLE     | Direct Submision                                                                                                                     |
| JOURNAL   | Submitted (12-JAN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA |
| COMMENT   | -----Genome Center<br>Center: Joint Genome Institute                                                                                 |

Center Code: JGI  
Web site: <http://www.jgi.doe.gov>

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-----Summary Statistics-----
Consensus quality: 113524 bases at least Q40
Consensus quality: 110053 bases at least Q30
Consensus quality: 1626852 bases at least Q20
Estimated insert size: 128562; sum-of-contigs estimation
Estimated insert size: 128002; pulse field gel estimation
Quality coverage: 7.48% in Q40 bases; pulse field gel estimation
Quality coverage: 7.48% in Q20 bases; sum-of-contigs estimation

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* NOTE: This is a 'working draft' sequence. It currently
* consists of 21 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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|            |   |       |                          |                               |
|------------|---|-------|--------------------------|-------------------------------|
|            | * | 1     | 1198:                    | contig of 1198 bp in length   |
|            | * |       | gap of unknown length    |                               |
|            | * | 1199  | 2531:                    | contig of 1333 bp in length   |
|            | * |       | gap of unknown length    |                               |
|            | * | 2532  | 4140:                    | contig of 1609 bp in length   |
|            | * |       | gap of unknown length    |                               |
|            | * | 4141  | 5328:                    | contig of 1188 bp in length   |
|            | * |       | gap of unknown length    |                               |
|            | * | 5329  | 6673:                    | contig of 1345 bp in length   |
|            | * |       | gap of unknown length    |                               |
|            | * | 6674  | 8037:                    | contig of 1364 bp in length   |
|            | * |       | gap of unknown length    |                               |
|            | * | 8038  | 9583:                    | contig of 1546 bp in length   |
|            | * |       | gap of unknown length    |                               |
|            | * | 9584  | 11046:                   | contig of 1463 bp in length   |
|            | * |       | gap of unknown length    |                               |
|            | * | 11047 | 12841:                   | contig of 1795 bp in length   |
|            | * |       | gap of unknown length    |                               |
|            | * | 12842 | 14056:                   | contig of 1215 bp in length   |
|            | * |       | gap of unknown length    |                               |
|            | * | 14057 | 15421:                   | contig of 1365 bp in length   |
|            | * |       | gap of unknown length    |                               |
|            | * | 15422 | 16973:                   | contig of 1552 bp in length   |
|            | * |       | gap of unknown length    |                               |
|            | * | 16974 | 18746:                   | contig of 1773 bp in length   |
|            | * |       | gap of unknown length    |                               |
|            | * | 18747 | 20176:                   | contig of 1430 bp in length   |
|            | * |       | gap of unknown length    |                               |
|            | * | 20177 | 21643:                   | contig of 1467 bp in length   |
|            | * |       | gap of unknown length    |                               |
|            | * | 21644 | 22955:                   | contig of 1312 bp in length   |
|            | * |       | gap of unknown length    |                               |
|            | * | 22956 | 24395:                   | contig of 1440 bp in length   |
|            | * |       | gap of unknown length    |                               |
|            | * | 24396 | 26493:                   | contig of 2098 bp in length   |
|            | * |       | gap of unknown length    |                               |
|            | * | 26494 | 46982:                   | contig of 20489 bp in length  |
|            | * |       | gap of unknown length    |                               |
|            | * | 46983 | 78189:                   | contig of 31207 bp in length  |
|            | * |       | gap of unknown length    |                               |
|            | * | 78190 | 128562:                  | contig of 50373 bp in length. |
| FEATURES   |   |       |                          |                               |
| source     |   |       |                          |                               |
|            |   |       | 1..128562                |                               |
|            |   |       | /organism="Mus musculus" |                               |
|            |   |       | /db_xref="taxon:10090"   |                               |
|            |   |       | /clone="RP21-126H5"      |                               |
| BASE COUNT |   | 31926 | a                        | 32661                         |
| ORIGIN     |   |       | c                        | 31576                         |
|            |   |       | g                        | 32269                         |
|            |   |       | t                        | 130                           |
|            |   |       | others                   |                               |

|                       |         |               |        |                |
|-----------------------|---------|---------------|--------|----------------|
| Query Match           | 3.2%;   | Score 19;     | DB 66; | Length 128562; |
| Best Local Similarity | 100.0%; | Pred. No. 28; |        |                |
| Matches               | 19;     | Conservative  | 0;     | Mismatches     |
|                       |         |               | 0;     | Indels         |
|                       |         |               |        | Gaps           |
|                       |         |               |        | 0;             |

QY 280 gccgcggcgatcgactg 298  
 Db 117029 GCCGCGCGGATCGGCTG 117047

RESULT 24  
 LOCUS AC073882 130734 bp DNA ROD 24-AUG-2000  
 DEFINITION Mus musculus chromosome 2 clone ct7-305f12 strain 129/SVES Cell  
 ACCESSION AC073882  
 KEYWORDS AC073882.4 GI:9690337  
 SOURCE HTG.  
 ORGANISM house mouse.  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
 AUTHORS Jia, H., Lin, S., Rithideck, K. and Roe, B.A.  
 TITLE 1 (bases 1 to 130734)  
 JOURNAL Unpublished  
 AUTHORS 2 (bases 1 to 130734)  
 TITLE Jia, H., Lin, S., Rithideck, K. and Roe, B.A.  
 JOURNAL Direct Submission  
 Submitted (01-JUL-2000) Department Of Chemistry And Biochemistry,  
 The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,  
 OK 73019, USA  
 REFERENCE 3 (bases 1 to 130734)  
 AUTHORS Jia, H., Lin, S., Rithideck, K. and Roe, B.A.  
 TITLE Direct Submission  
 Submitted (04-AUG-2000) Department Of Chemistry And Biochemistry,  
 The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,  
 OK 73019, USA  
 REFERENCE 4 (bases 1 to 130734)  
 AUTHORS Jia, H., Lin, S., Rithideck, K. and Roe, B.A.  
 TITLE Direct Submission  
 Submitted (24-AUG-2000) Department Of Chemistry And Biochemistry,  
 The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,  
 OK 73019, USA  
 COMMENT On Aug 4, 2000 this sequence version replaced g1:9280733.  
 FEATURES  
 source  
 1. .130734  
 /organism="Mus musculus"  
 /strain="129/SVES Cell Line Cj7"  
 /db\_xref="taxon:10090"  
 /chromosome="2"  
 /clone="ct7-305f12"  
 /clone\_1ib="Caltech CITB-BAC library"  
 BASE COUNT 41025 a 25364 c 26653 g 37692 t

Query Match 3.2%; Score 19; DB 94; Length 130734;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 537 gaacacacagagaaga 555  
 Db 65070 GAAACCAACAGAGAGAA 65088

RESULT 25  
 LOCUS HSJ1057D4 131888 bp DNA PRI 01-MAR-2001  
 DEFINITION Human DNA sequence from clone RP5-1057D4 on chromosome 20 contains  
 a spermidine synthase (SPDSY) pseudogene, a CpG island, ESTs, STS  
 and GSSs, complete sequence.  
 ACCESSION AL121777  
 VERSION AL121777.39 GI:10862842  
 KEYWORDS HTG; CpG island; spermidine synthase.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
 AUTHORS Blakey, S.  
 TITLE Direct Submission  
 JOURNAL Submitted (26-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire,  
 CB10 1SA, UK. E-mail enquiries: humquerrysanger.ac.uk  
 COMMENT  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 131888)  
 On Oct 17, 2000 this sequence version replaced g1:10716550.  
 During sequence assembly data is compared from overlapping clones.  
 Where differences are found these are annotated as variations  
 together with a note of the overlapping clone name. Note that the  
 variation annotation may not be found in the sequence submission  
 corresponding to the overlapping clone, as we submit sequences with  
 only a small overlap as described above.  
 The following abbreviations are used to associate primary accession  
 numbers given in the feature table with their source databases:  
 Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WormPeP; Information  
 on the WormPeP database can be found at  
 http://www.sanger.ac.uk/projects/c\_elegans/wormpep  
 This sequence was generated from part of bacterial clone contigs of human  
 chromosome 20, constructed by the Sanger Centre Chromosome 20  
 Mapping Group. Further information can be found at  
 http://www.sanger.ac.uk/HGP/Chr20  
 This sequence is the entire insert of clone RP5-1057D4 The true  
 left end of clone RP1-73E16 is at 71240 in this sequence. The true  
 right end of clone CTD-2653D5 is at 84358 in this sequence. This  
 sequence was finished as follows unless otherwise noted: all  
 regions were either double-stranded or sequenced with an alternate  
 chemistry or covered by high quality data (i.e., phred quality >=  
 30): an attempt was made to resolve all sequencing problems, such  
 as compressions and repeats; all regions were covered by at least  
 one plasmid subclone or more than one M13 subclone; and the  
 assembly was confirmed by restriction digest. RP5-1057D4 is from  
 the library RPCI-5 constructed by the group of Pieter de Jong. For  
 further details see  
 http://www.chori.org/bacpac/home.htm  
 VECTOR: pCYPAC2.  
 FEATURES  
 source  
 Location/Qualifiers  
 1. .131888  
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 /db\_xref="taxon:9606"  
 /chromosome="20"  
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 /clone\_1ib="RPCI-5"  
 repeat\_region  
 313..930  
 /note="12 repeat: matches 2043..2749 of consensus"  
 1411..1543  
 /note="MIR repeat: matches 80..222 of consensus"  
 1623..1934  
 /note="AluX repeat: matches 1..311 of consensus"  
 2162..2215  
 /note="12 repeat: matches 2696..2749 of consensus"  
 2444..2646  
 /note="12 repeat: matches 2353..2521 of consensus"  
 2929..3407  
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 3104..3214  
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 3638..3839  
 /note="MIR repeat: matches 32..256 of consensus"  
 3916..4051  
 /note="AluX repeat: matches 1..123 of consensus"  
 4052..4341  
 /note="AluX repeat: matches 1..295 of consensus"  
 4342..4477  
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 5436..5600  
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 5601..5892  
 /note="AluX repeat: matches 1..291 of consensus"  
 5893..6050  
 /note="AluX repeat: matches 1..170 of consensus"  
 6179..6230

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6186. .6565  
/note="L2 repeat: matches 2292. .2731 of consensus"  
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/note="L2 repeat: matches 2148. .2189 of consensus"  
repeat\_region 6607. .6913  
/note="AluYo repeat: matches 1. .307 of consensus"  
repeat\_region 6914. .7005  
/note="L2 repeat: matches 2064. .2148 of consensus"  
repeat\_region 7104. .7559  
/note="WTR1G repeat: matches 31. .512 of consensus"  
repeat\_region 8768. .8969  
/note="MER20 repeat: matches 1. .216 of consensus"  
repeat\_region 9696. .10011  
/note="L2 repeat: matches 2357. .2734 of consensus"  
repeat\_region 11637. .12065  
/note="WTR1H repeat: matches 20. .531 of consensus"  
repeat\_region 12302. .12377  
/note="MIR repeat: matches 115. .190 of consensus"  
repeat\_region 13520. .13783  
/note="L2 repeat: matches 2432. .2749 of consensus"  
repeat\_region 13953. .14155  
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repeat\_region 14420. .14705  
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misc\_feature /note="match: GSS: Em:AQ713490"  
complement(14589. .15060)  
misc\_feature /note="match: GSS: Em:AQ760291"  
complement(14602. .15072)  
misc\_feature /note="match: GSS: Em:AQ85065"  
15070. .15576  
/note="match: GSS: Em:AQ709181"  
15088. .15403  
/note="match: GSS: Em:AQ198342"  
15088. .15583  
/note="match: GSS: Em:AQ680811"  
15094. .15492  
/note="match: GSS: Em:AQ082327"  
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/note="L2 repeat: matches 1609. .1854 of consensus"  
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repeat\_region 15898. .16155  
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16156. .16457  
/note="AluXx repeat: matches 3. .304 of consensus"  
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21832. .22251  
/note="12 copies 35 mer 57% conserved"

repeat\_region 21934. .22123  
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repeat\_region 22000. .22257  
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repeat\_region 24041. .24328  
/note="AluYb repeat: matches 1. .288 of consensus"  
repeat\_region 24329. .24543  
/note="MER33 repeat: matches 23. .233 of consensus"  
25195. .25242  
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27239. .27425  
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27638. .27889  
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27900. .28343  
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29873. .30045  
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30349. .30598  
/note="WTR1C repeat: matches 163. .464 of consensus"  
30721. .30798  
/note="MER5B repeat: matches 44. .117 of consensus"  
30802. .30927  
/note="L1MB8 repeat: matches 6040. .6168 of consensus"  
30942. .31001  
/note="MER5B repeat: matches 113. .173 of consensus"  
31509. .31809  
/note="AluXx repeat: matches 1. .304 of consensus"  
32898. .33202  
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33556. .33701  
/note="MER5A repeat: matches 1. .146 of consensus"  
  
Query Match 3.2%; Score 19; DB 93; Length 131888;  
Best Local Similarity 100.0%; Pred. No. 28;  
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QY 215 cttccgctgtcattccccc 233  
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Db 22024 cttccgctgtcattccccc 22042  
  
RESULT 26  
AC084179/c  
LOCUS AC084179/c  
DEFINITION Homo sapiens chromosome 5 clone RP11-148P16 map 5, WORKING DRAFT  
SEQUENCE, 39 unordered pieces.  
AC084179  
AC084179.2 GI:12229370  
VERSION  
KEYWORDS HTG: HTGS\_PHASE1; HTGS\_DRAFT.  
SOURCE  
human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 147009)  
Birken,B., Linton,L., Nusbaum,C. and Lander,E.  
TITLE Homo sapiens chromosome 5, clone RP11-148P16  
JOURNAL Unpublished  
2 (bases 1 to 147009)  
Birken,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,  
REFERENCE  
Anderson,S., Barna,N., Bastien,V., Bada,F., Boguslavsky,L.,

TITLE  
JOURNAL  
COMMENT

Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A.,  
Choepe, Y., Colangelo, M., Collins, S., Collamore, A., Cooke, P.,  
Dearrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P.,  
Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Glade, S., Goyette, M.,  
Graham, L., Grand-pierre, N., Hagos, B., Heatford, A., Horton, L.,  
Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Larocque, K.,  
Lamasaras, R., Landers, T., Lengoczy, J., Levine, R., Lieu, C., Liu, G.,  
Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McKernan, K.,  
McPheeters, R., Meldrum, J., Meneus, L., Mihova, T., Mienga, V.,  
Morlow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T.,  
O'Donnell, P., O'Neill, D., Oliver, T.M., Oliver, J., Peterson, K.,  
Pierre, N., Pisan, C., Pollara, V., Raymond, C., Rieback, M., Riley, R.,  
Rogov, P., Rottman, D., Roy, A., Santos, R., Schauer, S., Severy, P.,  
Sougnuez, C., Spencer, B., Stange, Thoman, N., Stojanovic, N.,  
Straus, N., Subramanian, A., Talamas, J., Testfaye, S., Theodore, J.,  
Tirrell, A., Travers, M., Trigg, J., Vassiliev, H., Viel, R., Vo, A.,  
Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J.,  
Zimmer, A. and Zody, M.

Direct Submission  
Submitted (14-OCT-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Jan 15, 2001 this sequence version replaced gi:10801407.  
All repeats were identified using RepeatMasker:  
Sift, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute / MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

Project information

Center project name: L11428

Center clone name: 148\_P\_16

Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads  
Chemistry: Dye-terminator; Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 13223 bases at least Q40

Consensus quality: 139576 bases at least Q30

Consensus quality: 142136 bases at least Q20

Insert size: 176000; agarose-fp

Insert size: 143209; sum-of-contigs

Quality coverage: 3.0 in Q20 bases; agarose-fp

Quality coverage: 3.6 in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently  
\* consists of 39 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 1353: contig of 1353 bp in length  
\* 1354 1453: gap of 100 bp  
\* 1454 2001: contig of 548 bp in length  
\* 2002 2101: gap of 100 bp  
\* 2102 3124: contig of 1023 bp in length  
\* 3125 3224: gap of 100 bp  
\* 3225 4546: contig of 1322 bp in length  
\* 4547 4646: gap of 100 bp  
\* 4647 6015: contig of 1369 bp in length  
\* 6016 6115: gap of 100 bp  
\* 6116 7299: contig of 1184 bp in length  
\* 7300 7399: gap of 100 bp  
\* 7400 8836: contig of 1437 bp in length  
\* 8837 8936: gap of 100 bp  
\* 8937 10282: contig of 1346 bp in length  
\* 10283 10382: gap of 100 bp  
\* 10383 11352: contig of 970 bp in length  
\* 11353 11452: gap of 100 bp  
\* 11453 12856: contig of 1404 bp in length  
\* 12857 12956: gap of 100 bp

## FEATURES

## source

12957 14187: contig of 1231 bp in length  
\* 14188 14287: gap of 100 bp  
\* 14288 15977: contig of 1690 bp in length  
\* 15978 16077: gap of 100 bp  
\* 16078 17844: contig of 1767 bp in length  
\* 17845 17944: gap of 100 bp  
\* 17945 19861: contig of 1917 bp in length  
\* 19862 19961: gap of 100 bp  
\* 19962 22368: contig of 2407 bp in length  
\* 22369 22468: gap of 100 bp  
\* 22469 24485: contig of 2017 bp in length  
\* 24486 24585: gap of 100 bp  
\* 24586 26722: contig of 2137 bp in length  
\* 26723 26822: gap of 100 bp  
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\* 28984 29083: gap of 100 bp  
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\* 31859 31958: gap of 100 bp  
\* 31959 33783: contig of 1825 bp in length  
\* 33784 33883: gap of 100 bp  
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\* 36260 36359: gap of 100 bp  
\* 36360 39396: contig of 3037 bp in length  
\* 39397 39496: gap of 100 bp  
\* 39497 43329: contig of 3833 bp in length  
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\* 46058 46157: gap of 100 bp  
\* 46158 50066: contig of 3909 bp in length  
\* 50067 50166: gap of 100 bp  
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\* 53728 53827: gap of 100 bp  
\* 53828 57631: contig of 3804 bp in length  
\* 57632 57731: gap of 100 bp  
\* 57732 61304: contig of 3573 bp in length  
\* 61305 61404: gap of 100 bp  
\* 61405 63868: contig of 2464 bp in length  
\* 63869 63968: gap of 100 bp  
\* 63969 68393: contig of 4425 bp in length  
\* 68394 68493: gap of 100 bp  
\* 68494 72466: contig of 3973 bp in length  
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\* 72567 77027: contig of 4461 bp in length  
\* 77028 77127: gap of 100 bp  
\* 77128 81524: contig of 4397 bp in length  
\* 81525 81624: gap of 100 bp  
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\* 88874 88973: gap of 100 bp  
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\* 96288 96387: gap of 100 bp  
\* 96388 117899: contig of 21512 bp in length  
\* 117900 117999: gap of 100 bp  
\* 118000 123663: contig of 5664 bp in length  
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1. 1353  
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## misc\_feature

2102. 3124  
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misc_feature      36360..39396
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```

```

Query Match      3.2%  Score 19:  DB 76;  Length 147009;
Best Local Similarity 100.0%;  Pred. No. 27;
Matches 19;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

```

```

Oy  190 agtagcagtcataccaata 208
    |||||
Db  10253 AGTAGCAGTCATCAATCAATA 10235

```

```

RESULT 27
AC083840 156599 bp  DNA  HTG  03-MAR-2001
LOCUS    Homo sapiens chromosome 8 clone RP11-7319 map 8, WORKING DRAFT
DEFINITION
SEQUENCE 37 unordered pieces.
AC083840  AC083840.2 GI:13184085
VERSION   HTG; HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS  human.
SOURCE    Homo sapiens
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 156599)
AUTHORS  Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE     Homo sapiens chromosome 8, clone RP11-7319
JOURNAL   Unpublished
AUTHORS   2 (bases 1 to 156599)
          Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
          Anderson,S., Barna,N., Bastien,V., Beda,F., Boguslavsky,L.,
          Bouhagiel,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,
          Choeppel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
          Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Ferreira,P.,
          Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S., Glade,S., Goyette,M.,
          Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,C.,
          Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., LaRoque,K.,
          Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Lien,C., Liu,G.,

```

# TITLE JOURNAL COMMENT

Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McKernan, R., McPheeters, R., Meldrum, J., Meneus, L., Mihova, T., Mlepea, Y., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Olivari, T.M., Oliver, J., Peterson, K., Pierre, N., Pisanu, C., Pollara, V., Raymond, C., Rieback, M., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Sougnuez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Testa, S., Theodore, J., Tirelli, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A., and Zody, M.

Direct Submission  
Submitted (03-OCT-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Mar 2, 2001 this sequence version replaced gi:10518398.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: MIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
Project Information  
Center project name: 111308  
Center clone name: 73.1.9

Summary Statistics  
Sequencing vector: Plasmid; n/a; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.960731  
Consensus quality: 141695 bases at least Q40  
Consensus quality: 148947 bases at least Q30  
Consensus quality: 151617 bases at least Q20  
Insert size: 152899; sum-of-coverage  
Quality coverage: 4.0 in Q20 bases; sum-of-coverage

NOTE: This is a 'working draft' sequence. It currently consists of 37 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

```

1      816: contig of 816 bp in length
*      917 916: gap of 100 bp
*      917 2094: contig of 1178 bp in length
*      2095 2194: gap of 100 bp
*      2195 3169: contig of 975 bp in length
*      3170 3269: gap of 100 bp
*      3270 3766: contig of 497 bp in length
*      3767 3866: gap of 100 bp
*      3867 5257: contig of 1391 bp in length
*      5258 5357: gap of 100 bp
*      5358 7176: contig of 1819 bp in length
*      7177 7276: gap of 100 bp
*      7277 8366: contig of 1090 bp in length
*      8367 8466: gap of 100 bp
*      8467 9770: contig of 1304 bp in length
*      9771 9870: gap of 100 bp
*      9871 11023: contig of 1153 bp in length
*      11024 11123: gap of 100 bp
*      11124 12210: contig of 1087 bp in length
*      12211 12310: gap of 100 bp
*      12311 13716: contig of 1406 bp in length
*      13717 13816: gap of 100 bp
*      13817 14696: contig of 880 bp in length
*      14697 14796: gap of 100 bp
*      14797 16050: contig of 1254 bp in length
*      16051 16150: gap of 100 bp
*      16151 18691: contig of 2541 bp in length
*      18692 18791: gap of 100 bp
*      18792 20474: contig of 1683 bp in length

```

|        |         |           |       |    |           |
|--------|---------|-----------|-------|----|-----------|
| 2045   | 20574   | gap of    | 100   | bp |           |
| 20575  | 22566   | contlg of | 1990  | bp | in length |
| 22565  | 22664   | gap of    | 100   | bp |           |
| 22665  | 22349   | contlg of | 2665  | bp | in length |
| 25350  | 25449   | gap of    | 100   | bp |           |
| 25450  | 28733   | contlg of | 3282  | bp | in length |
| 28732  | 28831   | gap of    | 100   | bp |           |
| 28832  | 41793   | contlg of | 12662 | bp | in length |
| 41794  | 41893   | gap of    | 100   | bp |           |
| 41894  | 45562   | contlg of | 3669  | bp | in length |
| 45563  | 45662   | gap of    | 100   | bp |           |
| 45663  | 49244   | contlg of | 3563  | bp | in length |
| 49246  | 49345   | gap of    | 100   | bp |           |
| 49346  | 55701   | contlg of | 3366  | bp | in length |
| 52702  | 52801   | gap of    | 100   | bp |           |
| 52802  | 55787   | contlg of | 4766  | bp | in length |
| 55788  | 57687   | gap of    | 100   | bp |           |
| 57688  | 60742   | contlg of | 3055  | bp | in length |
| 60743  | 60842   | gap of    | 100   | bp |           |
| 60843  | 64655   | contlg of | 3813  | bp | in length |
| 64656  | 64755   | gap of    | 100   | bp |           |
| 64756  | 66878   | contlg of | 4123  | bp | in length |
| 66879  | 68978   | gap of    | 100   | bp |           |
| 68979  | 73540   | contlg of | 4562  | bp | in length |
| 73541  | 73640   | gap of    | 100   | bp |           |
| 73641  | 79164   | contlg of | 5524  | bp | in length |
| 79165  | 79264   | gap of    | 100   | bp |           |
| 79265  | 87667   | contlg of | 8403  | bp | in length |
| 87668  | 87767   | gap of    | 100   | bp |           |
| 87768  | 96110   | contlg of | 8343  | bp | in length |
| 96111  | 96210   | gap of    | 100   | bp |           |
| 96211  | 104171  | contlg of | 7961  | bp | in length |
| 104172 | 104271  | gap of    | 100   | bp |           |
| 104272 | 110622  | contlg of | 6331  | bp | in length |
| 110623 | 110722  | gap of    | 100   | bp |           |
| 110723 | 121728  | contlg of | 11006 | bp | in length |
| 121729 | 121828  | gap of    | 100   | bp |           |
| 121829 | 1329949 | contlg of | 8121  | bp | in length |
| 129950 | 130049  | gap of    | 100   | bp |           |
| 130050 | 1330747 | contlg of | 9698  | bp | in length |
| 139748 | 139847  | gap of    | 100   | bp |           |
| 139848 | 155810  | contlg of | 13663 | bp | in length |
| 153811 | 153910  | gap of    | 100   | bp |           |
| 153911 | 156599  | contlg of | 2669  | bp | in length |

## FEATURES

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|              | /db_xref="taxon:9606"               |
|              | /chromosome="8"                     |
|              | /map="8"                            |
|              | /clone="RP11-7319"                  |
|              | /clone.lib="RPCI-11 Human Male BAC" |
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|              | /note="assembly_fragment"           |
| misc_feature | clone_end:Sp6                       |
|              | vector_side:left"                   |
|              | 917..2094                           |
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|              | 3270..3766                          |
| misc_feature | /note="assembly_fragment"           |
|              | 3867..5257                          |
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|              | 5358..7176                          |
| misc_feature | /note="assembly_fragment"           |
|              | 7277..8366                          |
| misc_feature | /note="assembly_fragment"           |
|              | 8467..9770                          |
| misc_feature | /note="assembly_fragment"           |
|              | 9871..11023                         |
| misc_feature | /note="assembly_fragment"           |
|              | 11124..12210                        |

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12311. 13716
/note="assembly_fragment"
misc_feature      /note="assembly_fragment"
13817. 14696
/note="assembly_fragment"
misc_feature      /note="assembly_fragment"
14797. 16050
/note="assembly_fragment"
misc_feature      /note="assembly_fragment"
16151. 18631
/note="assembly_fragment"
misc_feature      /note="assembly_fragment"
18792. 20474
/note="assembly_fragment"
misc_feature      /note="assembly_fragment"
20575. 22564
/note="assembly_fragment"
misc_feature      /note="assembly_fragment"
22665. 25349
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misc_feature      /note="assembly_fragment"
25450. 28731
/note="assembly_fragment"
misc_feature      /note="assembly_fragment"
28832. 41793
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misc_feature      /note="assembly_fragment"
41894. 45562
/note="assembly_fragment"
misc_feature      /note="assembly_fragment"
45663. 49245
/note="assembly_fragment"
misc_feature      /note="assembly_fragment"
49346. 52701
/note="assembly_fragment"
misc_feature      /note="assembly_fragment"
52802. 57587
/note="assembly_fragment"
misc_feature      /note="assembly_fragment"
57688. 60742
/note="assembly_fragment"
misc_feature      /note="assembly_fragment"
60843. 64655

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|            | Query Match | Similarity          | 3.28; | Score 19;  | DB 76; | Length 156599; |
|------------|-------------|---------------------|-------|------------|--------|----------------|
| Best Local | 19;         | Conservative        | 0;    | Mismatches | 0;     | Gaps 0;        |
| Matches    | 19;         | Conservative        | 0;    | Mismatches | 0;     | Gaps 0;        |
| Qy         | 243         | ccctggttcagcgccagcc | 261   |            |        |                |
| Db         | 2492        | ccctgtttcagcgccagcc | 2510  |            |        |                |

[illegible]

|           |                               |
|-----------|-------------------------------|
| ACCESSION | Pages                         |
| VERSION   | AC015815                      |
| KEYWORDS  | AC015815.4 GI:7341971         |
| SOURCE    | HTG; HTGS_PHASE1; HTGS_DRAFT. |
| ORGANISM  | human.                        |
|           | Homo sapiens                  |

| REFERENCE   | AUTHORS                                                                   | TITLE | JOURNAL |
|-------------|---------------------------------------------------------------------------|-------|---------|
| REFERENCE 1 | (bases 1 to 161549)                                                       |       |         |
| AUTHORS     | Birren, B., Linton, L., Nusbaum, C., and Lander, E.                       |       |         |
| TITLE       | Homo sapiens, clone RP11-21015                                            |       |         |
| JOURNAL     | unpublished                                                               |       |         |
| REFERENCE 2 | (bases 1 to 161549)                                                       |       |         |
| AUTHORS     | Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., |       |         |

Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,  
Cooke, P., DeRellano, K., Dewar, K., Domingo, M., Donelan, L., Doyle, M.,  
Ferrelle, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D.,  
Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heathford, A., Horton, L.,  
Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,  
Lehocky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N.,  
Mcwan, P., McGurk, A., McKenna, K., McLaughlin, J., Meldrum, J.,  
Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,  
Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,  
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,  
Teftaye, S., Tirell, A., Vassiliou, H., Vo, A., Wheeler, J., Wu, X.,  
Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.

Direct Submission

TITLE

JOURNAL

Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome

## COMMENT

Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Mar 30, 2000 this sequence version replaced gi:6939989.  
All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research  
Web site: <http://www-seq.wi.mit.edu>

Contact: sequence.submissions@genome.wi.mit.edu

Project Information

Center project name: L4073

Center clone name: 21\_O\_15

Summary Statistics

Sequencing vector: M13; M77815; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 15133 bases at least Q40

Consensus quality: 155764 bases at least Q30

Consensus quality: 157650 bases at least Q20

Insert size: 157000; agarose-fp

Quality coverage: 4.9 in Q20 bases; agarose-fp

Quality coverage: 4.8 in Q20 bases; sum-of-coverage

NOTE: This is a 'working draft' sequence. It currently consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

```

1 1138: contig of 1138 bp in length
1139 1238: gap of 100 bp
1239 2713: contig of 1475 bp in length
2714 2813: gap of 100 bp
2814 4948: contig of 2135 bp in length
4949 5048: gap of 100 bp
5049 7939: contig of 2891 bp in length
7940 8039: gap of 100 bp
8040 9902: contig of 1863 bp in length
9903 10002: gap of 100 bp
10003 12571: contig of 2569 bp in length
12572 12671: gap of 100 bp
12672 16792: contig of 4121 bp in length
16793 16892: gap of 100 bp
16893 21320: contig of 4428 bp in length
21321 21420: gap of 100 bp
21421 28365: contig of 6945 bp in length
28366 28465: gap of 100 bp
28466 34699: contig of 6234 bp in length
34700 34799: gap of 100 bp
34800 40251: contig of 5452 bp in length
40252 40351: gap of 100 bp
40352 47897: contig of 7546 bp in length
47898 47997: gap of 100 bp
47998 55766: contig of 7769 bp in length
55767 55866: gap of 100 bp
55867 63968: contig of 8102 bp in length
63969 64068: gap of 100 bp
64069 74694: contig of 10626 bp in length
74695 74794: gap of 100 bp
74795 84737: contig of 9943 bp in length
84738 84837: gap of 100 bp
84838 98320: contig of 13483 bp in length
98321 98420: gap of 100 bp
98421 110611: contig of 12191 bp in length
110612 110711: gap of 100 bp
110712 122418: contig of 11707 bp in length
122419 122518: gap of 100 bp
122519 137004: contig of 14486 bp in length
137005 137104: gap of 100 bp

```

FEATURES \* 137105 161549: contig of 24445 bp in length.  
Location/Qualifiers

source

1. 161549

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="RP11-21015"

/clone\_11b="RPC1-11 Human Male BAC"

1. 1138

/note="assembly-fragment"

1239. 2713

/note="assembly-fragment"

2814. 4948

/note="assembly-fragment"

5049. 7939

/note="assembly-fragment"

8040. 9902

/note="assembly-fragment"

10003. 12571

/note="assembly-fragment"

12672. 16792

/note="assembly-fragment"

16893. 21320

/note="assembly-fragment"

21421. 28365

/note="assembly-fragment"

28466. 34699

/note="assembly-fragment"

clone\_end:596

vector\_side:left"

34800. 40251

/note="assembly-fragment"

40352. 47897

/note="assembly-fragment"

47998. 55766

/note="assembly-fragment"

/note="assembly-fragment"

clone\_end:77

vector\_side:left"

55867. 63968

/note="assembly-fragment"

64059. 74694

/note="assembly-fragment"

74795. 84737

/note="assembly-fragment"

84838. 98320

/note="assembly-fragment"

98421. 110611

/note="assembly-fragment"

110712. 122418

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122519. 137004

/note="assembly-fragment"

137105. 161549

/note="assembly-fragment"

BASE COUNT 41638 a 38819 c 39363 g 39720 t 2009 others

ORIGIN

Query Match 3.2% Score 19; DB 64; Length 161549;

Best Local Similarity 100.0%; Pred. No. 27;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 105 cagggaagaacagcagcca 123

Db 28267 CAGGSAAGACAGCAGCCA 28249

|||||

RESULT 29

AC009108 AC009108 170431 bp DNA HTG 02-SEP-2000

LOCUS Homo sapiens chromosome 16 clone RP11-46309, WORKING DRAFT

DEFINITION SEQUENCE, 4 ordered pieces.

AC009108 AC009108

VERSION AC009108.8 GI:9964740

```

KEYWORDS      HTG: HTGS_PHASE2; HTGS_DRAFT.
SOURCE        human.
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS       1 (bases 1 to 170431)
TITLE         DOE Joint Genome Institute.
JOURNAL       Sequencing of Human Chromosome 16
REFERENCE     Unpublished
AUTHORS       2 (bases 1 to 170431)
JOURNAL       DOE Joint Genome Institute.
COMMENT       Direct Submission
              Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
              Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
              On Sep 2, 2000 this sequence version replaced gi:8575957.
              -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: S84502
Center clone name: RPCI_11_46309
-----
Summary Statistics
Consensus quality: 167345 bases at least Q40
Consensus quality: 169423 bases at least Q30
Consensus quality: 169900 bases at least Q20
Estimated insert size: 181440; agarose-fp estimation
Quality coverage: 10.63 in Q20 bases; agarose-fp estimation
Quality coverage: 11.33 in Q20 bases; sum-of-contigs estimation.
NOTE: This is a 'working draft' sequence. It currently
consists of 4 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
provided by the submittor.
This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.
    1   24820: contig of 24820 bp in length
    *   24821   37862: gap of unknown length
    *   24921   37862: contig of 12942 bp in length
    *   37863   37962: gap of unknown length
    *   37963   114671: contig of 76709 bp in length
    *   114672   114771: gap of unknown length
    *   114772   170431: contig of 55660 bp in length.
Location/Qualifiers
    1..170431
organism="Homo sapiens"
db_xref="taxon:9606"
chromosome="16"
clone_id="RPCI-human BAC library 11"
BASE COUNT   41117 a 43130 c 42591 g 43290 t          303 others
ORIGIN
Query Match           3.2%; Score 19; DB 61; Length 170431;
Best Local Similarity 100.0%; Prid. No. 26;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      280 gccgcggcgcatgagctg 298
|||||
Db      21976 gccgcggcgcgatgcgtg 21994

RESULT  30
AC013343/c AC013343 175249 bp DNA HTG 30-MAR-2000
LOCUS      Homo sapiens clone RP11-22B10, WORKING DRAFT SEQUENCE, 13 unordered
DEFINITION pieces.
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ACCESSION AC013343  
VERSION AC013343.3 GI:7341972  
KEYWORDS HUG, HTGS\_PHASE1, HTGS\_DRAFT.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 175249)  
Barren,B., Linton,L., Nusbaum,C. and Lander,E.  
Homo sapiens, clone RP11-22B10  
Unpublished  
2 (bases 1 to 175249)  
Barren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M., Batdwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Boukhalter,B., Brown,A., Castle,A., Colangelo,M., Collins,S., Collamore,A., Cooke,P., Dacrellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M., Ferreira,P., Fitzhugh,W., Forrest,C., Funke,K., Gage,D., Galagan,J., Gardyna,S., Grant,G., Haas,B., Heaford,A., Horton,L., Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., Leheccky,J., Lien,C., Locke,K., Macdonald,P., Margulis,N., McManus,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrum,J., Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P., Strange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Testaye,S., Tirell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X., Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.  
Direct Submission  
Submitted (06-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Mar 30, 2000 this sequence version replaced gi:6478975.  
All repeats were identified using RepeatMasker:  
Smt, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html  
-----  
Center: Whitehead Institute/ MIT Center for Genome Research  
Genome Center  
Web site: http://www.seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
-----  
Project Information  
Center project name: L4088  
Center clone name: 22\_B\_10  
-----  
Summary Statistics  
Sequencing vector: M13; M77815; 100% of reads  
Chemistry: dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap, version 0.960731  
Consensus quality: 169195 bases at least Q40  
Consensus quality: 171919 bases at least Q30  
Consensus quality: 172990 bases at least Q20  
Insert size: 172000; agarose-fp  
Insert size: 174049; sum-of-contigs  
Quality coverage: 6.8 in Q20 bases; agarose-fp  
Quality coverage: 6.7 in Q20 bases; sum-of-contigs  
-----  
NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.  
-----  
1 1100: contig of 1100 bp in length  
\* 1101 1200: gap of 100 bp  
\* 1201 2923: contig of 1723 bp in length  
\* 2924 3023: gap of 100 bp  
\* 3024 6205: contig of 3182 bp in length  
\* 6206 6305: gap of 100 bp  
\* 6306 8632: contig of 2337 bp in length  
\* 8633 8732: gap of 100 bp  
\* 8733 16009: contig of 7277 bp in length  
\* 16010 16109: gap of 100 bp  
\* 16110 26909: contig of 10600 bp in length  
\* 26910 27009: gap of 100 bp



\* 27010 39473: contig of 12464 bp in length  
 \* 39474 39573: gap of 100 bp  
 \* 39574 51751: contig of 12178 bp in length  
 \* 51752 51851: gap of 100 bp  
 \* 51852 66815: contig of 14964 bp in length  
 \* 66816 66915: gap of 100 bp  
 \* 66916 79391: contig of 12476 bp in length  
 \* 79392 79491: gap of 100 bp  
 \* 79492 105904: contig of 26413 bp in length  
 \* 105905 106004: gap of 100 bp  
 \* 106005 130201: contig of 24197 bp in length  
 \* 130202 130301: gap of 100 bp  
 \* 130302 175249: contig of 44948 bp in length.

FEATURES  
 SOURCE

1. 175249  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="RP11-22B10"  
 /clone\_11b="RPC1-11 Human Male BAC"  
 1. 1100  
 /note="assembly-fragment"  
 1201. 2923  
 /note="assembly-fragment"  
 3024. 6205  
 /note="assembly-fragment"  
 6306. 8632  
 /note="assembly-fragment"  
 clone\_end:17  
 vector\_side:right"  
 8733. 16009  
 /note="assembly-fragment"  
 16110. 26909  
 /note="assembly-fragment"  
 27010. 39473  
 /note="assembly-fragment"  
 39574. 51751  
 /note="assembly-fragment"  
 51852. 66815  
 /note="assembly-fragment"  
 66916. 79391  
 /note="assembly-fragment"  
 79492. 105904  
 /note="assembly-fragment"  
 106005. 130201  
 /note="assembly-fragment"  
 130302. 175249  
 /note="assembly-fragment"  
 clone\_end:SP6  
 vector\_side:left"  
 BASE COUNT 55507 a 34489 c 33847 g 50204 t 1202 others  
 ORIGIN

Query Match 3.2%; Score 19; DB 63; Length 175249;  
 Best Local Similarity 100.0%; Pred. No. 26;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 190 agtagcagctaccata 208  
 |||  
 Db 68509 AGTAGCAGCTACCAATA 68491

RESULT 31  
 LOCUS AP002501/c 179844 bp DNA HTG 13-JUN-2000  
 DEFINITION Homo sapiens chromosome 18 clone RP11-680K13 map 18q12, WORKING  
 DRAFT SEQUENCE, 26 unordered pieces.  
 ACCESSION AP002501  
 VERSION AP002501.1 GI:8547586  
 KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
 SOURCE Homo sapiens DNA; clone:RP11-680K13.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

# REFERENCE

1 (bases 1 to 179844)  
 Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P.,  
 Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H., and Sakaki, Y.  
 Homo sapiens 179,844 genomic DNA of 18q12  
 Published Only in Database (2000) in press  
 2 (bases 1 to 179844)  
 Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P.,  
 Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H., and Sakaki, Y.  
 Direct Submission  
 Submitted (09-JUN-2000) Masahira Hattori, The Institute of Physical  
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
 Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,  
 Japan (E-mail: hattori@gsc.riken.go.jp,  
 URL: http://hgp.gsc.riken.go.jp/, Tel: 81-42-778-9923,  
 Fax: 81-42-778-9924)

## COMMENT

Center: RIKEN Genomic Sciences Center (GSC)  
 Center code: RIKEN  
 Web site: http://hgp.gsc.riken.go.jp/  
 Contact: hattori@gsc.riken.go.jp  
 Project Information  
 Center project name: HumDrafl18  
 Center clone name: RP11-680K13  
 ----- Summary Statistics -----  
 Sequencing vector: PCR products; 100% of reads  
 Chemistry: Dye-terminator ET-amersham; 100% of reads  
 Assembly program: Phrap; version 0.990329  
 Consensus quality: 15359 bases at least Q40  
 Consensus quality: 166513 bases at least Q30  
 Consensus quality: 173786 bases at least Q20  
 Insert size: 177344; sum-of-contigs  
 Quality coverage: 4.16x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of  
 26 contigs. The true order of the pieces is not known and their  
 order in this sequence record is arbitrary. Gaps between the  
 contigs are represented as runs N, but the exact sizes of the gaps  
 are unknown. This record will be updated with the finished sequence  
 as soon as it is available and the accession number will be  
 preserved

1 18994 contig of 18994 bp in length  
 19995 39625 contig of 19631 bp in length  
 39726 54530 contig of 14805 bp in length  
 54631 68239 contig of 13609 bp in length  
 68340 78114 contig of 9775 bp in length  
 78215 89873 contig of 11659 bp in length  
 89974 99848 contig of 9875 bp in length  
 99949 109211 contig of 9263 bp in length  
 109312 116907 contig of 7596 bp in length  
 117008 121661 contig of 4654 bp in length  
 121762 128613 contig of 6852 bp in length  
 128714 132862 contig of 4149 bp in length  
 132963 137321 contig of 4359 bp in length  
 137422 142209 contig of 4788 bp in length  
 142310 146753 contig of 4444 bp in length  
 146854 152208 contig of 5355 bp in length  
 152309 158467 contig of 6159 bp in length  
 158568 162542 contig of 3975 bp in length  
 162643 165710 contig of 3068 bp in length  
 165811 168812 contig of 3002 bp in length  
 168913 170572 contig of 1660 bp in length  
 170673 172454 contig of 1782 bp in length  
 172555 175531 contig of 2977 bp in length  
 175632 177476 contig of 1845 bp in length  
 177577 178671 contig of 1095 bp in length  
 178772 179844 contig of 1073 bp in length.

NOTE: This is a 'working draft' sequence. It currently  
 consists of 26 contigs. The true order of the pieces  
 is not known and their order in this sequence record is  
 arbitrary. Gaps between the contigs are represented as  
 runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence

\* as soon as it is available and the accession number will  
\* be preserved.

```
1 19894: contig of 19894 bp in length
19895 19994: gap of 100 bp
19995 39625: contig of 19631 bp in length
39626 39725: gap of 100 bp
39726 54530: contig of 14805 bp in length
54531 54630: gap of 100 bp
54631 68239: contig of 13609 bp in length
68240 68339: gap of 100 bp
68340 78114: contig of 9775 bp in length
78115 78214: gap of 100 bp
78215 89873: contig of 11659 bp in length
89874 89973: gap of 100 bp
89974 99848: contig of 9875 bp in length
99849 99948: gap of 100 bp
109212 109311: contig of 9263 bp in length
109312 116907: contig of 7596 bp in length
116908 117007: gap of 100 bp
117008 121661: contig of 4654 bp in length
121662 121761: gap of 100 bp
121762 128613: contig of 6852 bp in length
128614 128713: gap of 100 bp
128714 132862: contig of 4149 bp in length
132863 132962: gap of 100 bp
132963 137321: contig of 4359 bp in length
137322 137421: gap of 100 bp
137422 142209: contig of 4788 bp in length
142210 142309: gap of 100 bp
142310 146753: contig of 4444 bp in length
146754 146853: gap of 100 bp
146854 152208: contig of 5355 bp in length
152209 152308: gap of 100 bp
152309 158467: contig of 6159 bp in length
158468 158567: gap of 100 bp
158568 162542: contig of 3975 bp in length
162543 162642: gap of 100 bp
162643 165710: contig of 3068 bp in length
165711 165810: gap of 100 bp
165811 168812: contig of 3002 bp in length
168813 168912: gap of 100 bp
168913 170572: contig of 1660 bp in length
170573 170672: gap of 100 bp
170673 172454: contig of 1782 bp in length
172455 172554: gap of 100 bp
172555 175531: contig of 2977 bp in length
175532 175631: gap of 100 bp
175632 177476: contig of 1845 bp in length
177477 177576: gap of 100 bp
177577 178671: contig of 1095 bp in length
178672 178771: gap of 100 bp
178772 179844: contig of 1073 bp in length.
```

FEATURES  
source

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1. 179844
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="18"
/map="18q12"
/clone="RP11-680K13"
1. 19894
/note="assembly_fragment"
19995. .39625
/note="assembly_fragment"
39726. .54530
/note="assembly_fragment"
54631. .68239
/note="assembly_fragment"
68340. .78114
/note="assembly_fragment"
78215. .89873
/note="assembly_fragment"
89974. .99848
```

```
misc_feature /note="assembly_fragment clone_end:SP6 vector_side:left"
99949. .109211
/note="assembly_fragment"
misc_feature /note="assembly_fragment"
109312. .116907
/note="assembly_fragment"
117008. .121661
/note="assembly_fragment clone_end:r7 vector_side:right"
121762. .128613
/note="assembly_fragment"
128714. .132862
/note="assembly_fragment"
132963. .137321
/note="assembly_fragment"
137422. .142209
/note="assembly_fragment"
142310. .146753
/note="assembly_fragment"
146854. .152208
/note="assembly_fragment"
152309. .158467
/note="assembly_fragment"
158568. .162542
/note="assembly_fragment"
162643. .165710
/note="assembly_fragment"
165811. .168812
/note="assembly_fragment"
168913. .170572
/note="assembly_fragment"
170673. .172454
/note="assembly_fragment"
172555. .175531
/note="assembly_fragment"
175632. .177476
/note="assembly_fragment"
177577. .178671
/note="assembly_fragment"
178772. .179844
/note="assembly_fragment"
misc_feature /note="assembly_fragment"
42717 a 45958 c 47394 g 41275 t 2500 others
```

BASE COUNT  
ORIGIN

```
Query Match 3.28: Score 19; DB 83; Length 179844;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 243 cccgtttcagcgcagcc 261
DB 99697 CCTGTTCACGCCACGC 99679
```

```
RESULT 32
AC068169/c DNA HNG 15-NOV-2000
LOCUS Homo sapiens chromosome 17 clone RP11-651B2 map 17, WORKING DRAFT
DEFINITION
SEQUENCE 15 unordered pieces.
ACCESSION AC068169.3 GI:11136767
VERSION AC068169.3
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 180717)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens chromosome 17, clone RP11-651B2
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 180717)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
Boguslavsky,L., Boukhalter,B., Brown,A., Burkett,G.,
Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
```



REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 181853)  
Birren,B., Linton,L., Nusbaum,C. and Lander,E.  
Homo sapiens chromosome 1, clone RP11-153j19  
unpublished  
2 (bases 1 to 181853)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,  
Anderson,S., Baldwin,J., Barna,N., Beda,F., Boguslavsky,L.,  
Bouknight,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,  
Chapel,Y., Colangelo,M., Collins,S., Collamore,A., Cooke,P.,  
Dearlano,K., Dewar,K., Diaz,J.S., Dodge,S., Domino,M., Doyle,M.,  
Fenster,J., Ferreira,P., Fitzhugh,M., Forrest,C., Gage,D.,  
Gallagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,  
Grand-Pierre,N., Grant,G., Hages,B., Heaford,A., Horton,L.,  
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,  
Klein,J., Landers,T., Larcocque,K., Lehocsky,J., Levine,R.,  
Lieu,C., Liu,G., Locke,K., Macdonald,P., Margulis,N., McCarthy,M.,  
McEwan,P., McGuirk,A., McKernan,K., McNeeters,R., Meldrum,J.,  
Meneus,L., Milhova,T., Miranda,C., Mlenka,V., Morrow,J., Naylor,J.,  
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Olivar,T.M.,  
Peterson,K., Pierre,N., Pisan,C., Pollara,V., Raymond,C.,  
Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S.,  
Severy,P., Spencer,B., Strange-Thomann,N., Stojanovic,N.,  
Subramanian,A., Talamas,J., Testaye,S., Theodore,J., Tirrell,A.,  
Travers,M., Triggillo,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B.,  
Wu,X., Wymen,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and  
Zody,M.

TITLE  
JOURNAL

## COMMENT

Submitted (28-FEB-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Mar 16, 2000 this sequence version replaced g1:108303.  
All repeats were identified using RepeatMasker:  
Smit,A.F.A. & Green, P. (1996.1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

----- Project Information

Center project name: L7202

Center clone name: 153\_J19

-----  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 55 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 1225: contig of 1225 bp in length  
\* 1226 1325: gap of 100 bp  
\* 1326 2383: contig of 1058 bp in length  
\* 2384 2483: gap of 100 bp  
\* 2484 3638: contig of 1155 bp in length  
\* 3639 3738: gap of 100 bp  
\* 3739 4871: contig of 1133 bp in length  
\* 4872 4971: gap of 100 bp  
\* 4972 6453: contig of 1482 bp in length  
\* 6454 6553: gap of 100 bp  
\* 6554 7651: contig of 1098 bp in length  
\* 7652 7751: gap of 100 bp  
\* 7752 8917: contig of 1166 bp in length  
\* 8918 9017: gap of 100 bp  
\* 9018 10865: contig of 1848 bp in length  
\* 10866 10965: gap of 100 bp  
\* 10966 12050: contig of 1085 bp in length  
\* 12051 12150: gap of 100 bp  
\* 12151 13291: contig of 1141 bp in length  
\* 13292 13391: gap of 100 bp  
\* 13392 14491: contig of 1100 bp in length

14492 14591: gap of 100 bp  
\* 14592 15649: contig of 1058 bp in length  
\* 15650 15749: gap of 100 bp  
\* 15750 17150: contig of 1401 bp in length  
\* 17151 17250: gap of 100 bp  
\* 17251 18421: contig of 1171 bp in length  
\* 18422 18521: gap of 100 bp  
\* 18522 20045: contig of 1524 bp in length  
\* 20046 20145: gap of 100 bp  
\* 20146 21485: contig of 1340 bp in length  
\* 21486 21585: gap of 100 bp  
\* 21586 23169: contig of 1584 bp in length  
\* 23170 23269: gap of 100 bp  
\* 23270 24275: contig of 1006 bp in length  
\* 24276 24375: gap of 100 bp  
\* 24376 25509: contig of 1134 bp in length  
\* 25510 25609: gap of 100 bp  
\* 25610 26831: contig of 1222 bp in length  
\* 26832 26931: gap of 100 bp  
\* 26932 27248: contig of 317 bp in length  
\* 27249 27348: gap of 100 bp  
\* 27349 28595: contig of 1247 bp in length  
\* 28596 28695: gap of 100 bp  
\* 28696 30616: contig of 1921 bp in length  
\* 30617 30716: gap of 100 bp  
\* 30717 32613: contig of 1897 bp in length  
\* 32614 32713: gap of 100 bp  
\* 32714 33958: contig of 1245 bp in length  
\* 33959 34058: gap of 100 bp  
\* 34059 35732: contig of 1674 bp in length  
\* 35733 35832: gap of 100 bp  
\* 35833 37422: contig of 1590 bp in length  
\* 37423 37522: gap of 100 bp  
\* 37523 38306: contig of 784 bp in length  
\* 38307 38406: gap of 100 bp  
\* 38407 40880: contig of 2474 bp in length  
\* 40881 40980: gap of 100 bp  
\* 40981 42955: contig of 1975 bp in length  
\* 42956 43055: gap of 100 bp  
\* 43056 45418: contig of 2363 bp in length  
\* 45419 45518: gap of 100 bp  
\* 45519 48193: contig of 2675 bp in length  
\* 48194 48293: gap of 100 bp  
\* 48294 50938: contig of 2645 bp in length  
\* 50939 51038: gap of 100 bp  
\* 51039 54450: contig of 3412 bp in length  
\* 54451 54550: gap of 100 bp  
\* 54551 57303: contig of 2753 bp in length  
\* 57304 57403: gap of 100 bp  
\* 57404 60335: contig of 2932 bp in length  
\* 60336 60435: gap of 100 bp  
\* 60436 64090: contig of 3655 bp in length  
\* 64091 64190: gap of 100 bp  
\* 64191 67400: contig of 3210 bp in length  
\* 67401 67500: gap of 100 bp  
\* 67501 70359: contig of 2859 bp in length  
\* 70360 70459: gap of 100 bp  
\* 70460 74596: contig of 4137 bp in length  
\* 74597 74696: gap of 100 bp  
\* 74697 78944: contig of 4248 bp in length  
\* 78945 79044: gap of 100 bp  
\* 79045 83836: contig of 4792 bp in length  
\* 83837 83936: gap of 100 bp  
\* 83937 89561: contig of 5625 bp in length  
\* 89562 89661: gap of 100 bp  
\* 89662 95570: contig of 5909 bp in length  
\* 95571 95670: gap of 100 bp  
\* 95671 100625: contig of 4955 bp in length  
\* 100626 100725: gap of 100 bp  
\* 100726 106496: contig of 5771 bp in length  
\* 106497 106596: gap of 100 bp  
\* 106597 113908: contig of 7312 bp in length  
\* 113909 114008: gap of 100 bp

\* 114009 119847: contig of 5839 bp in length  
\* 119848 119947: gap of 100 bp  
\* 119948 126028: contig of 6081 bp in length  
\* 126028 126128: gap of 100 bp  
\* 126129 132814: contig of 6686 bp in length  
\* 132815 132914: gap of 100 bp  
\* 132915 139664: contig of 6750 bp in length  
\* 139665 139764: gap of 100 bp  
\* 139765 149495: contig of 9731 bp in length  
\* 149496 149595: gap of 100 bp  
\* 149596 157948: contig of 8353 bp in length  
\* 157949 158048: gap of 100 bp  
\* 158049 167045: contig of 8997 bp in length  
\* 167046 167145: gap of 100 bp  
\* 167146 181853: contig of 14708 bp in length.

## FEATURES

## SOURCE

/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="1"  
/map="1"  
/clone="RP11-153J19"  
/clone\_id="RPC1-11 Human Male BAC"  
1. .1225  
misc\_feature  
/note="assembly\_fragment"  
1326. .2383  
misc\_feature  
/note="assembly\_fragment"  
2484. .3638  
misc\_feature  
/note="assembly\_fragment"  
3739. .4871  
misc\_feature  
/note="assembly\_fragment"  
4972. .6453  
misc\_feature  
/note="assembly\_fragment"  
6554. .7651  
misc\_feature  
/note="assembly\_fragment"  
7752. .8917  
misc\_feature  
/note="assembly\_fragment"  
9018. .10865  
misc\_feature  
/note="assembly\_fragment"  
10966. .12050  
misc\_feature  
/note="assembly\_fragment"  
12151. .13291  
misc\_feature  
/note="assembly\_fragment"  
13392. .14491  
misc\_feature  
/note="assembly\_fragment"  
14592. .15649  
misc\_feature

## Query Match

Best Local Similarity 3.2%; Score 19; DB 68; Length 181853;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 484 ttgtgtgcagctaatatg 502  
|||||

Db 142035 TTGTGTGCAGCTAATATG 142053

## RESULT 34

LOCUS AC090652 185892 bp DNA HTG 17-APR-2001  
DEFINITION Mus musculus clone rp23-116a10, WORKING DRAFT SEQUENCE, 37  
unordered pieces.  
ACCESSION AC090652  
VERSION AC090652.12 GI:13654354  
KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
SOURCE house mouse.  
ORGANISM Mus musculus.

REFERENCE 1 (bases 1 to 185892)  
AUTHORS Jiang,X., Song,L. and Roe,B.A.  
TITLE Mus musculus BAC Clone rp23-116a10  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 185892)

AUTHORS  
TITLE  
JOURNAL

## COMMENT

Jiang,X., Song,L. and Roe,B.A.  
Direct Submission  
Submitted (07-MAR-2001) Department Of Chemistry And Biochemistry,  
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,  
Ok 73019, USA  
On Apr 17, 2001 this sequence version replaced gi:13592216.  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 37 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
1  
2257 2256: contig of 2256 bp in length  
2357 2356: gap of unknown length  
4895 4894: contig of 2538 bp in length  
4995 4994: gap of unknown length  
7125 7124: contig of 2130 bp in length  
7225 7224: gap of unknown length  
9314 9313: contig of 2089 bp in length  
9414 9413: gap of unknown length  
11676 11675: contig of 2262 bp in length  
11776 11775: gap of unknown length  
13996 13995: contig of 2220 bp in length  
14096 14095: gap of unknown length  
16201 16200: contig of 2105 bp in length  
16301 16300: gap of unknown length  
19351 19350: contig of 3050 bp in length  
22099 22099: gap of unknown length  
22100 22100: gap of unknown length  
22200 22200: contig of 3196 bp in length  
25396 25395: gap of unknown length  
25496 25495: gap of unknown length  
28785 28784: contig of 3290 bp in length  
28886 28885: gap of unknown length  
31919 31919: contig of 3034 bp in length  
32019 32019: gap of unknown length  
34426 34426: contig of 2407 bp in length  
34526 34526: gap of unknown length  
34527 34527: contig of 3850 bp in length  
38377 38376: gap of unknown length  
38477 38477: contig of 2887 bp in length  
41363 41363: gap of unknown length  
41464 41463: gap of unknown length  
43857 43857: contig of 2394 bp in length  
43958 43958: gap of unknown length  
47633 47633: contig of 3676 bp in length  
47733 47733: gap of unknown length  
51680 51680: contig of 3947 bp in length  
51780 51780: gap of unknown length  
56459 56459: contig of 4679 bp in length  
56559 56559: gap of unknown length  
61682 61682: contig of 5123 bp in length  
61782 61782: gap of unknown length  
68058 68058: contig of 6276 bp in length  
68158 68158: gap of unknown length  
68159 68159: gap of unknown length  
73468 73468: contig of 5310 bp in length  
73568 73568: gap of unknown length  
73659 73659: gap of unknown length  
79967 79966: contig of 6398 bp in length  
80066 80066: gap of unknown length  
85383 85383: contig of 5317 bp in length  
85483 85483: gap of unknown length  
85484 85484: gap of unknown length  
91631 91630: contig of 6147 bp in length  
91730 91730: gap of unknown length  
97583 97583: contig of 5853 bp in length  
97683 97683: gap of unknown length  
104398 104398: contig of 6715 bp in length  
104498 104498: gap of unknown length  
111386 111386: contig of 6688 bp in length  
111486 111486: gap of unknown length  
118341 118341: contig of 6855 bp in length  
118441 118441: gap of unknown length  
125657 125657: contig of 7216 bp in length

125658 125757: gap of unknown length  
\* 125758 132358: contig of 6601 bp in length  
\* 132359 132458: gap of unknown length  
\* 132459 140201: contig of 7743 bp in length  
\* 140202 140301: gap of unknown length  
\* 140302 145956: contig of 5655 bp in length  
\* 145957 146056: gap of unknown length  
\* 146057 153447: contig of 7291 bp in length  
\* 153448 162532: contig of 9085 bp in length  
\* 162533 162632: gap of unknown length  
\* 162633 173314: contig of 10682 bp in length  
\* 173315 173415: gap of unknown length  
\* 173415 185892: contig of 12478 bp in length.  
Location/Qualifiers  
1. 185892  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/clone="rp23-116a10"  
BASE COUNT 46626 a 44442 c 44049 g 46981 t 3794 others  
ORIGIN

Query Match 3.2%; Score 19; DB 78; Length 185892;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 108 ggaagacacagcagcagc 126  
|||||  
DB 64904 GGAAGAACACAGCAGCAGC 64922

RESULT 35  
LOCUS AC069560  
DEFINITION Mus musculus chromosome 2 clone ct7-22f10 strain 129/Sv ES cell  
line Cj7, WORKING DRAFT SEQUENCE, 28 unordered pieces.  
AC069560 191257 bp DNA HTG 28-MAR-2001  
AC069560  
VERSION AC069560.17 GI:13470162  
KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
SOURCE house mouse.  
ORGANISM Mus musculus.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 191257)  
Shauli, S., Rahhal, R., Yao, Z., Rithidech, K. and Roe, B.A.  
Mus musculus Chromosome 2 BAC Clone ct7b-22f10  
Unpublished  
2 (bases 1 to 191257)  
Shauli, S., Rahhal, R., Yao, Z., Rithidech, K. and Roe, B.A.  
Direct Submission  
Submitted (03-JUN-2000) Department of Chemistry and Biochemistry,  
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,  
OK 73019, USA  
On Mar 28, 2001, this sequence version replaced gi:11992964.  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 28 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
1  
2130 2129: contig of 2129 bp in length  
\* 2230 2229: gap of unknown length  
\* 4410 4410: contig of 2181 bp in length  
\* 4411 4510: gap of unknown length  
\* 4511 6827: contig of 2317 bp in length  
\* 6828 6927: gap of unknown length  
\* 6928 9607: contig of 2680 bp in length  
\* 9608 9707: gap of unknown length  
\* 9708 11753: contig of 2046 bp in length  
\* 11754 11853: gap of unknown length

11854 14087: contig of 2234 bp in length  
\* 14088 14187: gap of unknown length  
\* 14188 16271: contig of 2084 bp in length  
\* 16272 16371: gap of unknown length  
\* 16372 19053: contig of 2682 bp in length  
\* 19054 19153: gap of unknown length  
\* 19154 21327: contig of 2174 bp in length  
\* 21328 21427: gap of unknown length  
\* 21428 24279: contig of 2852 bp in length  
\* 24280 24379: gap of unknown length  
\* 24380 26574: contig of 2195 bp in length  
\* 26575 26674: gap of unknown length  
\* 26675 29819: contig of 3145 bp in length  
\* 29820 29919: gap of unknown length  
\* 29920 32658: contig of 2739 bp in length  
\* 32659 32758: gap of unknown length  
\* 32759 35340: contig of 2582 bp in length  
\* 35341 35440: gap of unknown length  
\* 35441 38430: contig of 2990 bp in length  
\* 38431 38530: gap of unknown length  
\* 38431 41853: contig of 3323 bp in length  
\* 41854 41953: gap of unknown length  
\* 41954 45151: contig of 3198 bp in length  
\* 45152 45251: gap of unknown length  
\* 45252 49105: contig of 3854 bp in length  
\* 49106 49205: gap of unknown length  
\* 49206 53586: contig of 4381 bp in length  
\* 53587 53686: gap of unknown length  
\* 53687 57668: contig of 3982 bp in length  
\* 57669 57768: gap of unknown length  
\* 57769 63349: gap of 5581 bp in length  
\* 63350 63449: gap of unknown length  
\* 63450 67562: contig of 4113 bp in length  
\* 67563 74350: gap of unknown length  
\* 74351 74450: contig of 6688 bp in length  
\* 74451 78798: gap of unknown length  
\* 78799 78898: contig of 4348 bp in length  
\* 78899 78899: gap of unknown length  
\* 78899 84605: contig of 5707 bp in length  
\* 84606 84706: gap of unknown length  
\* 84706 99565: contig of 14860 bp in length  
\* 99566 99665: gap of unknown length  
\* 99666 136994: contig of 37329 bp in length  
\* 136995 137094: gap of unknown length  
\* 137095 191257: contig of 54183 bp in length.  
Location/Qualifiers  
1. 191257  
/organism="Mus musculus"  
/strain="129/Sv ES cell line Cj7"  
/db\_xref="taxon:10090"  
/chromosome="2"  
/clone="ct7-22f10"  
/clone\_lib="Caltech Cj7B-BAC library"

BASE COUNT 54814 a 40040 c 40978 g 52695 t 2730 others  
ORIGIN

Query Match 3.2%; Score 19; DB 74; Length 191257;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 537 gaaacacagcagcagc 555  
|||||  
DB 130319 GAAACCAACAGAGAGAGAA 130337

RESULT 36  
LOCUS AL512653  
DEFINITION Homo sapiens chromosome 1 clone RP11-523K4, \*\*\* SEQUENCING IN  
PROGRESS \*\*\*  
ACCESSION AL512653  
VERSION AL512653.4 GI:13235023

KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 194575)  
 AUTHORS McIay, K.  
 TITLE Direct Submission  
 JOURNAL Submitted (28-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire,  
 CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk  
 Requests: clonerequests@sanger.ac.uk  
 On Mar 5, 2001 this sequence version replaced gi:13169575.  
 ----- Genome Center  
 Center: Sanger Centre  
 Center code: SC  
 Web site: http://www.sanger.ac.uk  
 Contact: humquerry@sanger.ac.uk  
 ----- Project Information  
 Center project name: ba523k4  
 ----- Summary Statistics  
 Sequencing program: XGAP4; version 4.5  
 Chemistry: Dye-terminator Big Dye; 98% of reads  
 Dye-terminator Big Dye; 98% of reads  
 Consensus quality: 171678 bases at least Q40  
 Consensus quality: 180206 bases at least Q30  
 Consensus quality: 185635 bases at least Q20  
 Insert size: 190375; sum-of-contigs  
 Insert size: 152230; 3.3% error; agarose-fp  
 Quality coverage: 3.14x in Q20 bases; sum-of-contigs Quality  
 coverage: 4.72x in Q20 bases; agarose-fp  
 -----

\* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 43 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.  
 \* 1 4458: contig of 4458 bp in length  
 \* 4459 4558: gap of 100 bp  
 \* 4559 6602: contig of 2044 bp in length  
 \* 6603 6702: gap of 100 bp  
 \* 6703 9078: contig of 2376 bp in length  
 \* 9079 9178: gap of 100 bp  
 \* 9179 12224: contig of 3046 bp in length  
 \* 12225 12324: gap of 100 bp  
 \* 12325 15579: contig of 3255 bp in length  
 \* 15580 15679: gap of 100 bp  
 \* 15680 22986: contig of 7307 bp in length  
 \* 22987 23086: gap of 100 bp  
 \* 23087 25938: contig of 2852 bp in length  
 \* 25939 26038: gap of 100 bp  
 \* 26039 38837: contig of 12799 bp in length  
 \* 38838 38937: gap of 100 bp  
 \* 38938 45337: contig of 6400 bp in length  
 \* 45338 45437: gap of 100 bp  
 \* 45438 49342: contig of 3905 bp in length  
 \* 49343 49442: gap of 100 bp  
 \* 49443 61905: contig of 12463 bp in length  
 \* 61906 62005: gap of 100 bp  
 \* 62006 64568: contig of 2563 bp in length  
 \* 64569 64668: gap of 100 bp  
 \* 64669 67376: contig of 2708 bp in length  
 \* 67377 67476: gap of 100 bp  
 \* 67477 69819: contig of 2343 bp in length  
 \* 69820 69919: gap of 100 bp  
 \* 69920 76132: contig of 6213 bp in length  
 \* 76133 76232: gap of 100 bp  
 \* 76233 78236: contig of 2004 bp in length  
 \* 78237 78336: gap of 100 bp  
 \* 78337 86544: contig of 8208 bp in length

\* 86545 86644: gap of 100 bp  
 \* 86645 89369: contig of 2725 bp in length  
 \* 89370 89469: gap of 100 bp  
 \* 89470 93493: contig of 4024 bp in length  
 \* 93494 93593: gap of 100 bp  
 \* 93594 96676: contig of 3083 bp in length  
 \* 96677 96776: gap of 100 bp  
 \* 96777 99971: contig of 3195 bp in length  
 \* 99972 100071: gap of 100 bp  
 \* 100072 105701: contig of 5630 bp in length  
 \* 105702 105801: gap of 100 bp  
 \* 105802 109322: contig of 3521 bp in length  
 \* 109323 109422: gap of 100 bp  
 \* 109423 112011: contig of 2589 bp in length  
 \* 112012 112111: gap of 100 bp  
 \* 112112 114284: contig of 2173 bp in length  
 \* 114285 114384: gap of 100 bp  
 \* 114385 122566: contig of 8182 bp in length  
 \* 122567 122666: gap of 100 bp  
 \* 122667 129674: contig of 7008 bp in length  
 \* 129675 129774: gap of 100 bp  
 \* 129775 132589: contig of 2815 bp in length  
 \* 132590 132689: gap of 100 bp  
 \* 132690 134777: contig of 2088 bp in length  
 \* 134778 134877: gap of 100 bp  
 \* 134878 141445: contig of 6568 bp in length  
 \* 141446 141545: gap of 100 bp  
 \* 141546 149107: contig of 7562 bp in length  
 \* 149108 149207: gap of 100 bp  
 \* 149208 152744: contig of 3537 bp in length  
 \* 152745 152844: gap of 100 bp  
 \* 152845 158786: contig of 5942 bp in length  
 \* 158787 158886: gap of 100 bp  
 \* 158887 161331: contig of 2345 bp in length  
 \* 161332 161331: gap of 100 bp  
 \* 161332 163923: contig of 2592 bp in length  
 \* 163924 164023: gap of 100 bp  
 \* 164024 167292: contig of 3269 bp in length  
 \* 167293 167392: gap of 100 bp  
 \* 167393 169608: contig of 2216 bp in length  
 \* 169609 169708: gap of 100 bp  
 \* 169709 175744: contig of 6036 bp in length  
 \* 175745 175844: gap of 100 bp  
 \* 175845 180590: contig of 4746 bp in length  
 \* 180591 180690: gap of 100 bp  
 \* 180691 183185: contig of 2495 bp in length  
 \* 183186 183285: gap of 100 bp  
 \* 183286 185116: contig of 2231 bp in length  
 \* 185117 185616: gap of 100 bp  
 \* 185617 192097: contig of 6481 bp in length  
 \* 192098 192197: gap of 100 bp  
 \* 192198 194575: contig of 2378 bp in length.  
 \* Location/Qualifiers  
 \* 1..194575  
 \* /organism="Homo sapiens"  
 \* /db\_xref="taxon:9606"  
 \* /chromosome="1"  
 \* /clone="RP11-523K4"  
 \* /clone\_lib="RPCT-11.2"  
 \* 1..4458  
 \* /note="assembly-fragment:00856  
 \* fragment\_chain:1"  
 \* 4459..6602  
 \* /note="assembly-fragment:00764  
 \* fragment\_chain:1"  
 \* 6703..9078  
 \* /note="assembly-fragment:01170  
 \* fragment\_chain:1"  
 \* 9179..12224  
 \* /note="assembly-fragment:00852  
 \* fragment\_chain:1"  
 \* 12325..15579  
 \* /note="assembly-fragment:01087

## FEATURES

source

1..194575

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/chromosome="1"

/clone="RP11-523K4"

/clone\_lib="RPCT-11.2"

1..4458

/note="assembly-fragment:00856  
fragment\_chain:1"

4459..6602

/note="assembly-fragment:00764  
fragment\_chain:1"

6703..9078

/note="assembly-fragment:01170  
fragment\_chain:1"

9179..12224

/note="assembly-fragment:00852  
fragment\_chain:1"

12325..15579

/note="assembly-fragment:01087

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misc_feature      fragment_chain:2"
15680..22986
/note="assembly_fragment:00246
fragment_chain:2"
misc_feature      /note="assembly_fragment:01976
23087..25938
/note="assembly_fragment:01976
26039..38837
fragment_chain:2"
/note="assembly_fragment:01200
fragment_chain:2"
misc_feature      /note="assembly_fragment:00679
38938..45337
fragment_chain:3"
/note="assembly_fragment:00679
45438..49342
fragment_chain:3"
/note="assembly_fragment:01991
fragment_chain:3"
misc_feature      /note="assembly_fragment:00239
49443..61905
fragment_chain:3"
/note="assembly_fragment:00239
62006..64568
fragment_chain:3"
/note="assembly_fragment:00334
fragment_chain:4"
misc_feature      /note="assembly_fragment:00402
64669..67376
fragment_chain:4"
/note="assembly_fragment:00402
67477..69819
fragment_chain:4"
/note="assembly_fragment:00376
fragment_chain:5"
misc_feature      /note="assembly_fragment:01449
69920..76132
fragment_chain:5"
/note="assembly_fragment:01449
76233..78236
fragment_chain:5"
/note="assembly_fragment:00418
78337..86544
fragment_chain:6"
/note="assembly_fragment:00432
86645..89369
fragment_chain:6"
misc_feature      /note="assembly_fragment:00503
89470..93493
fragment_chain:7"
/note="assembly_fragment:00747
93594..96676
fragment_chain:7"
/note="assembly_fragment:00956
96777..99971
fragment_chain:8"
/note="assembly_fragment:00401
fragment_chain:8"
misc_feature

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Query Match 3.2%: Score 19; DB 81; Length 194575;  
 Best Local Similarity 100.0%; Pred. No. 26;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

547 gggagagaaagcgtcg 565  
 |||  
 Db 187810 GGAGAGAAAAGCCTCG 187828

RESULT 37  
 AC011359 198453 bp DNA HTG 14-FEB-2001  
 LOCUS Homo sapiens chromosome 5 clone CTC-370H24, WORKING DRAFT SEQUENCE,  
 DEFINITION 6 ordered pieces.  
 AC011359  
 VERSION AC011359.4 GI:12830128  
 KEYWORDS HTG; HTGS\_PHASE2; HTGS\_DRAFT.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 198453)  
 REFERENCE DOE Joint Genome Institute.  
 AUTHORS

```

TITLE      Sequencing of Human Chromosome 5
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 198453)
AUTHORS    DOE Joint Genome Institute.
TITLE      Direct Submission
JOURNAL    Submitted (06-OCT-1999) Production Sequencing Facility, DOE Joint
           Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
           On Feb 14, 2001 this sequence version replaced gi:7710570.
COMMENT    -----Genome Center
           Center: Joint Genome Institute
           Center Code: JGI
           Web site: http://www.jgi.doe.gov
           -----
           Project Information
           Center Project Name: 327450, H224
           Center clone name: CTF-HSPC_370H24
           -----
           Summary Statistics
           Consensus quality: 192637 bases at least Q40
           Consensus quality: 195977 bases at least Q30
           Consensus quality: 196983 bases at least Q20
           Estimated insert size: 196000; pulse field gel estimation
           Estimated insert size: 197953; sum-of-contrigs estimation
           Quality coverage: 8.4 in Q20 bases; pulse field gel estimation
           Quality coverage: 8.32 in Q20 bases; sum-of-contrigs estimation.
           * NOTE: This is a 'working draft' sequence. It currently
           * consists of 6 contrigs. Gaps between the contrigs
           * are represented as runs of N. The order of the pieces
           * is believed to be correct as given, however the sizes
           * of the gaps between them are based on estimates that have
           * provided by the submitter.
           * This sequence will be replaced
           * by the finished sequence as soon as it is available and
           * the accession number will be preserved.
           *
           1 80992: contrig of 80992 bp in length
           * 80993 81092: gap of unknown length
           * 81093 98177: contrig of 17085 bp in length
           * 98178 98277: gap of unknown length
           * 98278 113101: contrig of 14824 bp in length
           * 113102 113201: gap of unknown length
           * 113202 132185: contrig of 18984 bp in length
           * 132186 132285: gap of unknown length
           * 132286 157259: contrig of 24973 bp in length
           * 157259 157359: gap of unknown length
           * 157359 198453: contrig of 41095 bp in length.
           Location/Qualifiers
           source      1. 198453
                   /organism="Homo sapiens"
                   /db_xref="taxon:9606"
                   /chromosome="5"
                   /clone_lib="Caltech human BAC library C"
                   /clone_id="CTC-370H24"
BASE COUNT  54938 a 39611 c 41079 g 62319 t 506 others
ORIGIN

```

Query Match 3.2%: Score 19; DB 62; Length 198453;  
 Best Local Similarity 100.0%; Pred. No. 26;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

484 ttggtgcagctatagtg 502  
 |||  
 Db 134128 TTGGTGCAGCTATAGTG 134146

RESULT 38  
 AL445211 200860 bp DNA HTG 06-MAR-2001  
 LOCUS Homo sapiens chromosome 1 clone RP5-882B12, \*\*\* SEQUENCING IN  
 DEFINITION PROGRESS \*\*\*, 38 unordered pieces.  
 AC011359  
 VERSION AL445211.5 GI:13273841  
 KEYWORDS HTG; HTGS\_PHASE1.



SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS 1 (bases 1 to 200860)  
TITLE McIlroy, K.  
JOURNAL Direct Submission  
Submitted (03-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk Clone  
requests: clonerequests@sanger.ac.uk  
On Mar 11, 2001 this sequence version replaced gi:13234984.  
----- Genome Center  
Center: Sanger Centre  
Center code: SC  
Web site: http://www.sanger.ac.uk  
Contact: humquerry@sanger.ac.uk  
----- Project Information  
Center project name: d082812  
----- Summary Statistics  
Assembly program: XGAP4; version 4.5  
Sequencing vector: plasmid; 108752; 100% of reads  
Chemistry: dye-terminator Big Dye; 100% of reads  
Consensus quality: 17636 bases at least Q40  
Consensus quality: 186827 bases at least Q30  
Consensus quality: 192595 bases at least Q20  
Insert size: 197160; sum-of-contigs  
Quality coverage: 2.89x in Q20 bases; sum-of-contigs Quality  
coverage: 5.60x in Q20 bases; agarose-1p  
-----  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 38 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
\* 1 4569: contig of 4569 bp in length  
\* 4570 4669: gap of 100 bp  
\* 9273 9372: contig of 4603 bp in length  
\* 9373 15080: contig of 5708 bp in length  
\* 15081 15180: gap of 100 bp  
\* 15181 18588: contig of 3678 bp in length  
\* 18589 18958: gap of 100 bp  
\* 18959 23944: contig of 4986 bp in length  
\* 23945 24044: gap of 100 bp  
\* 24045 27176: contig of 3132 bp in length  
\* 27177 27276: gap of 100 bp  
\* 27277 31044: contig of 3768 bp in length  
\* 31045 31144: gap of 100 bp  
\* 31145 41645: contig of 10501 bp in length  
\* 41646 41745: gap of 100 bp  
\* 41746 44420: contig of 2675 bp in length  
\* 44421 44520: gap of 100 bp  
\* 44521 51070: contig of 6550 bp in length  
\* 51071 51170: gap of 100 bp  
\* 51171 56439: contig of 5269 bp in length  
\* 56440 56539: gap of 100 bp  
\* 56540 62931: contig of 6392 bp in length  
\* 62932 63031: gap of 100 bp  
\* 63032 66281: contig of 3250 bp in length  
\* 66282 66381: gap of 100 bp  
\* 66382 71591: contig of 5210 bp in length  
\* 71592 71691: gap of 100 bp  
\* 71692 74032: contig of 2341 bp in length  
\* 74033 74132: gap of 100 bp  
\* 74133 78618: contig of 4486 bp in length  
\* 78619 78718: gap of 100 bp  
\* 78719 85194: contig of 6476 bp in length  
\* 85195 85294: gap of 100 bp  
\* 85295 90909: contig of 5615 bp in length

90910 91009: gap of 100 bp  
\* 91010 94589: contig of 3580 bp in length  
\* 94590 94689: gap of 100 bp  
\* 94690 101003: contig of 6316 bp in length  
\* 101006 101105: gap of 100 bp  
\* 101106 113385: contig of 12280 bp in length  
\* 113386 113485: gap of 100 bp  
\* 113486 116348: contig of 2863 bp in length  
\* 116349 116448: gap of 100 bp  
\* 116449 118882: contig of 2334 bp in length  
\* 118883 119082: gap of 100 bp  
\* 119083 121185: contig of 2103 bp in length  
\* 121186 121285: gap of 100 bp  
\* 121286 129849: contig of 8564 bp in length  
\* 129850 129948: gap of 100 bp  
\* 129950 133006: contig of 3057 bp in length  
\* 133007 133106: gap of 100 bp  
\* 133107 141678: contig of 8572 bp in length  
\* 141679 141778: gap of 100 bp  
\* 141779 150289: contig of 8511 bp in length  
\* 150290 150389: gap of 100 bp  
\* 150390 156647: contig of 6258 bp in length  
\* 156648 156747: gap of 100 bp  
\* 156748 160777: contig of 4030 bp in length  
\* 160778 160877: gap of 100 bp  
\* 160878 163439: contig of 2562 bp in length  
\* 163440 163539: gap of 100 bp  
\* 163540 169473: contig of 5934 bp in length  
\* 169474 169573: gap of 100 bp  
\* 169574 173317: contig of 3744 bp in length  
\* 173318 173417: gap of 100 bp  
\* 173418 179971: contig of 6554 bp in length  
\* 179972 180071: gap of 100 bp  
\* 180072 184603: contig of 4532 bp in length  
\* 184604 184703: gap of 100 bp  
\* 184704 193498: contig of 8795 bp in length  
\* 193499 193598: gap of 100 bp  
\* 193599 197774: contig of 4176 bp in length  
\* 197775 197874: gap of 100 bp  
\* 197875 200860: contig of 286 bp in length.  
-----  
FEATURES  
Location/Qualifiers  
source  
1..200860  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="1"  
/clone="RP5-882B12"  
/clone\_lib="RPCT-5"  
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fragment\_chain:1"  
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15181..18588  
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24045..27176  
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27277..31044  
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31145..41645  
/note="assembly\_fragment:00802  
fragment\_chain:3"  
41746..44420  
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misc_feature      63032..66281
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misc_feature      71692..74032
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misc_feature      94690..101005
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misc_feature      119083..121185
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Query Match 3.28; Score 19; DB 81; Length 200860;  
 Best Local Similarity 100.0%; Pred. No. 25;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 547 ggaagaagaagcctccg 565  
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 Db 113569 GGAGAGAGAAAGCCTCCG 113587

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RESULT 39
AC004615      AC004615      235141 bp      DNA      PRI      03-FEB-2000
DEFINITION    Homo sapiens BAC clone GSI-405L21 from 5p15.2, complete sequence.
ACCESSION    AC004615
VERSION      AC004615.1 GI:3080660
KEYWORDS
SOURCE       human.
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE    1 (bases 1 to 235141)
AUTHORS      Kallio, J. and Harmon, G.
TITLE        The sequence of Homo sapiens BAC clone GSI-405L21
JOURNAL      Unpublished

```

```

REFERENCE      2 (bases 1 to 235141)
AUTHORS       Waterston, R.
TITLE         Direct Submision
JOURNAL       Submitted (24-APR-1998) Department of Genetics, Washington
              University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
              3 (bases 1 to 235141)
REFERENCE     Waterston, R.
AUTHORS       Direct Submision
JOURNAL       Submitted (03-FEB-2000) Department of Genetics, Washington
              University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT
-----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
-----
Center project name: H_GSI405L21
-----

```

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:  
 Mapping information for this clone was provided by Dr. Michael Lovett, Departments of Otorhinolaryngology, Molecular Biology and Oncology, University of Texas Southwestern Medical Center, Dallas TX. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:  
 This clone is from the first BAC library from Genome Systems, Inc. (<http://www.genomesystems.com>).  
 Cell line: Lymphoblastoid  
 Haplotypes: two  
 VECTOR: pBelOBAC  
 Selection: chloramphenicol  
 NEIGHBORING SEQUENCE INFORMATION:  
 The actual start of this clone is at base position 1 of GSI-405L21; actual end is at 235141 of GSI-405L21.

This clone contains STS HSA0552D9 (NID:q1233025).

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FEATURES
  source
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      1..235141
      /organism="Homo sapiens"
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      /map="5p15.2"
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      /clone_1lb="GSBAC1"
      /rpt_family="Alu"
      rpt_region
        181..480
        3000..3303
        /rpt_family="Alu"
      rpt_region
        4356..4559
        /rpt_family="Alu"
      rpt_region
        4576..4744
        /rpt_family="(TAGA)n"
      rpt_region
        6769..7074
        /rpt_family="MER1_type"
      rpt_region
        7096..7157
        /rpt_family="Alu"
      rpt_region
        7286..7384
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        7491..7742
        /rpt_family="MALR"
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9154..>234415  
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162076..162174,164155..164368,186819..187104,  
191786..191921,198574..198778,234207..>234415)  
/gene="SEMAF"  
/note="match to U52840 (PID:g2772584);but note  
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/db\_xref="GI:3080661"  
/translation="MKCTCVIAMLFSSSLGLMRLAHPAOGTTCOCRTHEPYSKEIG  
PWLREPRKNAVDLSOLFDPGKELVGAARYLFLQLEDLSLQAVEMECDEATRK  
ACYSKSKSECCNYIRVLVVGDRLETCGTNATTPCTNRSLSNLEIHDQISGAR  
CPTSPDHNSTALTAGGELYAATMDPFGKDPATYRSGLIIPPLTKQVNSKWLNEFN  
VSSSDIGNFTYFEFRENAAVHDCGKTFSRAARVCKNDIGRFLDPTWTFFMKRL  
NCSRPGEVPYVNELSTFELPELDLYGIFETPVNVAIASAVCFMISAIAQAFSGP  
FKYQENRSAMLPYPNPMPHOCGTDOGLVNLTERNLQDAQKFLIMHEVVOPTVY  
PSFMEDNSRSHVADVVOGRALVHITLATDGTGTLKKVRVPLNQNSSCLLEIEL  
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11271..11381  
/rpt\_family="L1"  
12176..12392  
/rpt\_family="L1"  
13349..13391  
/rpt\_family="MER81"  
13453..13898  
/rpt\_family="MAltR"  
19001..19202  
/rpt\_family="L2"  
19350..19841  
/rpt\_family="L1"  
19893..20700  
/rpt\_family="L1"  
21002..21401  
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21797..21994  
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22413..22710  
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27381..27411  
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29733..29893  
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30444..30532  
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33961..34048  
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34057..34316  
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34390..34520  
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36072..36286  
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36464..36604  
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36622..36732  
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38061..38641  
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38939..39082  
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39096..39399  
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39415..39483  
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repeat\_region  
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42862..43091  
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46106..46225  
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47785..47839  
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51495..51731  
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53061..53183  
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54138..54238  
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54275..54314  
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54348..54495  
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58611..58868  
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59061..59261  
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59571..59768  
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60224..60521  
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62226..62479  
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62480..62757  
/rpt\_family="Alu"  
63954..64048  
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64650..64950  
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65069..65357  
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repeat\_region

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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 160 ggggtgctgtctcctcgagca 178  
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Db 96608 GGGTGTGTCTCTCGGCA 96626

RESULT 40  
AL354813 296050 bp DNA HTG 13-APR-2001  
LOCUS Homo sapiens chromosome 20 clone CTD-2653D5, \*\*\* SEQUENCING IN  
DEFINITION PROGRESS \*\*\*, 14 unordered pieces.  
ACCESSION AL354813  
VERSION AL354813.25 GI:13624971  
KEYWORDS HTG; HTGS\_PHASE1; HTGS\_ACTIVEFIN; HTGS\_DRAFT; HTGS\_FULLTOP.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 296050)  
AUTHORS Wallis,J.  
TITLE Direct Submission  
JOURNAL Submitted (12-APR-2001) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk  
requests: clonerequests@sanger.ac.uk  
On Apr 14, 2001 this sequence version replaced gi:13568011.  
COMMENT \*\*\*\*\* Genome Center  
Center: Sanger Centre  
Center code: SC



AUTHORS Paranhos-Baccala,G., Lesenechal,M. and Jolivet,M.  
 TITLE NOVEL TRYPAOSOMA CRUZI ANTIGEN, AND GENE CODING THEREFOR; THEIR  
 APPLICATION TO THE DETECTION OF CHAGAS' DISEASE  
 JOURNAL Patent: WO 9605312-A 8 22-FEB-1996;

COMMENT BIO MERIEUX (FR)  
 Other publication CA 2173957 960222  
 Other publication AU 3169195 960307  
 Other publication FR 2723589 960216.

FEATURES location/Qualifiers

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Query Match 3.0%; Score 18; DB 9; Length 18;  
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 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 211 actctgcgcgtcgtcga 228  
 Db 18 ACTCTGCCGCTGCTGCA 1

RESULT 43  
 LOCUS AR047923 18 bp DNA PAT 29-SEP-1999  
 DEFINITION Sequence 5 from patent US 5820864.  
 ACCESSION AR047923  
 VERSION AR047923.1 GI:5970266  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 18)  
 AUTHORS Paranhos-Baccala,G., Lesenechal,M. and Jolivet,M.  
 TITLE Trypanosoma cruzi antigen, gene encoding therefor and methods of  
 detecting and treating chagas disease  
 JOURNAL Patent: US 5820864-A 5 13-OCT-1998;  
 FEATURES location/Qualifiers

source 1..18 /organism="unknown"  
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Query Match 3.0%; Score 18; DB 9; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 172 tcgggcactgaacggcg 189  
 Db 1 TCGGCGACTGACGCGCG 18

RESULT 44  
 LOCUS AR047926 18 bp DNA PAT 29-SEP-1999  
 DEFINITION Sequence 8 from patent US 5820864.  
 ACCESSION AR047926  
 VERSION AR047926.1 GI:5970269  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 18)  
 AUTHORS Paranhos-Baccala,G., Lesenechal,M. and Jolivet,M.  
 TITLE Trypanosoma cruzi antigen, gene encoding therefor and methods of  
 detecting and treating chagas disease  
 JOURNAL Patent: US 5820864-A 8 13-OCT-1998;  
 FEATURES location/Qualifiers

source 1..18

BASE COUNT 5 a 4 c 7 g 2 t  
 ORIGIN /organism="unknown"

Query Match 3.0%; Score 18; DB 9; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 211 actctgcgcgtcgtcga 228  
 Db 18 ACTCTGCCGCTGCTGCA 1

RESULT 45  
 LOCUS AU049339 339 bp DNA STS 20-JAN-2000  
 DEFINITION Rattus norvegicus, OTSUKA clone, 862e02, microsatellite sequence,  
 sequence tagged site.  
 ACCESSION AU049339  
 VERSION AU049339.1 GI:6722510  
 KEYWORDS  
 SOURCE Rattus norvegicus (strain:Brown Norway) liver hepatocyte DNA,  
 clone:862e02.  
 ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.

REFERENCE 1 (sites)  
 AUTHORS Watanabe,T.K., Hishigaki,H., Okuno,S., Mizoguchi,A., Oga,K.,  
 Tsuji,A., Ono,T., Yamasaki,Y., Kanemoto,N., Takahashi,E., Irie,Y.,  
 Nakamura,Y., Takagi,Y. and Tanigami,A.  
 TITLE The large-scale mapping of rat microsatellite markers  
 JOURNAL Unpublished (1998)  
 REFERENCE 2 (bases 1 to 339)  
 AUTHORS Watanabe,T.K.  
 TITLE Direct Submission  
 JOURNAL Submitted (11-DEC-1998) to the DDBJ/EMBL/GenBank databases. Takeshi  
 K Watanabe, Otsuka GEN Research Institute, Otsuka Pharmaceutical  
 Co., Ltd; 463-10, Kagasuno, Kawauchi-cho, Tokushima, Tokushima  
 771-0192, Japan (E-mail:watanabe@otsuka.gr.jp, Tel:+81-886-65-2888,  
 Fax:+81-886-37-1035)

FEATURES location/Qualifiers  
 source 1..339 /organism="Rattus norvegicus"

/strain="Brown Norway"  
 /db\_xref="taxon:10116"  
 /cell\_type="hepatocyte"  
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 /tissue\_type="liver"  
 /note="862e02F-5'-TCGGTGCACCTGAGTTCAT-3',  
 862e02R-5'-GACATGACACCCACATCATAC-3'."  
 BASE COUNT 61 a 73 c 76 g 128 t  
 ORIGIN

Query Match 3.0%; Score 18; DB 53; Length 339;  
 Best Local Similarity 100.0%; Pred. No. 3e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 537 gaaccacagagagaaga 554  
 Db 23 GAACCAACAGAGAGA 6

RESULT 46  
 LOCUS AX086831 1589 bp DNA PAT 09-MAR-2001  
 DEFINITION Sequence 783 from Patent WO0112659.  
 ACCESSION AX086831  
 VERSION AX086831.1 GI:13276044  
 KEYWORDS  
 SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1589)  
AUTHORS Wiemann, S.  
TITLE Human dna sequences  
JOURNAL Patent: WO 0112659-A 783 22-FEB-2001;  
German Human Genome Project (DE)  
FEATURES  
Source  
Location/Qualifiers  
1. 1589  
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/db\_xref="taxon:9606"  
BASE COUNT 442 a 374 c 353 g 420 t  
ORIGIN

Query Match 3.0%; Score 18; DB 10; Length 1589;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 211 actctgcgcgtctgca 228  
|||||  
Db 333 ACTTCTGCCGCTGCTCA 316

RESULT 47  
HSM801826/c 1589 bp mRNA PRI 10-MAR-2001  
LOCUS HSM801826  
DEFINITION Homo sapiens mRNA: cDNA DKFZp434N2435 (from clone DKFZp434N2435);  
complete cds.  
ACCESSION AL136858  
VERSION AL136858.1 GI:12053220  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1589)  
AUTHORS Wiemann, S., Weill, B., Wellenreuther, R., Gassenhuber, J., Glassl, S.,  
Ansorge, W., Boecker, M., Bloeker, H., Bauersachs, S., Blum, H.,  
Lauber, J., Duesterhoeft, A., Beyer, A., Koehrer, K., Strack, N.,  
Mewes, H.W., Ottenwälder, B., Obermaler, B., Tampe, J., Heubner, D.,  
Mambitt, R., Korn, B., Klein, M., and Poustka, A.  
TITLE Toward a Catalog of Human Genes and Proteins: Sequencing and  
Analysis of 500 Novel Complete Protein Coding Human cDNAs  
JOURNAL Genome Res. 11 (3), 422-435 (2001)  
PUBMED 11230166  
REFERENCE 2 (bases 1 to 1589)  
AUTHORS Poustka, A., Klein, M., Mewes, H.W., Gassenhuber, J. and Wiemann, S.  
TITLE Direct Submission  
JOURNAL Submitted (18-JAN-2000) MIPS, Am Klopferstr. 18a, D-82152  
Martinsried, GERMANY  
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;  
Heidelberg/Germany) within the cDNA sequencing consortium of the  
German Genome Project  
This clone is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further  
information about the clone and the sequencing project is available  
at http://www.mips.blochem.mpg.de/proj/cDNA/  
Location/Qualifiers  
1. 1589  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="DKFZp434N2435"  
/tissue.type="testis"  
/clone\_lib="434 (synonym: htess3). Vector psport1; host  
DH10B; sites NotI + SalI"  
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78. 1175  
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CDS 78. 1175  
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/note="unknown protein"  
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/protein\_id="CA66792.1"  
/db\_xref="GI:12053221"  
/translation="MNVLYPLAVPKGRRLCEVCEAPAEARVCAACTVITYCGVHOKA  
DMDVSIHEKICQLILPLRTSMPEYNSEERQHQLOQROKYLIEFCYTIARQYLIEG  
KHEDAVPALQSLRFKRVKLYGLSSVELVAYPLAASIGLRIYQAEYLFQAOQWTV  
LKSTDCSNATHSLIHRNLGILYIARKNVEARHYLANDYFASCAGTDIRTSGYF  
HLANIFYDKLIDLPATLYTKVSEIYHAILNNHYQVLSAHHIQOQNLKLEFENDGL  
DEQDERATILRLSTLNRESYSDKAPQKTFVLYLKLTVMLYTLMMNSRAQETGMAL  
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1561. 1566  
polya\_signal  
polya\_site 1579  
BASE COUNT 442 a 374 c 353 g 420 t  
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 211 actctgcgcgtctgca 228  
|||||  
Db 333 ACTTCTGCCGCTGCTCA 316

RESULT 48  
AR051480 2520 bp DNA PAT 29-SEP-1999  
LOCUS AR051480  
DEFINITION Sequence 50 from patent US 5830670.  
ACCESSION AR051480  
VERSION AR051480.1 GI:5974844  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2520)  
AUTHORS de la Monte, S. and Wands, J.R.  
TITLE Neural thread protein gene expression and detection of Alzheimer's  
disease  
JOURNAL Patent: US 5830670-A 50 03-NOV-1998;  
Location/Qualifiers  
Source  
1. 2520  
/organism="unknown"  
BASE COUNT 660 a 578 c 581 g 701 t  
ORIGIN

Query Match 3.0%; Score 18; DB 9; Length 2520;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 230 cccctgcatacccccgcg 247  
|||||  
Db 298 CCCCTGCATCACCCCTCG 315

RESULT 49  
AR072620 2520 bp DNA PAT 28-AUG-2000  
LOCUS AR072620  
DEFINITION Sequence 50 from patent US 5948634.  
ACCESSION AR072620  
VERSION AR072620.1 GI:9999384  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2520)  
AUTHORS de la Monte, S. and Wands, J.R.  
TITLE Neural thread protein gene expression and detection of Alzheimer's

disease  
JOURNAL Patent: US 5948634-A 50 07-SEP-1999;  
FEATURES Location/Qualifiers  
SOURCE 1..2520  
/organism="unknown"  
BASE COUNT 660 a 578 c 581 g 701 t  
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Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 230 cccctgcacccccctg 247  
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DB 298 CCCCTGCATCACCCCTG 315

RESULT 50  
AR073165  
LOCUS AR073165 2520 bp DNA PAT 28-AUG-2000  
DEFINITION Sequence 50 from patent US 5948688.  
ACCESSION AR073165  
VERSION AR073165.1 GI:9999928  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2520)  
AUTHORS de la Monte,S. and Wands,J.R.  
TITLE Neural thread protein gene expression and detection of Alzheimer's  
disease  
JOURNAL Patent: US 5948688-A 50 07-SEP-1999;  
FEATURES Location/Qualifiers  
SOURCE 1..2520  
/organism="unknown"  
BASE COUNT 660 a 578 c 581 g 701 t  
ORIGIN

Query Match 3.0%; Score 18; DB 9; Length 2520;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 230 cccctgcacccccctg 247  
|||||  
DB 298 CCCCTGCATCACCCCTG 315

Search completed: September 21, 2001, 21:10:19  
Job time: 25839 sec

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OM nucleic - nucleic search, using sw model

Run on: September 21, 2001, 13:47:10 : Search time 646.95 Seconds  
(without alignments)  
576.511 Million cell updates/sec

Title: US-09-138-735-1\_COPY\_1232\_1825

Perfect score: 594  
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Scoring table:  
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Gapop 60.0 , Gapext 60.0

Searched: 730101 seqs, 313950809 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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| 12 | 18 | 3.0 | 1302   | 21 | AAH59435  | Human secreted pro  |
| 13 | 18 | 3.0 | 2520   | 15 | AAH07884  | Neural thread prot  |
| 14 | 18 | 3.0 | 2520   | 17 | AAH27766  | AD 16c human neuro  |
| 15 | 18 | 3.0 | 68750  | 21 | AAH35887  | Sorangium cellulos  |
| 16 | 18 | 3.0 | 71989  | 21 | AAH29349  | Sorangium cellulos  |
| 17 | 17 | 2.9 | 198    | 20 | AAH84320  | Stealth virus nucl  |
| 18 | 17 | 2.9 | 353    | 21 | AAH09227  | Human secreted pro  |
| 19 | 17 | 2.9 | 386    | 21 | AAH01025  | Human secreted pro  |
| 20 | 17 | 2.9 | 513    | 21 | AAH38084  | Human secreted pro  |
| 21 | 17 | 2.9 | 673    | 19 | AAH16884  | Arabidopsis thalia  |
| 22 | 17 | 2.9 | 673    | 19 | AAH26019  | Human prostate can  |
| 23 | 17 | 2.9 | 697    | 21 | AAH87504  | Prostate disease m  |
| 24 | 17 | 2.9 | 697    | 21 | AAH33534  | Prostate, breast a  |
| 25 | 17 | 2.9 | 763    | 21 | AAH39218  | Human prostate can  |
| 26 | 17 | 2.9 | 800    | 21 | AAH9839   | Arabidopsis thalia  |
| 27 | 17 | 2.9 | 1148   | 21 | AAH42507  | Human secreted pro  |
| 28 | 17 | 2.9 | 1273   | 21 | AAH4984   | Arabidopsis thalia  |
| 29 | 17 | 2.9 | 1338   | 19 | AAH37359  | Arabidopsis thalia  |
| 30 | 17 | 2.9 | 1338   | 19 | AAH64526  | Arabidopsis thalia  |
| 31 | 17 | 2.9 | 1338   | 19 | AAH44417  | Mycobacterium tube  |
| 32 | 17 | 2.9 | 1338   | 20 | AAH19327  | M. tuberculosis an  |
| 33 | 17 | 2.9 | 1338   | 20 | AAH19115  | M. tuberculosis re  |
| 34 | 17 | 2.9 | 1647   | 21 | AAH79935  | Human secreted pro  |
| 35 | 17 | 2.9 | 3337   | 17 | AAH34620  | P. vivax ESP-1 blo  |
| 36 | 17 | 2.9 | 3337   | 20 | AAH15174  | DNA encoding a sec  |
| 37 | 17 | 2.9 | 6171   | 17 | AAH74895  | Human ORFX ORF450   |
| 38 | 17 | 2.9 | 11212  | 21 | AAH58762  | DNA encoding a cyc  |
| 39 | 17 | 2.9 | 11672  | 21 | AAH01009  | Escherichia coli p  |
| 40 | 17 | 2.9 | 15611  | 21 | AAH01008  | Escherichia coli p  |
| 41 | 17 | 2.9 | 240825 | 22 | AAH24497  | Human PG-3 gene.    |
| 42 | 16 | 2.7 | 41     | 15 | AAH36842  | Adaptor-primer. S   |
| 43 | 16 | 2.7 | 222    | 15 | AAH03710  | Retrotransposon pro |
| 44 | 16 | 2.7 | 334    | 20 | AAH25170  | HIV-1 group O Isol  |
| 45 | 16 | 2.7 | 371    | 20 | AAH21399  | 3' fragment of Abs  |
| 46 | 16 | 2.7 | 398    | 21 | AAH01286  | Human secreted pro  |
| 47 | 16 | 2.7 | 413    | 21 | AAH79394  | Eucalyptus grandis  |
| 48 | 16 | 2.7 | 489    | 21 | AAH01726  | Human secreted pro  |
| 49 | 16 | 2.7 | 541    | 19 | AAH76907  | S. glaucosens Hst   |
| 50 | 16 | 2.7 | 624    | 18 | AAH84039  | DNA encoding a Sta  |
| 51 | 16 | 2.7 | 651    | 18 | AAH15445  | Human gene fragmen  |
| 52 | 16 | 2.7 | 774    | 19 | AAH28667  | Ripening banana pu  |
| 53 | 16 | 2.7 | 774    | 20 | AAH16622  | Human gene express  |
| 54 | 16 | 2.7 | 1185   | 19 | AAH05039  | Alcaligenes eutrop  |
| 55 | 16 | 2.7 | 1185   | 20 | AAH08784  | A. eutrophus beta-  |
| 56 | 16 | 2.7 | 1185   | 21 | AAH71692  | A. eutrophus bktB   |
| 57 | 16 | 2.7 | 1234   | 21 | AAH35983  | Arabidopsis thalia  |
| 58 | 16 | 2.7 | 1314   | 19 | AAH00732  | Arabidopsis thalia  |
| 59 | 16 | 2.7 | 1314   | 19 | AAH09626  | A. terreus FAOD-L   |
| 60 | 16 | 2.7 | 1314   | 20 | AAH07721  | Heat-resistant fru  |
| 61 | 16 | 2.7 | 1411   | 14 | AAH041260 | Encodes repressor   |
| 62 | 16 | 2.7 | 1411   | 15 | AAH072717 | Dialkylglycine dec  |
| 63 | 16 | 2.7 | 1669   | 20 | AAH25204  | Mai ze cinnamate-4- |
| 64 | 16 | 2.7 | 1864   | 20 | AAH24942  | Wild type A.eutrop  |
| 65 | 16 | 2.7 | 2063   | 22 | AAH84244  | Signal transductio  |
| 66 | 16 | 2.7 | 2214   | 19 | AAH22682  | New DNA sequence i  |
| 67 | 16 | 2.7 | 2274   | 21 | AAH47059  | zsa mayas DNA fragm |
| 68 | 16 | 2.7 | 2310   | 20 | AAH21502  | Secchiaropolyspora  |
| 69 | 16 | 2.7 | 2610   | 21 | AAH90578  | Human death induce  |
| 70 | 16 | 2.7 | 2886   | 21 | AAH51244  | Murine TANCO 130 c  |
| 71 | 16 | 2.7 | 3045   | 20 | AAH21885  | Neisseria meningit  |
| 72 | 16 | 2.7 | 3045   | 20 | AAH21885  | Neisseria gonorrhoe |
| 73 | 16 | 2.7 | 3331   | 19 | AAH22683  | New DNA sequence i  |
| 74 | 16 | 2.7 | 3331   | 20 | AAH23021  | Human METHI relate  |
| 75 | 16 | 2.7 | 3331   | 22 | AAH90078  | DB6074 cDNA clone.  |
| 76 | 16 | 2.7 | 5117   | 21 | AAH06027  | hudep-1 cDNA. Hom   |
| 77 | 16 | 2.7 | 6242   | 21 | AAH99495  | Human cDNA encodin  |
| 78 | 16 | 2.7 | 6545   | 17 | AAH27537  | Maltose binding pr  |
| 79 | 16 | 2.7 | 7732   | 20 | AAH77723  | pV22 vector. Synt   |
| 80 | 16 | 2.7 | 9243   | 21 | AAH81534  | N. meningitidis pa  |
| 81 | 16 | 2.7 | 9551   | 20 | AAH22301  | cDNA encoding a hu  |
| 82 | 16 | 2.7 | 16510  | 21 | AAH21086  | Human low adenosin  |
| 83 | 16 | 2.7 | 16510  | 21 | AAH34964  | Human adenosine re  |
| 84 | 16 | 2.7 | 17634  | 21 | AAH21087  | Human low adenosin  |

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|-------|----|-----|---------|----|-----------|--------------------|-------|------|----|-----------|--------------------|
| C 85  | 16 | 2.7 | 17634   | 21 | AAA34965  | Human adenosine re | C 158 | 1102 | 22 | AAE222774 | Human prostate can |
| C 86  | 16 | 2.7 | 21721   | 20 | AAH83427  | Human lipolysis st | C 159 | 1129 | 21 | AAE545524 | Arabidopsis thalia |
| C 87  | 16 | 2.7 | 22976   | 20 | AAH83426  | Genomic region con | C 160 | 1144 | 21 | AAE33490  | Arabidopsis thalia |
| C 88  | 16 | 2.7 | 23187   | 21 | AAA50273  | Human lipolysis st | C 161 | 1189 | 21 | AAE07514  | Fusarium venenatum |
| C 89  | 16 | 2.7 | 23187   | 22 | AAE2331   | Human leptin fragm | C 162 | 1200 | 22 | AAE71690  | Corynebacterium gl |
| C 90  | 16 | 2.7 | 39796   | 21 | AAE61681  | Nucleotide sequenc | C 163 | 1211 | 21 | AAE41977  | Arabidopsis thalia |
| C 91  | 16 | 2.7 | 47475   | 21 | AAA81465  | N. meningitidis pa | C 164 | 1221 | 21 | AAE97139  | Arabidopsis thalia |
| C 92  | 16 | 2.7 | 102634  | 21 | AAH81464  | N. meningitidis pa | C 165 | 1223 | 21 | AAE99054  | Human gene 75 DNA  |
| C 93  | 16 | 2.7 | 349980  | 21 | AAE21608  | Neisseria meningit | C 166 | 1263 | 21 | AAE35285  | Human pancreatic c |
| C 94  | 16 | 2.7 | 349980  | 21 | AAE21609  | Neisseria meningit | C 167 | 1278 | 20 | AAE90824  | Plant retroelement |
| C 95  | 16 | 2.7 | 349980  | 21 | AAE21610  | Neisseria meningit | C 168 | 1281 | 20 | AAE90824  | DNA encoding human |
| C 96  | 16 | 2.7 | 349980  | 21 | AAE21612  | Neisseria meningit | C 169 | 1287 | 20 | AAE15146  | Coding region for  |
| C 97  | 16 | 2.7 | 837096  | 21 | AAA81489  | N. meningitidis pa | C 170 | 1294 | 21 | AAE13611  | Corynebacterium gl |
| C 98  | 16 | 2.7 | 1437668 | 21 | AAA81490  | N. meningitidis pa | C 171 | 1313 | 16 | AAE91637  | Aspergillus oryzae |
| C 99  | 15 | 2.5 | 20      | 21 | AAAL4833  | PCR primer HG52.16 | C 172 | 1313 | 16 | AAE91637  | Mouse sonic hedgeh |
| C 100 | 15 | 2.5 | 40      | 18 | AAE58819  | DNP DU labelled ol | C 173 | 1313 | 20 | AAE25620  | Mouse sonic hedgeh |
| C 101 | 15 | 2.5 | 44      | 18 | AAE58819  | Glycerol-based DNP | C 174 | 1313 | 20 | AAE25101  | Mouse sonic hedgeh |
| C 102 | 15 | 2.5 | 44      | 18 | AAE58825  | Glycerol DNP/DNP D | C 175 | 1313 | 20 | AAE07274  | Mouse sonic hedgeh |
| C 103 | 15 | 2.5 | 81      | 16 | AAE06202  | HIV-1 reverse tran | C 176 | 1313 | 20 | AAE16185  | Mouse shh hedgehog |
| C 104 | 15 | 2.5 | 168     | 21 | AAE44666  | Human secreted exp | C 177 | 1313 | 21 | AAE50449  | Mouse sonic hedgeh |
| C 105 | 15 | 2.5 | 196     | 21 | AAE41667  | Human secreted exp | C 178 | 1313 | 21 | AAE30277  | Mouse sonic hedgeh |
| C 106 | 15 | 2.5 | 295     | 16 | AAE21139  | Human gene signalu | C 179 | 1313 | 21 | AAE52260  | Mouse sonic hedgeh |
| C 107 | 15 | 2.5 | 297     | 21 | AAE77752  | CDNA encoding huma | C 180 | 1313 | 22 | AAE87077  | Mouse sonic hedgeh |
| C 108 | 15 | 2.5 | 300     | 20 | AAE214302 | Human gene express | C 181 | 1313 | 22 | AAE27016  | Nucleotide sequenc |
| C 109 | 15 | 2.5 | 300     | 20 | AAE212540 | Human gene express | C 182 | 1314 | 22 | AAE37897  | Mouse sonic hedgeh |
| C 110 | 15 | 2.5 | 300     | 21 | AAE00491  | Human colon cancer | C 183 | 1340 | 21 | AAE26964  | Human coenzyme A-u |
| C 111 | 15 | 2.5 | 325     | 20 | AAE86047  | Exon 1 of the huma | C 184 | 1362 | 21 | AAE50399  | Human angiotensin  |
| C 112 | 15 | 2.5 | 325     | 21 | AAE60344  | Human neurotrophin | C 185 | 1362 | 21 | AAE35278  | Soybean retroelme  |
| C 113 | 15 | 2.5 | 325     | 21 | AAE60344  | Human secreted pro | C 186 | 1368 | 21 | AAE53670  | Neisseria gonorrhe |
| C 114 | 15 | 2.5 | 328     | 21 | AAE12718  | Human secreted pro | C 187 | 1368 | 21 | AAE53672  | Neisseria meningit |
| C 115 | 15 | 2.5 | 362     | 22 | AAE93718  | CDNA encoding SFR  | C 188 | 1368 | 22 | AAE72256  | Corynebacterium gl |
| C 116 | 15 | 2.5 | 384     | 22 | AAE65140  | Novel human polyu  | C 189 | 1368 | 22 | AAE72257  | Corynebacterium gl |
| C 117 | 15 | 2.5 | 397     | 19 | AAE44835  | Novel human polyu  | C 190 | 1374 | 21 | AAE51258  | Arabidopsis thalia |
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| C 120 | 15 | 2.5 | 403     | 22 | AAE66880  | Nucleotide encodin | C 193 | 1381 | 20 | AAE84482  | Human secreted pro |
| C 121 | 15 | 2.5 | 426     | 20 | AAE08739  | Human secreted exp | C 194 | 1386 | 22 | AAE60982  | P. putida KT240-a  |
| C 122 | 15 | 2.5 | 430     | 21 | AAA43600  | Polynucleotide seq | C 195 | 1396 | 22 | AAE33740  | Arabidopsis thalia |
| C 123 | 15 | 2.5 | 462     | 20 | AAE20850  | Porcine BAC-PIGF2- | C 196 | 1423 | 17 | AAE39049  | CDNA encoding cell |
| C 124 | 15 | 2.5 | 500     | 21 | AAE65460  | Eucalyptus grandis | C 197 | 1437 | 20 | AAE484973 | Human secreted pro |
| C 125 | 15 | 2.5 | 574     | 21 | AAE65056  | Human prostate can | C 198 | 1448 | 20 | AAE42009  | Human endometriu   |
| C 126 | 15 | 2.5 | 603     | 22 | AAE22775  | Human prostate can | C 199 | 1486 | 21 | AAE38414  | Arabidopsis thalia |
| C 127 | 15 | 2.5 | 628     | 22 | AAE22779  | Human prostate can | C 200 | 1498 | 21 | AAE45265  | Arabidopsis thalia |
| C 128 | 15 | 2.5 | 631     | 21 | AAE54906  | Arabidopsis thalia | C 201 | 1572 | 20 | AAE02671  | T. versicolor lac  |
| C 129 | 15 | 2.5 | 633     | 21 | AAE36696  | Arabidopsis thalia | C 202 | 1572 | 20 | AAE09786  | AAE09786           |
| C 130 | 15 | 2.5 | 633     | 21 | AAE31309  | Arabidopsis thalia | C 203 | 1591 | 16 | AAE09786  | AAE09786           |
| C 131 | 15 | 2.5 | 637     | 21 | AAE37714  | Arabidopsis thalia | C 204 | 1608 | 14 | AAE041461 | AAE041461          |
| C 132 | 15 | 2.5 | 658     | 21 | AAE54905  | Arabidopsis thalia | C 205 | 1631 | 21 | AAE298141 | AAE298141          |
| C 133 | 15 | 2.5 | 659     | 21 | AAE81591  | N. meningitidis pa | C 206 | 1632 | 14 | AAE42976  | AAE42976           |
| C 134 | 15 | 2.5 | 672     | 21 | AAE52269  | Human colon cancer | C 207 | 1667 | 21 | AAE51207  | AAE51207           |
| C 135 | 15 | 2.5 | 674     | 21 | AAE02040  | Human prostate can | C 208 | 1715 | 16 | AAE04588  | AAE04588           |
| C 136 | 15 | 2.5 | 675     | 22 | AAE22781  | Human secreted can | C 209 | 1738 | 21 | AAE51206  | AAE51206           |
| C 137 | 15 | 2.5 | 686     | 21 | AAE60054  | Human secreted pro | C 210 | 1755 | 20 | AAE06232  | AAE06232           |
| C 138 | 15 | 2.5 | 791     | 21 | AAE54902  | Arabidopsis thalia | C 211 | 1779 | 20 | AAE12073  | AAE12073           |
| C 139 | 15 | 2.5 | 792     | 21 | AAE52503  | Arabidopsis thalia | C 212 | 1779 | 20 | AAE12074  | AAE12074           |
| C 140 | 15 | 2.5 | 799     | 20 | AAE16224  | Human gene express | C 213 | 1779 | 20 | AAE12075  | AAE12075           |
| C 141 | 15 | 2.5 | 800     | 19 | AAE63926  | Mycobacterium tube | C 214 | 1779 | 21 | AAE53673  | AAE53673           |
| C 142 | 15 | 2.5 | 800     | 20 | AAE81033  | Nucleotide sequenc | C 215 | 1779 | 21 | AAE53674  | AAE53674           |
| C 143 | 15 | 2.5 | 810     | 21 | AAE39970  | Murine TANGO 188 c | C 216 | 1779 | 21 | AAE53675  | AAE53675           |
| C 144 | 15 | 2.5 | 837     | 21 | AAE30334  | Nucleotide sequenc | C 217 | 1788 | 22 | AAE32651  | AAE32651           |
| C 145 | 15 | 2.5 | 838     | 16 | AAE090275 | Human beta-kinesin | C 218 | 1827 | 21 | AAE69692  | AAE69692           |
| C 146 | 15 | 2.5 | 841     | 22 | AAE75381  | Rattus eutrophia   | C 219 | 1831 | 20 | AAE26880  | AAE26880           |
| C 147 | 15 | 2.5 | 846     | 20 | AAE25129  | Soybean chalcone 1 | C 220 | 1831 | 21 | AAE09889  | AAE09889           |
| C 148 | 15 | 2.5 | 846     | 21 | AAE38424  | Soybean chalcone 1 | C 221 | 1831 | 21 | AAE30190  | AAE30190           |
| C 149 | 15 | 2.5 | 876     | 8  | AAE70094  | Sequence of region | C 222 | 1858 | 22 | AAE85599  | AAE85599           |
| C 150 | 15 | 2.5 | 901     | 20 | AAE86270  | DNA encoding a hum | C 223 | 1862 | 22 | AAE02606  | AAE02606           |
| C 151 | 15 | 2.5 | 921     | 21 | AAE45812  | Arabidopsis thalia | C 224 | 1863 | 21 | AAE28268  | AAE28268           |
| C 152 | 15 | 2.5 | 948     | 22 | AAE90012  | Clone HYAS03 codi  | C 225 | 1869 | 20 | AAE33970  | AAE33970           |
| C 153 | 15 | 2.5 | 1005    | 21 | AAE51280  | Arabidopsis thalia | C 226 | 1869 | 21 | AAE60537  | AAE60537           |
| C 154 | 15 | 2.5 | 1014    | 21 | AAE34499  | Arabidopsis thalia | C 227 | 1869 | 21 | AAE50126  | AAE50126           |
| C 155 | 15 | 2.5 | 1029    | 17 | AAE72718  | g protein coupled  | C 228 | 1869 | 22 | AAE97388  | AAE97388           |
| C 156 | 15 | 2.5 | 1065    | 21 | AAE14557  | Aspergillus oryzae | C 229 | 1873 | 22 | AAE27220  | AAE27220           |
| C 157 | 15 | 2.5 | 1078    | 20 | AAE08745  | Nucleotide encodin | C 230 | 1876 | 12 | AAE04498  | AAE04498           |

|       |       |      |    |           |                    |       |    |     |        |    |           |                     |
|-------|-------|------|----|-----------|--------------------|-------|----|-----|--------|----|-----------|---------------------|
| 231   | c 231 | 1676 | 12 | AAQ14499  | Clone 2 for trunca | c 304 | 15 | 2.5 | 9706   | 21 | AA65342   | NDO related comple  |
| c 232 | c 232 | 1876 | 20 | AAAI5144  | cDNA encoding huma | c 305 | 15 | 2.5 | 9840   | 21 | AA655340  | NDO related comple  |
| c 233 | c 233 | 1879 | 21 | AAZ45850  | Human muscle angio | c 306 | 15 | 2.5 | 9994   | 22 | AA655191  | S. avermitilis 10   |
| c 234 | c 234 | 1879 | 22 | AAF29701  | Human angiotensin  | c 307 | 15 | 2.5 | 10427  | 21 | AAZ36325  | Mechanical stress   |
| c 235 | c 235 | 1894 | 20 | AAH87588  | Human fibrinogen d | c 308 | 15 | 2.5 | 10897  | 17 | AAZ09187  | Murty putative onco |
| c 236 | c 236 | 1911 | 21 | AAF22396  | Human secreted pro | c 309 | 15 | 2.5 | 10898  | 21 | AAAS2462  | Human MN gene. Ho   |
| c 237 | c 237 | 1913 | 21 | AAE97138  | Human gene 75 DNA  | c 310 | 15 | 2.5 | 10898  | 21 | AAAI6543  | Human MN complete   |
| c 238 | c 238 | 1921 | 22 | AAF44835  | RP55-like protein  | c 311 | 15 | 2.5 | 11279  | 21 | AAAB38389 | Pseudomonas sp. WF  |
| c 239 | c 239 | 1931 | 21 | AAZ97093  | Human secreted pro | c 312 | 15 | 2.5 | 11871  | 20 | AAAI3108  | Enterococcus faeca  |
| c 240 | c 240 | 1955 | 21 | AAZ95588  | cDNA encoding a hu | c 313 | 15 | 2.5 | 12286  | 21 | AAZ35261  | Plant generic retr  |
| c 241 | c 241 | 1973 | 21 | AAZ60998  | Human vesicle asso | c 314 | 15 | 2.5 | 12571  | 21 | AAZ35272  | Soybean retroelene  |
| c 242 | c 242 | 2044 | 17 | AAAT13167 | Rat interleukin-1  | c 315 | 15 | 2.5 | 12808  | 21 | AAAB5347  | NDO related comple  |
| c 243 | c 243 | 2044 | 18 | AAAT84010 | DNA encoding a Sta | c 316 | 15 | 2.5 | 12886  | 21 | AAAB09084 | Human patched-like  |
| c 244 | c 244 | 2051 | 20 | AAZ28069  | Heparin sulphate 6 | c 317 | 15 | 2.5 | 13518  | 20 | AAAZ0563  | Polynucleotide seq  |
| c 245 | c 245 | 2051 | 21 | AAZ99186  | Human H56S71 cDNA. | c 318 | 15 | 2.5 | 13574  | 21 | AAAB15529 | N. meningitidis pa  |
| c 246 | c 246 | 2084 | 21 | AAZ52492  | Human secreted pro | c 319 | 15 | 2.5 | 16020  | 21 | AAAB39283 | Streptomyces nogal  |
| c 247 | c 247 | 2102 | 21 | AAZ39969  | Human secreted pro | c 320 | 15 | 2.5 | 24417  | 18 | AAI972221 | Pseudomonas aerugi  |
| c 248 | c 248 | 2104 | 22 | AAAC87120 | Nucleotide sequenc | c 321 | 15 | 2.5 | 25871  | 21 | AAAB09888 | Human genomic OCTN  |
| c 249 | c 249 | 2160 | 20 | AAAB8635  | Nucleotide sequenc | c 322 | 15 | 2.5 | 42000  | 21 | AAAB63349 | Streptomyces globi  |
| c 250 | c 250 | 2187 | 21 | AAZ29701  | Wild-type human c- | c 323 | 15 | 2.5 | 44576  | 21 | AAZ61522  | Cosmid CVO14 contra |
| c 251 | c 251 | 2200 | 22 | AAF27713  | Human transport pr | c 324 | 15 | 2.5 | 50341  | 19 | AAAZ2674  | DNA sequence of a   |
| c 252 | c 252 | 2221 | 20 | AAZ00370  | Partial nucleotide | c 325 | 15 | 2.5 | 50341  | 21 | AAAZ39519 | L5 shuttle phasmid  |
| c 253 | c 253 | 2249 | 21 | AAAS37055 | Human PRO1374 (UNO | c 326 | 15 | 2.5 | 50937  | 21 | AAAB09469 | Streptococcus olea  |
| c 254 | c 254 | 2255 | 22 | AAAF54285 | DNA encoding prote | c 327 | 15 | 2.5 | 52297  | 21 | AAAB09469 | Streptococcus olea  |
| c 255 | c 255 | 2263 | 20 | AAAB0628  | Kidney injury asso | c 328 | 15 | 2.5 | 52298  | 16 | AAAT1411  | Mycobacteriophage   |
| c 256 | c 256 | 2271 | 11 | AAO06844  | Anyase gene from   | c 329 | 15 | 2.5 | 58857  | 21 | AAAS84737 | L5 mycobacterioph   |
| c 257 | c 257 | 2276 | 18 | AAAT86164 | PHA depolymerase g | c 330 | 15 | 2.5 | 63164  | 21 | AAAS3438  | Nucleotide sequenc  |
| c 258 | c 258 | 2291 | 9  | AAAB0309  | Entire amylase gen | c 331 | 15 | 2.5 | 78845  | 21 | AAAB1463  | N. meningitidis pa  |
| c 259 | c 259 | 2311 | 21 | AAAF18225 | Lung cancer associ | c 332 | 15 | 2.5 | 109973 | 21 | AAAF22288 | BAC containing rep  |
| c 260 | c 260 | 2324 | 21 | AAAI5288  | cDNA encoding prot | c 333 | 15 | 2.5 | 172325 | 21 | AAAF21613 | Nelisseria meningit |
| c 261 | c 261 | 2332 | 21 | AAAF7398  | Human nucleic acid | c 334 | 15 | 2.5 | 235033 | 19 | AAAV57926 | Hereditary haemoch  |
| c 262 | c 262 | 2420 | 21 | AAZ46489  | PKA substrate, Csk | c 335 | 15 | 2.5 | 237326 | 19 | AAAV57903 | Hereditary haemoch  |
| c 263 | c 263 | 2501 | 21 | AAAS2499  | 2.5 kb human MN ge | c 336 | 15 | 2.5 | 349980 | 21 | AAAF21608 | Nelisseria meningit |
| c 264 | c 264 | 2501 | 21 |           |                    |       |    |     |        |    |           |                     |





|       |    |      |    |          |                     |       |    |      |    |          |                      |
|-------|----|------|----|----------|---------------------|-------|----|------|----|----------|----------------------|
| c 669 | 14 | 1147 | 21 | AA664274 | Human membrane-ass  | 742   | 14 | 1392 | 18 | AA799938 | Bovine dipeptidyl    |
| c 670 | 14 | 1149 | 21 | AA51824  | Human melancortin   | c 743 | 14 | 1394 | 9  | AA82030  | Synthetic Hydroxym   |
| c 671 | 14 | 1149 | 21 | AA51825  | Human melancortin   | c 744 | 14 | 1394 | 9  | AA82030  | Encodes human 3-hy   |
| c 672 | 14 | 1149 | 21 | AA51826  | Human melancortin   | c 745 | 14 | 1401 | 19 | AA734002 | S. penicellus dnrx   |
| c 673 | 14 | 1149 | 21 | AA51827  | Human melancortin   | c 746 | 14 | 1414 | 20 | AA728679 | Clone HP01766 enco   |
| c 674 | 14 | 1149 | 21 | AA51828  | Human melancortin   | c 747 | 14 | 1417 | 18 | AA793887 | CDNA encoding a no   |
| c 675 | 14 | 1149 | 21 | AA51829  | Human melancortin   | c 748 | 14 | 1417 | 18 | AA87401  | Ad/AD3LP sequence    |
| c 676 | 14 | 1149 | 21 | AA51830  | Human melancortin   | c 749 | 14 | 1417 | 20 | AA87401  | Human phosphorilas   |
| c 677 | 14 | 1149 | 21 | AA51832  | Human melancortin   | c 750 | 14 | 1419 | 21 | AA38239  | Novel human phosph   |
| c 678 | 14 | 1149 | 21 | AA51834  | Human melancortin   | c 751 | 14 | 1420 | 21 | AA42087  | Arbidopsis thalia    |
| c 679 | 14 | 1149 | 21 | AA51836  | Human melancortin   | c 752 | 14 | 1423 | 19 | AA19156  | Human XAG growth f   |
| c 680 | 14 | 1149 | 21 | AA51838  | Human melancortin   | c 753 | 14 | 1423 | 22 | AA63315  | Human huxAG-2/cscg   |
| c 681 | 14 | 1149 | 21 | AA60917  | Phanerocchaete sord | c 754 | 14 | 1428 | 20 | AA808799 | Human homologue of   |
| c 682 | 14 | 1159 | 21 | AA60917  | Human secreted pro  | c 755 | 14 | 1437 | 18 | AA770130 | Max-interacting pr   |
| c 683 | 14 | 1161 | 21 | AA60917  | Arbidopsis thalia   | c 756 | 14 | 1437 | 21 | AA805493 | Streptococcus pneu   |
| c 684 | 14 | 1164 | 19 | AAV35131 | Mouse WRN helicase  | c 757 | 14 | 1446 | 21 | AA53032  | Murine beta-1,3-ga   |
| c 685 | 14 | 1164 | 21 | AA639983 | Arbidopsis thalia   | c 758 | 14 | 1448 | 21 | AA66643  | Human secreted pro   |
| c 686 | 14 | 1170 | 21 | AA648952 | Arbidopsis thalia   | c 759 | 14 | 1455 | 21 | AA68152  | Eucalyptus grandis   |
| c 687 | 14 | 1172 | 21 | AA636439 | Arbidopsis thalia   | c 760 | 14 | 1466 | 21 | AA639078 | Human secreted pro   |
| c 688 | 14 | 1175 | 21 | AA633905 | Human secreted pro  | c 761 | 14 | 1469 | 20 | AA28654  | Nucleotide sequenc   |
| c 689 | 14 | 1193 | 21 | AA636257 | Pinus radiata tran  | c 762 | 14 | 1469 | 21 | AA440574 | Xenopus sp embryo    |
| c 690 | 14 | 1198 | 21 | AA632888 | Arbidopsis thalia   | c 763 | 14 | 1478 | 21 | AA42221  | Arbidopsis thalia    |
| c 691 | 14 | 1199 | 21 | AA616672 | Human secreted pro  | c 764 | 14 | 1488 | 20 | AA39661  | Renal cancer assoc   |
| c 692 | 14 | 1200 | 12 | AA011650 | FB-FB-UK fusion co  | c 765 | 14 | 1491 | 20 | AA300070 | Aspergillus oryzae   |
| c 693 | 14 | 1200 | 20 | AAV74138 | Mouse FLAME-2 cDNA  | c 766 | 14 | 1491 | 20 | AA82521  | Aspergillus oryzae   |
| c 694 | 14 | 1204 | 21 | AA633604 | Arbidopsis thalia   | c 767 | 14 | 1491 | 20 | AA800018 | Aspergillus oryzae   |
| c 695 | 14 | 1205 | 21 | AA608110 | Human ATP synthase  | c 768 | 14 | 1498 | 21 | AA86796  | Human protein kina   |
| c 696 | 14 | 1205 | 21 | AA635906 | Human ATP synthase  | c 769 | 14 | 1515 | 19 | AA770118 | Plasmidom falcpa     |
| c 697 | 14 | 1209 | 17 | AA739519 | Flea calreticulin   | c 770 | 14 | 1518 | 19 | AA734595 | M. vaccae pota hom   |
| c 698 | 14 | 1209 | 17 | AA739517 | Flea calreticulin   | c 771 | 14 | 1518 | 20 | AA113330 | M. vaccae pota gen   |
| c 699 | 14 | 1212 | 21 | AA640247 | Arbidopsis thalia   | c 772 | 14 | 1519 | 21 | AA69883  | Human secreted pro   |
| c 700 | 14 | 1221 | 21 | AA643461 | Arbidopsis thalia   | c 773 | 14 | 1521 | 19 | AAV01533 | Human acylcoenzyme   |
| c 701 | 14 | 1225 | 21 | AA648624 | Arbidopsis thalia   | c 774 | 14 | 1527 | 22 | AA631528 | C. glutamicum phosph |
| c 702 | 14 | 1228 | 22 | AA633098 | Human secreted pro  | c 775 | 14 | 1529 | 21 | AA659076 | Human secreted pro   |
| c 703 | 14 | 1234 | 15 | AA670415 | Full length pre-pr  | c 776 | 14 | 1530 | 6  | AA50275  | Sequence from PATK   |
| c 704 | 14 | 1245 | 22 | AA644651 | Novel protein kina  | c 777 | 14 | 1530 | 21 | AA51831  | Human melancortin    |
| c 705 | 14 | 1258 | 22 | AA633083 | Human secreted pro  | c 778 | 14 | 1530 | 21 | AA51835  | Human melancortin    |
| c 706 | 14 | 1261 | 16 | AA680230 | Rat NDF clone 40 D  | c 779 | 14 | 1532 | 21 | AA653022 | Human beta-1,3-gal   |
| c 707 | 14 | 1268 | 16 | AA638969 | Sequence of delet   | c 780 | 14 | 1533 | 21 | AA660047 | Human secreted pro   |
| c 708 | 14 | 1268 | 16 | AA701482 | Tobacco promoter T  | c 781 | 14 | 1536 | 21 | AA65886  | S. lavendulae Mmcl   |
| c 709 | 14 | 1268 | 18 | AA74891  | Human neurogenic D  | c 782 | 14 | 1537 | 21 | AA645667 | Arbidopsis thalia    |
| c 710 | 14 | 1268 | 19 | AAV42932 | DNA encoding human  | c 783 | 14 | 1540 | 21 | AA51833  | Human melancortin    |
| c 711 | 14 | 1269 | 14 | AA648087 | Sequence of the an  | c 784 | 14 | 1540 | 21 | AA51837  | Human melancortin    |
| c 712 | 14 | 1269 | 21 | AA642289 | Arbidopsis thalia   | c 785 | 14 | 1544 | 21 | AA633610 | Arbidopsis thalia    |
| c 713 | 14 | 1270 | 15 | AA644340 | Sequence encoding   | c 786 | 14 | 1547 | 21 | AA647981 | Arbidopsis thalia    |
| c 714 | 14 | 1272 | 21 | AA633124 | Arbidopsis thalia   | c 787 | 14 | 1553 | 21 | AA697082 | Human secreted pro   |
| c 715 | 14 | 1274 | 21 | AA648616 | Arbidopsis thalia   | c 788 | 14 | 1586 | 21 | AA69327  | Agrobacterium KNR7   |
| c 716 | 14 | 1275 | 19 | AAV05044 | DNA encoding the v  | c 789 | 14 | 1589 | 17 | AA739516 | Flea calreticulin    |
| c 717 | 14 | 1275 | 19 | AAV05044 | DNA encoding the v  | c 790 | 14 | 1589 | 17 | AA739518 | Flea calreticulin    |
| c 718 | 14 | 1287 | 21 | AA676396 | Human ORFX ORF1951  | c 791 | 14 | 1591 | 20 | AA622715 | Human cytochrome p   |
| c 719 | 14 | 1287 | 22 | AA671411 | Corynebacterium g1  | c 792 | 14 | 1593 | 20 | AA601021 | DNA sequence of 5N   |
| c 720 | 14 | 1289 | 16 | AA699001 | Bovine herpes viru  | c 793 | 14 | 1599 | 21 | AA680531 | Human secreted pro   |
| c 721 | 14 | 1290 | 11 | AA603061 | Human T-cell leuk   | c 794 | 14 | 1601 | 18 | AA613395 | T72 promoter regio   |
| c 722 | 14 | 1305 | 21 | AA616092 | Human prostate can  | c 795 | 14 | 1605 | 18 | AA67531  | H. pylori putative   |
| c 723 | 14 | 1305 | 21 | AA645454 | Arbidopsis thalia   | c 796 | 14 | 1607 | 21 | AA651800 | Arbidopsis thalia    |
| c 724 | 14 | 1317 | 18 | AA79937  | Bovine dipeptidyl   | c 797 | 14 | 1607 | 21 | AA694052 | Human endothelial    |
| c 725 | 14 | 1321 | 21 | AA677590 | Human ORFX ORF3145  | c 798 | 14 | 1608 | 20 | AA660803 | Human secreted pro   |
| c 726 | 14 | 1332 | 21 | AA696757 | Nuclear transpor    | c 799 | 14 | 1617 | 18 | AA67947  | H. pylori putative   |
| c 727 | 14 | 1339 | 21 | AA69968  | Human secreted pro  | c 800 | 14 | 1621 | 21 | AA65004  | Membrane-bound pro   |
| c 728 | 14 | 1348 | 21 | AA644931 | Arbidopsis thalia   | c 801 | 14 | 1621 | 22 | AA644150 | Human Prol134 (UNC   |
| c 729 | 14 | 1351 | 18 | AA676800 | Human ORFX ORF2355  | c 802 | 14 | 1633 | 14 | AA651227 | Human MSH-R gene     |
| c 730 | 14 | 1353 | 18 | AA676800 | Burkholderia cepac  | c 803 | 14 | 1633 | 19 | AA619136 | Human melanocyte s   |
| c 731 | 14 | 1371 | 21 | AA676887 | Human ORFX ORF2442  | c 804 | 14 | 1636 | 20 | AA663703 | Human melanocyte s   |
| c 732 | 14 | 1376 | 21 | AA639392 | Arabidopsis thalia  | c 805 | 14 | 1636 | 21 | AA677774 | Human cancer assoc   |
| c 733 | 14 | 1380 | 18 | AA651051 | Human amine recept  | c 806 | 14 | 1640 | 21 | AA645188 | Aspergillus sojae    |
| c 734 | 14 | 1380 | 20 | AA681288 | Human amine recept  | c 807 | 14 | 1650 | 15 | AA674684 | Early ripening Tom   |
| c 735 | 14 | 1383 | 19 | AAV42055 | Kurthia sp. biotin  | c 808 | 14 | 1653 | 22 | AA674435 | Human pro4 nucleot   |
| c 736 | 14 | 1385 | 14 | AA638968 | Sequence of delet   | c 809 | 14 | 1659 | 22 | AA661037 | P. putida KT2440-a   |
| c 737 | 14 | 1385 | 16 | AA701481 | Tobacco promoter T  | c 810 | 14 | 1663 | 20 | AA633162 | Potato isomylase     |
| c 738 | 14 | 1386 | 22 | AA671410 | Corynebacterium g1  | c 811 | 14 | 1671 | 21 | AA679977 | Human secreted pro   |
| c 739 | 14 | 1387 | 18 | AA672332 | Pseudomonas aeru    | c 812 | 14 | 1673 | 22 | AA672835 | Secreted protein g   |
| c 740 | 14 | 1391 | 22 | AA626301 | Pseudomonas sp. TYP | c 813 | 14 | 1675 | 21 | AA642587 | Arbidopsis thalia    |
| c 741 | 14 | 1391 | 22 | AA693793 | Human CDNA encodin  | c 814 | 14 | 1680 | 19 | AA639818 | Scenedesmus D1 pro   |





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C 961 14 2.4 2430 16 AA080232 Rat NDF clone 42A
C 962 14 2.4 2464 18 AA030752 Porcine TNFalpha-c
C 963 14 2.4 2492 20 AA227265 Human secreted pro
C 964 14 2.4 2499 21 AA51776 S. cerevisiae esse
C 965 14 2.4 2516 19 AA52606 Human GTP binding
C 966 14 2.4 2516 21 AA59323 DNA encoding a hum
C 967 14 2.4 2529 18 AA87468 Hamster Ubiquitin/
C 968 14 2.4 2531 16 AA080227 Rat NDF clone 20 D
C 969 14 2.4 2534 21 AA46152 CDNA sequence enco
C 970 14 2.4 2536 19 AA533196 Secreted protein D
C 971 14 2.4 2578 17 AA12323 DNA encoding Sulfo
C 972 14 2.4 2609 20 AA24345 Human p101/P13 kin
C 973 14 2.4 2611 11 AA006281 Sequence encoding
C 974 14 2.4 2625 21 AA51567 Human phosphatidy
C 975 14 2.4 2631 20 AA34135 Mycobacterium spec
C 976 14 2.4 2633 12 AA010351 PLUXSPARC-2 encodi
C 977 14 2.4 2638 21 AA46664 CDNA of a human di
C 978 14 2.4 2642 12 AA010350 PLUXSPARC-1 encodi
C 979 14 2.4 2660 20 AA89196 Human DRK1 protei
C 980 14 2.4 2660 20 AA89197 Human DRK1 antise
C 981 14 2.4 2660 22 AA59632 Human cell cycle a
C 982 14 2.4 2664 20 AA34136 Mycobacterium spec
C 983 14 2.4 2669 20 AA24345 Human p101/P13 kin
C 984 14 2.4 2678 21 AA21760 Human breast and o
C 985 14 2.4 2693 20 AA24344 Human p101/P13 kin
C 986 14 2.4 2697 13 AA022957 S. tuberosum isom
C 987 14 2.4 2706 20 AA27061 Neuropilin-1
C 988 14 2.4 2709 20 AA211759 Human p101 protei
C 989 14 2.4 2711 19 AA68056 Neurodegenerative
C 990 14 2.4 2717 21 AA46676 CDNA of a human di
C 991 14 2.4 2720 22 AA72833 Secreted protein g
C 992 14 2.4 2730 20 AA58961 Human Transcrip
C 993 14 2.4 2733 17 AA14604 Human serotonin va
C 994 14 2.4 2733 19 AA48282 Human 5-HT2C serot
C 995 14 2.4 2743 16 AA080231 Rat NDF clone 41 D
C 996 14 2.4 2755 20 AA52230 Protein PRO266 con
C 997 14 2.4 2755 21 AA52205 Human PRO266 prote
C 998 14 2.4 2755 22 AA72388 Human PRO266 CDNA
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## ALIGNMENTS

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RESULT 1
ID AAX84092 standard; cDNA; 3402 BP.
XX
AC AAX84092;
XX
XX 27-AUG-1999 (first entry)
XX
DE T. cruzi PTC40 coding sequence.
XX
KM PTC40; Tc40; infection; diagnosis; immune complex; antigenic determinant;
KM therapy; antibody; ds.
XX
OS Trypanosoma cruzi.
XX
PN WO9229867-A1.
XX
PD 17-JUN-1999.
XX
PF 10-DEC-1998; 98WO-IB01987.
XX
PR 10-DEC-1997; 97US-0988242.
XX
XX (INMR ) BIO MERIEUX.
XX PA Jolivet M, Lesenechal M, Mandrand B, Paranhos-Baccala G;
XX PI WPI; 1999-394978/33.
DR
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DR P-PSDB: AAY22124.
XX New Trypanosoma cruzi antigen
XX
XX Claim 1; Page 52-56; 65pp; English.
XX
CC This sequence encodes the Trypanosoma cruzi PTC40 protein of the
CC invention, and is designated Tc40. The PTC40 antigenic determinant is
CC useful as a reagent for detection and/or monitoring of Trypanosoma cruzi
CC infection from samples including blood serum or plasma, urine, saliva, or
CC tears, by contacting with the sample and detecting an immune complex. The
CC PTC40 antigenic determinant, the vector, expression cassette, cell or
CC antibody are useful for treatment or prevention (vaccine) of a
CC Trypanosoma cruzi infection in a man or animal. Current Trypanosoma cruzi
CC antigens are obtained from protein fractions of the noninfectious stage
CC of the parasite, and these do not allow sufficient production of antigens
CC for use in reliable serological diagnostic tests. The strain to strain
CC polymorphism reduces reliability of the tests.
XX
SQ Sequence 3402 BP; 888 A; 821 C; 956 G; 737 T; 0 other;
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Query Match 100.0%; Score 594; DB 20; Length 3402;  
Best Local Similarity 100.0%; Pred. No. 1,2e-295;  
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 gacatgtcgtatcgtatgacgattcctcattcctcgtctcccgaggaagcaacag 120
DB 1392 gacatgtcgtatcgtatgacgattcctcattcctcgtctcccgaggaagcaacag 1351
QY 121 ccagagcaaaaacatcgtgtagtgcagcagcagcagcagcagcagcagcagcagcagc 180
DB 1352 ccagagcaaaaacatcgtgtagtgcagcagcagcagcagcagcagcagcagcagcagc 1411
QY 181 gacgcgcgcagtagcagtcatacacaatacgaattcgcgcgtgtgtaacccctgacatca 240
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DB 1532 ccgcacgtgggagcaagatcattgtaattagtaacagcgtgggagtaattgtaacac 1591
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DB 1592 caaagagcgtcgtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1651
QY 421 acgactacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 480
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QY 481 ggattgtgtgcagcctaagtggtgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 540
DB 1712 ggattgtgtgcagcctaagtggtgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 1771
QY 541 ccaacagagagaagaagagcctccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 594
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RESULT 2
ID AAT27310 standard; cDNA; 3402 BP.
XX
AC AAT27310;
XX
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| Accession                                                                                                                                    | Gene                                    | Location/Qualifiers |
|----------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------|---------------------|
| 26-NOV-1996                                                                                                                                  | (first entry)                           |                     |
| Trypanosoma cruzi                                                                                                                            | epimastigotic Prc100t antigen gene.     |                     |
| Antigen: Trypanosoma cruzi; epimastigote; serum; Chagas disease; probe; Primer; PCR; polymerase chain reaction; amplification; antibody; ds. |                                         |                     |
| Trypanosoma cruzi.                                                                                                                           |                                         |                     |
| Key                                                                                                                                          | Location/Qualifiers                     |                     |
| CDS                                                                                                                                          | 266..3013                               |                     |
| FT                                                                                                                                           | /*tag= a                                |                     |
| FT                                                                                                                                           | /product= Prc100t epimastigotic antigen |                     |
| FR27233589-A1.                                                                                                                               |                                         |                     |
| 16-FEB-1996.                                                                                                                                 |                                         |                     |
| 12-AUG-1994; 94FR-0010132.                                                                                                                   |                                         |                     |
| 12-AUG-1994; 94FR-0010132.                                                                                                                   |                                         |                     |
| (INMR ) BIO MERIEUX.                                                                                                                         |                                         |                     |
| Jolivet M, Lesenechal M, Paranhos-Baccala G;                                                                                                 |                                         |                     |
| WPI; 1996-190287/20.                                                                                                                         |                                         |                     |
| P-PSDB; AAR91615.                                                                                                                            |                                         |                     |
| New nucleic acid encoding Trypanosoma cruzi epimastigotic antigen -                                                                          |                                         |                     |
| useful for diagnosis, monitoring and therapy of Chagas disease                                                                               |                                         |                     |
| Claim 1; Page 24-26; 55pp; French.                                                                                                           |                                         |                     |
| This is the nucleotide sequence encoding a novel isolated antigenic                                                                          |                                         |                     |
| protein from Trypanosoma cruzi epimastigotes, designated Prc100t.                                                                            |                                         |                     |
| The clone Tc50 was isolated from a T. cruzi genomic expression library in                                                                    |                                         |                     |
| Lambda gt11, using a mixture of sera from patients with Chagas disease.                                                                      |                                         |                     |
| Clone Tc50 contained an 594 bp insert corresp. to nucleotides 1232-1825                                                                      |                                         |                     |
| of this sequence. The Tc50 sequence was subsequently used to probe a                                                                         |                                         |                     |
| Southern blot of restriction enzyme digested T. cruzi DNA and also screen                                                                    |                                         |                     |
| a lambda gt10 library to isolate a 1041 bp EcoRI fragment corresp. to                                                                        |                                         |                     |
| nucleotides 1403-2443 of Prc100t. Primers (AAT27311-5) were synthesised                                                                      |                                         |                     |
| based on the sequences of the 594 and 1041 bp fragments and used to                                                                          |                                         |                     |
| amplify the Prc100t clone as 3 fragments from cDNA derived from mRNA                                                                         |                                         |                     |
| purified from T. cruzi epimastigotes. The protein or antibodies raised                                                                       |                                         |                     |
| against it can be used in the detection and monitoring of T. cruzi                                                                           |                                         |                     |
| infection i.e. Chagas disease.                                                                                                               |                                         |                     |
| Sequence 3402 BP; 889 A; 818 C; 958 G; 737 T; 0 other;                                                                                       |                                         |                     |
| Query Match                                                                                                                                  | 82.8%; Score 492; DB 17; Length 3402;   |                     |
| Best Local Similarity                                                                                                                        | 99.7%; Pred. No. 3e-243;                |                     |
| Matches 592; Conservative 0; Mismatches 2; Indels 0; Gaps 0.                                                                                 |                                         |                     |
| 1 cagtagcagcgtaaacgcttctgtctcaatcgttaacgcccagcagtagctgcgtctgact 60                                                                           |                                         |                     |
| 1232 cagtagcagcgtaaacgcttctgtctcaatcgttaacgcccagcagtagctgcgtctgact 1291                                                                      |                                         |                     |
| 61 gacatgctcagatcgatgaacgattctccatctcgcgtccctccgcgaaggaaacacagcag 120                                                                        |                                         |                     |
| 1292 gacatgctcagatcgatgaacgattctccatctcgcgtccctccgcgaaggaaacacagcag 1351                                                                     |                                         |                     |
| 121 ccagggcgaacaaacatcggttagtgccgacgcggaacccgggtgtgtgtctcccgggcaat 180                                                                       |                                         |                     |
| 1332 ccagggcgaacaaacatcggttagtgccgacgcggaacccgggtgtgtgtctcccgggcaat 1411                                                                     |                                         |                     |
| 181 gacgagcgagtagcagcatcatcacaatacgaactctgcgcgctgcgcgcatccctcgtcata 240                                                                      |                                         |                     |
| 1412 gacgagcgagtagcagcatcatcacaatacgaactctgcgcgctgcgcgcatccctcgtcata 1471                                                                    |                                         |                     |
| 241 cccctgttccagcgccacgaagcagcggtccctcgtccgcgcgcgatccggttag 300                                                                              |                                         |                     |

[illegible]

RESULT 3  
 ID AAT27313 standard; cDNA, 22 BP.  
 XX  
 XX AAT27313;  
 XX  
 DT 26-NOV-1996 (first entry)  
 DE T.cruzi epimastigotic Prc100t antigen primer corresp. to bases 1266-87.  
 XX  
 XX Antigen; Trypanosoma cruzi; epimastigote; serum; Chagas disease; probe;  
 KW Primer; PCR; polymerase chain reaction; amplification; antibody; ss.  
 XX  
 OS Synthetic.  
 XX  
 EN FR2723589-A1.  
 XX  
 PD 16-FEB-1996.  
 XX  
 PF 12-AUG-1994; 94FR-0010132.  
 XX  
 PR 12-AUG-1994; 94FR-0010132.  
 XX  
 PA (INMR ) BIO MERIEUX.  
 XX  
 PI Jolivet M, Lesenechal M, Paranhos-Baccala G;  
 XX  
 DR WPI: 1996-190287/20.  
 XX  
 PT New nucleic acid encoding Trypanosoma cruzi epimastigotic antigen -  
 PT useful for diagnosis, monitoring and therapy of Chagas disease  
 XX  
 PS Claim 29; Page 37; 55pp; French.  
 XX  
 CC The primers AAT27311-5 were used to PCR amplify the sequence encoding a  
 CC novel isolated antigenic protein from Trypanosoma cruzi epimastigotes,  
 CC designated Prc100t (AAT27310). The primers, derived from the sequences  
 CC of a 594 and 1041 bp fragment of Prc100t, amplified from the gene as 3  
 CC fragments. This primer corresponds to nucleotides 1266-87 of the Prc100t  
 CC sequence, derived from the 594 bp fragment. The 594 bp fragment was  
 CC isolated from a T.cruzi genomic expression library in lambda g11, using  
 CC a mixture of sera from patients with Chagas disease. It corresponds to  
 CC nucleotides 1237-1825 of Prc100t. The 1041 bp fragment was isolated from  
 CC a lambda g110 library using the 594 bp fragment as a probe. The protein,  
 CC or antibodies raised against it, can be used in the detection and  
 CC monitoring of T.cruzi infection i.e. Chagas disease.  
 XX  
 SE Sequence 22 BP; 3 A; 8 C; 7 G; 4 T; 0 other;

Query Match 3.7%; Score 22; DB 17; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 35 cagcgacggtagctgctct 56  
|||||  
DB 1 cagcgacggtagctgctct 22

## RESULT 4

AAV30199 standard; DNA: 22 BP.

AC AAV30199;

DE 27-AUG-1999 (first entry)

XX PCR primer for T. cruzi PTC40 coding sequence.

XX PTC40; Tc40; infection; diagnosis; immune complex; antigenic determinant;  
KM therapy; antibody; PCR primer; ss.

XX Synthetic.

OS Trypanosoma cruzi.

XX WO99239867-A1.

PD 17-JUN-1999.

PF 10-DEC-1998; 98WO-IB01987.

XX 10-DEC-1997; 97US-0988242.

PA (INMR ) BIO MERIEUX.

PI Jolivet M, Lesenechal M, Mandrand B, Paranhos-Baccala G;

DR WPI; 1999-394978/33.

PT New Trypanosoma cruzi antigen

PS Disclosure; Page 21; 65pp; English.

XX This sequence is a PCR primer for DNA encoding the Trypanosoma cruzi

CC PTC40 protein of the invention. The PTC40 antigenic determinant is

CC useful as a reagent for detection and/or monitoring of Trypanosoma cruzi

CC infection from samples including blood serum or plasma, urine, saliva, or

CC tears, by contacting with the sample and detecting an immune complex. The

CC PTC40 antigenic determinant, the vector, expression cassette, cell or

CC antibody are useful for treatment or prevention (vaccine) of a

CC Trypanosoma cruzi infection in a man or animal. Current Trypanosoma cruzi

CC antigens are obtained from protein fractions of the noninfectious stage

CC of the parasite, and these do not allow sufficient production of antigens

CC for use in reliable serological diagnostic tests. The strain to strain

CC polymorphism reduces reliability of the tests.

Sequence 22 BP; 3 A; 8 C; 7 G; 4 T; 0 other;

Query Match 3.7%; Score 22; DB 20; Length 22;

Best Local Similarity 100.0%; Pred. No. 0.12; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 35 cagcgacggtagctgctct 56  
|||||

DB 1 cagcgacggtagctgctct 22

## RESULT 5

AAV30199/c

ID AAV30199 standard; DNA: 11878 BP.

AC AAV30199;

XX 14-SEP-1998 (first entry)

DE Protein kinase catalytic subunit gene.

XX Severe combined immunodeficiency disease; SCID; horse; diagnosis;

KM DNA-dependent protein kinase; ds.

OS Equus caballus.

PN WO9821367-A1.

PD 22-MAY-1998.

PF 14-NOV-1997; 97WO-US21066.

PR 15-NOV-1996; 96US-0031261.

PA (TEXA ) UNIV TEXAS SYSTEM.

PI Weeks K;

DR WPI; 1998-297967/26.

PT DNA-dependent protein kinase catalytic subunit - useful for

PS determining equine severe combined immunodeficiency alleles

XX This isolated DNA molecule encodes an equine DNA-dependent protein

CC kinase catalytic subunit (DNA-PKcs). A claimed method of

CC identifying an Arabian horse that is a carrier of equine severe

CC combined immunodeficiency (SCID) comprises determining whether the

CC horse has a mutation in a SCID determinant region of the DNA-PKcs

CC gene (see also AAV30196 and AAV30197). Sequence analysis of DNA-PKcs

CC genes from normal and SCID equine fibroblasts shows that a 5 bp

CC deletion is present in SCID foals at a site that corresponds to

CC nucleotide 9454 of the 12,381 nucleotide coding sequence of the

CC human transcript. This results in premature termination of the

CC DNA-PKcs at amino acid 3160 (see AAV56642). Oligonucleotide probes

CC (see AAV30194 and AAV30195) are provided that precisely span the SCID

CC determinant region of the DNA-PKcs gene, and which are diagnostic

CC for the normal and SCID alleles, respectively. Methods are also

CC provided for identifying for differentiating SCID homozygotes,

CC heterozygotes and normal horses.

Sequence 11878 BP; 3586 A; 2323 C; 2668 G; 3301 T; 0 other;

Query Match 3.2%; Score 19; DB 19; Length 11878;

Best Local Similarity 100.0%; Pred. No. 3.4; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 211 actctgcgctgctgcat 229  
|||||

DB 6446 ACTTCTGCCCTGCTGCA 6428

RESULT 6

AAV30198/c

ID AAV30198 standard; DNA: 11883 BP.

AC AAV30198;

DE 14-SEP-1998 (first entry)

XX Protein kinase catalytic subunit gene.

XX Severe combined immunodeficiency disease; SCID; horse; diagnosis;

KM DNA-dependent protein kinase; ds.

OS Equus caballus.

XX M09821367-A1.  
 PN 22-MAY-1998.  
 XX 14-NOV-1997; 97WO-US21066.  
 XX 15-NOV-1996; 96US-0031261.  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 XX Weeks K;  
 PI WPI: 1998-297967/26.  
 DR P-PSDB: AAW56642.  
 XX DNa-dependent protein kinase catalytic subunit - useful for  
 PT determining equine severe combined immunodeficiency alleles  
 XX  
 PS Claim 1; Page 39-44; 98pp; English.  
 CC This isolated DNA molecule encodes a DNA-dependent protein kinase  
 CC catalytic subunit (DNA-PKcs, see AAW56642) found in Arabian horses.  
 CC A claimed method of identifying an Arabian horse that is a carrier  
 CC of equine severe combined immunodeficiency (SCID) comprises  
 CC determining whether the horse has a mutation in a SCID determinant  
 CC region of the DNA-PKcs gene (see also AAV30196 and AAV30197). Sequence  
 CC analysis of DNA-PKcs genes from normal and SCID equine fibroblasts  
 CC shows that a 5 bp deletion is present in SCID foals at a site that  
 CC corresponds to nucleotide 9454 of the 12,381 nucleotide coding  
 CC sequence of the human transcript. This results in premature  
 CC termination of the DNA-PKcs at amino acid 3160. Oligonucleotide  
 CC probes (see AAV30194 and AAV30195) are provided that precisely span the  
 CC SCID determinant region of the DNA-PKcs gene, and which are  
 CC diagnostic for the normal and SCID alleles, respectively. Methods  
 CC are also provided for identifying for differentiating SCID  
 CC homozygotes, heterozygotes and normal horses. A claimed plasmid  
 CC contains the DNA-PKcs DNA and regulatory elements necessary for  
 CC expression of the DNA in a recombinant cell.  
 CC  
 SO Sequence 11883 BP; 3588 A; 2324 C; 2669 G; 3302 T; 0 other;

Query Match 3.2%; Score 19; DB 19; Length 11883;  
 Best Local Similarity 100.0%; Pred. No. 3.4;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 211 actctgcgcgtcgtcat 229  
 ||||||||||||||||  
 DB 6449 ACTCTGCCGCTGTCGAT 6431

RESULT 7  
 AAT27312/c  
 ID AAT27312 standard; cDNA: 18 BP.  
 AC AAT27312;  
 XX  
 DT 26-NOV-1996 (first entry)  
 XX  
 DE T. cruzi epimastigotic PTC100t antigen primer corresp. to bases 1442-59.  
 XX  
 KW Antigen: Trypanosoma cruzi; epimastigote; serum; Chagas disease; probe;  
 KW Primer: PCR; polymerase chain reaction; amplification; antibody; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX FR2723589-A1.  
 XX  
 XX 16-FEB-1996.  
 PD  
 XX 12-AUG-1994; 94FR-0010132.  
 PF  
 XX

PR 12-AUG-1994; 94FR-0010132.  
 XX  
 PA (INMR ) BIO MERIEUX.  
 XX  
 PI Jolivet M, Lesenechal M, Paranhos-Baccala G;  
 XX  
 DR WPI: 1996-190287/20.  
 XX  
 XX  
 PT New nucleic acid encoding Trypanosoma cruzi epimastigotic antigen -  
 PI useful for diagnosis, monitoring and therapy of Chagas disease  
 XX  
 PS Claim 29; Page 36; 55pp; French.  
 CC The primers AAT27311-5 were used to PCR amplify the sequence encoding a  
 CC novel isolated antigenic protein from Trypanosoma cruzi epimastigotes,  
 CC designated PTC100t (AAT27310). The primers, derived from the sequences  
 CC of a 594 and 1041 bp fragment of PTC100t, amplified the gene as 3  
 CC fragments. This primer corresponds to nucleotides 1442-59 of the PT100t  
 CC sequence, derived from the 594 bp fragment. The 594 bp fragment was  
 CC isolated from a T. cruzi genomic expression library in lambda gtl1, using  
 CC a mixture of sera from patients with Chagas disease. It corresponds to  
 CC nucleotides 1232-1825 of PTC100t. The 1041 bp fragment was isolated from  
 CC a lambda gt10 library using the 594 bp fragment as a probe. The protein,  
 CC or antibodies raised against it, can be used in the detection and  
 CC monitoring of T. cruzi infection i.e. Chagas disease.  
 CC  
 SO Sequence 18 BP; 5 A; 4 C; 7 G; 2 T; 0 other;

Query Match 3.0%; Score 18; DB 17; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 211 actctgcgcgtcgtcat 228  
 ||||||||||||||||  
 DB 18 ACTCTGCCGCTGTCGCA 1

RESULT 8  
 AAX84094/c  
 ID AAX84094 standard; DNA: 18 BP.  
 AC AAX84094;  
 XX  
 DT 27-AUG-1999 (first entry)  
 XX  
 DE PCR primer for T. cruzi PTC40 coding sequence.  
 XX  
 KW PTC40; Tcd0; infection; diagnosis; immune complex; antigenic determinant;  
 KW therapy; antibody; PCR primer; ss.  
 XX  
 OS Synthetic.  
 OS Trypanosoma cruzi.  
 OS  
 OS WO929867-A1.  
 XX  
 PD 17-JUN-1999.  
 XX  
 PF 10-DEC-1998; 98WO-IB01987.  
 XX  
 PR 10-DEC-1997; 97US-0988242.  
 XX  
 PA (INMR ) BIO MERIEUX.  
 XX  
 PI Jolivet M, Lesenechal M, Mandrand B, Paranhos-Baccala G;  
 XX  
 DR WPI: 1999-394978/33.  
 XX  
 PT New Trypanosoma cruzi antigen  
 PS Disclosure: Page 21; 65pp; English.  
 PS  
 XX This sequence is a PCR primer for DNA encoding the Trypanosoma cruzi

CC pTc40 protein of the invention. The pTc40 antigenic determinant is  
 CC useful as a reagent for detection and/or monitoring of *Trypanosoma cruzi*  
 CC infection from samples including blood serum or plasma, urine, saliva, or  
 CC tears, by contacting with the sample and detecting an immune complex. The  
 CC pTc40 antigenic determinant, the vector, expression cassette, cell or  
 CC antibody are useful for treatment or prevention (vaccine) of a  
 CC *Trypanosoma cruzi* infection in a man or animal. Current *Trypanosoma cruzi*  
 CC antigens are obtained from protein fractions of the noninfectious stage  
 CC of the parasite, and these do not allow sufficient production of antigens  
 CC for use in reliable serological diagnostic tests. The strain to strain  
 CC polymorphism reduces reliability of the tests.

SQ Sequence 18 BP; 5 A; 4 C; 7 G; 2 T; 0 other;

Query Match 3.0%; Score 18; DB 20; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 211 actctgcgcgcctctgca 228  
 ||||||||||||||||  
 Db 18 ACTTCTCGCCGCTGCTGCA 1

## RESULT 9

AAFO9309 standard; cDNA; 454 BP.

AAFO9309;

13-MAR-2001 (first entry)

*Fusarium venenatum* EST SEQ ID NO:1832.

Multiple gene expression; filamentous fungal cell; EST;

expressed sequence tag; *Fusarium venenatum*; *Aspergillus niger*;

*Aspergillus oryzae*; *Trichoderma reesei*; identification; recombination;

culture condition; environmental stress; spore morphogenesis;

metabolic pathway engineering; catabolic pathway engineering; ss.

*Fusarium venenatum*.

WO200056762-A2.

28-SEP-2000.

22-MAR-2000; 2000WO-US07781.

22-MAR-1999; 99US-0273623.

(NOVO ) NOVO NORDISK BIOTECH INC.  
 (NOVO ) NOVO NORDISK AS.

Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;  
 WPI; 2000-594572/56.

Monitoring differential expression of genes in filamentous fungal cells  
 uses fluorescence-labeled nucleic acids isolated from the cells and a  
 substrate of expressed sequence tags -

Claim 86; Page 1066; 3161pp; English.

The present invention describes a method for monitoring differential  
 expression of genes in a first filamentous fungal (FF) cell relative to  
 expression of the same genes in one or more second filamentous fungal  
 cells. The method uses fluorescence-labeled nucleic acids isolated from  
 the FF cells and a substrate of expressed sequence tags (EST). The ESTs  
 are used in the methods for monitoring differential expression of genes  
 in a first filamentous fungal (FF) cell relative to expression of the  
 same genes in one or more second filamentous fungal cells. Monitoring  
 the global expression of genes from FF cells allows the production  
 potential of the microorganisms to be improved. New genes may be

CC discovered, possible functions of unknown open reading frames can be  
 CC identified and gene copy number variation and stability can be  
 CC monitored. The expression of genes can be used to study how FF cells  
 CC adapt to changes in culture conditions, environmental stress, spore  
 CC morphogenesis, recombination, metabolic or catabolic pathway  
 CC engineering. Using ESTs provides several advantages over genomic or  
 CC random cDNA clones including elimination of redundancy as one spot on an  
 CC array equals one gene or open reading frame, and organization of the  
 CC microarrays based on function of the gene products to facilitate  
 CC analysis of the results. AAFO7478 to AAFL1247 represents ESTs from  
 CC *Fusarium venenatum*. AAFL1248 to AAFL1853 represents ESTs from *Aspergillus*  
 CC *niger*. AAFL1854 to AAFL4878 represents ESTs from *Aspergillus*  
 CC AAFL4879 to AAFL1537 represents ESTs from *Trichoderma reesei*, which are  
 CC all specifically claimed in the present invention.

SQ Sequence 454 BP; 141 A; 116 C; 89 G; 108 T; 0 other;

Query Match 3.0%; Score 18; DB 21; Length 454;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 220 gctgcgtcaccctctgca 237  
 ||||||||||||||||  
 Db 205 gctgcgtcaccctctgca 222

## RESULT 10

AAFO4783 standard; cDNA; 479 BP.

AAFO4783;

06-OCT-2000 (first entry)

Human secreted protein 5' EST, SEQ ID NO: 8858.

Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;

gene therapy; chromosome mapping; ss.

*Homo sapiens*.

EP1033401-A2.

06-SEP-2000.

21-FEB-2000; 2000EP-0200610.

26-FEB-1999; 99US-0122487.

(GEST ) GENSET.  
 Dumas Mline Edwards J, Duclert A, Giordano J;

WPI; 2000-500381/45.

New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
 obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for  
 diagnostic, forensic, gene therapy and chromosome mapping procedures -

Claim 1; SEQ ID 8858; 71pp + CD-ROM; English.

The present sequence is one of a large number of 5' ESTs derived from  
 CC mRNAs encoding secreted proteins. No ORF has yet been conclusively  
 CC identified within the present sequence. The 5' ESTs were prepared from  
 CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST  
 CC sequences usually correspond mainly to the 3' untranslated region (UTR)  
 CC of the mRNA because they are often obtained from oligo-dT primed cDNA  
 CC libraries. Such ESTs are not well suited for isolating cDNA sequences  
 CC derived from the 5' ends of mRNAs and even in those cases where longer  
 CC cDNA sequences have been obtained, the full 5' UTR is rarely included.  
 CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be  
 CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used

CC In diagnostic, forensic, gene therapy and chromosome mapping procedures.  
CC They are used to obtain upstream regulatory sequences and to design  
CC expression and secretion vectors.

XX  
SQ Sequence 479 BP, 109 A; 109 C; 99 G; 160 T; 2 other;

Query Match 3.0%; Score 18; DB 21; Length 479;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 492 agcataatagtggtccag 509  
|||||  
DB 64 agcataatagtggtccag 81

RESULT 11  
AA39943  
ID AAX39943 standard; DNA; 866 BP.

AC AAX39943;

DT 02-JUL-1999 (first entry)

DE Gastric cancer associated gene.

XX  
KW Cancer associated antigen; diagnosis; research; treatment; human;  
KW breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;  
KW prostate cancer; ss.

XX  
OS Homo sapiens.

XX  
PN WO9904265-A2.

PD 28-JAN-1999.

PE 15-JUL-1998; 98WO-US14679.

PR 22-JUN-1998; 98US-0102322.

PR 17-JUL-1997; 97US-0886164.

PR 10-OCT-1997; 97US-0061599.

PR 10-OCT-1997; 97US-0061765.

PR 10-OCT-1997; 97US-0948705.

PR 11-OCT-1997; 97GB-0021697.

XX  
PA (LUDM-) LUDMIG INST CANCER RES.

XX  
PI Chen Y, Gout I, Gure A, O'Hare M, Obata Y, Old LJ;

PI Pfeundschnuh M, Sahin U, Scanlan MJ, Stockert E;

PI Tureci O;

XX  
DR WPI; 1999-132448/11.

XX  
PT New isolated cancer associated nucleic acids and polypeptides -  
PT isolated using sera from cancer patients, used to develop products  
PT for the diagnosis, monitoring or treatment of cancers

PS Claim 67, Page 607; 787pp; English.  
XX  
CC The invention relates to a method for diagnosing a disorder characterised  
CC by expression of a human cancer associated antigen precursor coded for by  
CC a nucleic acid molecule (NAM). The method comprises: (a) contacting a  
CC biological sample isolated from a subject with an agent that specifically  
CC binds to the NAM, an expression product or a fragment of an expression  
CC product complexed with an HLA molecule; and (b) determining the  
CC interaction between the agent and the NAM or the expression product as a  
CC determination of the disorder. The products and methods can be used in  
CC the diagnosis, monitoring, research, or treatment of conditions  
CC characterised by the expression of various cancer associated antigens.  
CC The invention provides nucleic acid sequences and encoded polypeptides  
CC which are cancer associated antigen precursors expressed in human breast  
CC cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and  
CC lung cancer.

XX  
SQ Sequence 866 BP, 222 A; 235 C; 197 G; 206 T; 6 other;

Query Match 3.0%; Score 18; DB 20; Length 866;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 230 cccctgcatcaccctg 247  
|||||  
DB 37 cccctgcatcaccctg 54

RESULT 12  
AAC59435/C  
ID AAC59435 standard; cDNA; 1302 BP.

AC AAC59435;

DT 02-FEB-2001 (first entry)

DE Human secreted protein cDNA #44.

XX  
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;  
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; anticancer;  
KW vulnery; anticonvulsant; antibacterial; antifungal; antiparasitic;  
KW cardiact; gene therapy; cancer; immune disorder; cardiovascular disorder;  
KW neurological disease; infection; human; secreted protein; ss.

XX  
OS Homo sapiens.

XX  
PN WO200056765-A1.

PD 28-SEP-2000.

PE 16-MAR-2000; 2000WO-US06823.

PR 19-MAR-1999; 99US-0125364.

PR 08-DEC-1999; 99US-0169623.

XX  
PA (HUMA-) HUMAN GENOME SCI INC.

XX  
PI Rosen CA, Ruben SM, Komatsoulis G;

XX  
DR WPI; 2000-602215/57.

XX  
PI P-PSDB; AAB34002.

XX  
PT Nucleic acid molecules encoding human secreted proteins, used in  
PT preventing, treating or ameliorating a disorder, e.g. Alzheimer's and  
PT Parkinson's diseases and cancers -

PS Claim 1; Page 355; 410pp; English.  
XX  
CC The invention relates to the isolation of genes AAC59392-C59439 encoding  
CC 48 human secreted proteins AAB33963-B34006. The genes can be used to  
CC generate fusion proteins by linking to the gene for the human  
CC immunoglobulin G-Fc portion (SEQID1) for increasing the stability of  
CC the fusion protein as compared to the human protein only. The genes and  
CC proteins are useful for preventing, ameliorating or treating medical  
CC conditions, e.g. by protein or gene therapy. The genes are isolated  
CC from a range of human tissues disclosed in the specification. The  
CC nucleic acids, proteins, antibodies and (ant)agonists are useful in  
CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast  
CC and ovarian cancer, and other cancers of the adrenal gland, bone, bone  
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;  
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune  
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's  
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative  
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d)  
CC wound healing; (e) neurological diseases e.g. cerebral anoxia and  
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal  
CC and parasitic infections.

SQ Sequence 1302 BP; 249 A; 470 C; 338 G; 230 T; 15 other;

Query Match 3.0%; Score 18; DB 21; Length 1302;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 44 gtagctgcgtctgctgctg 61  
|||||  
DB 669 GTAGCTGCGTCTGCTG 652

## RESULT 13

AAO77884  
ID AAO77884 standard; cDNA; 2520 BP.

XX  
AC AAO77884;

XX  
DT 06-JUL-1995 (first entry)

XX  
DE Neural thread protein AD16c cDNA.

XX  
KM Neural thread protein AD16c; Alzheimer's; neuroectodermal tumours;  
KW malignant astrocytomas; glioblastomas; ss.

XX  
OS Rattus rattus.

XX  
PN MO9423756-A.

XX  
PD 27-OCT-1994.

XX  
PF 20-APR-1994; 94MO-US04321.

XX  
PR 20-APR-1993; 93US-0050559.

XX  
PA (GEHO ) GEN HOSPITAL CORP.

XX  
PI De la Monte SM, Wands JR;

XX  
DR WPI; 1994-341497/42.

XX  
PT Detection of neural thread proteins - to detect sporadic and  
familial Alzheimer's disease, neuroectodermal tumours, malignant  
astrocytomas and glioblastomas (Eng).

XX  
PS Example 4; Fig 16S; 158bp; English.

XX  
CC AAO77884 is the AD16c neural thread protein (NTP) cDNA.. This  
CC sequence was used in the development of an antibody dependent  
CC method, for the detection of NTPs. This new method could be  
CC used to diagnose Alzheimer's disease (differentiating between  
CC sporadic and familial), neuroectodermal tumours, malignant  
CC astrocytomas and glioblastomas.

XX  
SQ Sequence 2520 BP; 661 A; 577 C; 581 G; 701 T; 0 other;

Query Match 3.0%; Score 18; DB 15; Length 2520;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 230 cccctgcatacccccctg 247  
|||||  
DB 298 cccctgcatacccccctg 315

## RESULT 14

AA727766  
ID AA727766 standard; cDNA; 2520 BP.

XX  
AC AA727766;

XX  
DT 14-NOV-1996 (first entry)

XX  
DE AD 16c human neural thread protein clone (partial sequence).

XX  
KM Neural thread protein; NTP; diagnosis; detection;

KW Alzheimer's disease; neuroectodermal tumour; malignant astrocytoma;  
KW monoclonal antibody; binding fragment; ds.

XX  
OS Homo sapiens.

XX  
PN MO9615272-A1.

XX  
PD 23-MAY-1996.

XX  
PF 14-NOV-1995; 95MO-US17111.

XX  
PR 14-NOV-1994; 94US-0340426.

XX  
PA (GEHO ) GEN HOSPITAL CORP.

XX  
PI De la MONTE S, Wands JR;

XX  
DR WPI; 1996-259865/26.

XX  
PT Detection of neural thread protein in diagnosis of Alzheimer's  
disease - also NTP DNA and protein sequences used in gene and  
anti:sense therapy

XX  
PS Example 4c; Figure 16S; 238bp; English.

XX  
CC A method for detecting the presence of neural thread protein (NTP)  
CC having a molecular weight of 8, 14, 17, 21, 26 or 42 kD in a human  
CC subject comprises (a) contacting a sample from a human subject that  
CC is suspected of containing the NTP with at least one molecule  
CC capable of binding to the protein; and (b) detecting any of the  
CC molecule bound to the protein. The binding molecule is selected  
CC from an antibody free of natural impurities, a monoclonal antibody  
CC or a binding fragment of either of these. The method may be used for  
CC diagnosing the presence of Alzheimer's disease, neuroectodermal  
CC tumours and a malignant astrocytoma in a human. A number of clones  
CC of neural thread protein were isolated from healthy 17-18 week old  
CC foetal human brain (HB) 2 year old temporal lobe neocortex and end  
CC stage Alzheimer's disease (AD) cerebral cortex. See AA727753-75.

XX  
SQ Sequence 2520 BP; 661 A; 577 C; 581 G; 701 T; 0 other;

Query Match 3.0%; Score 18; DB 17; Length 2520;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 230 cccctgcatacccccctg 247  
|||||  
DB 298 cccctgcatacccccctg 315

## RESULT 15

AAZ55887/c  
ID AAZ55887 standard; DNA; 68750 BP.

XX  
AC AAZ55887;

XX  
DT 10-APR-2000 (first entry)

XX  
DE Sorangium cellulosum 68.75 kb contig.

XX  
KM Epithione biosynthesis; type I polyketide synthase; taxol substitute;  
KW anticancer; ds.

XX  
OS Sorangium cellulosum.

XX  
FH Key location/Qualifiers

FT CDS 1..1826  
/\*tag= a

```

FT /partial
FT /product= "Partial Orf 1 protein (AAV58580)"
FT /note= "No initiation codon given in the .specification"
FT CDS
FT /tag= b
FT /product= "Orf 2 protein (AAV58581)"
FT 3415..5556
FT /tag= c
FT /product= "Orf 3 protein (AAV58582)"
FT complement (5612..5992)
FT CDS
FT /tag= d
FT /product= "Orf 4 protein (AAV58583)"
FT 6226..6675
FT /tag= e
FT /product= "Orf 5 protein (AAV58584)"
FT 7610..11875
FT /tag= f
FT /product= "Type I polyketide synthase, EPOS A
FT 11872..116104
FT (AAV58573)" CDS
FT /tag= g
FT /product= "Non-ribosomal peptide synthetase, EPOS P
FT 16251..21749
FT /tag= h
FT /product= "Type I polyketide synthase, EPOS B
FT 21746..43519
FT (AAV58575)" CDS
FT /tag= i
FT /product= "Type I polyketide synthase, EPOS C
FT 43524..54920
FT (AAV58576)" CDS
FT /tag= j
FT /product= "Type I polyketide synthase, EPOS D
FT 54935..62254
FT (AAV58577)" CDS
FT /tag= k
FT /product= "Type I polyketide synthase, EPOS E
FT 62369..63628
FT (AAV58578)" CDS
FT /tag= l
FT /product= "Cytochrome P450 oxygenase homologue, EPOS F
FT 63779..64333
FT (AAV58579)" CDS
FT /tag= m
FT /product= "Orf 6 protein (AAV58585)"
FT complement (63853..64290)
FT CDS
FT /tag= n
FT /product= "Orf 7 protein (AAV58586)"
FT 64363..64920
FT CDS
FT /tag= o
FT /product= "Orf 8 protein (AAV58587)"
FT complement (64287..64727)
FT CDS
FT /tag= p
FT /product= "Orf 9 protein (AAV58588)"
FT 65063..65767
FT CDS
FT /tag= q
FT /product= "Orf 10 protein"
FT complement (65008..65874)
FT CDS
FT /tag= r
FT /product= "Orf 11 protein (AAV58590)"
FT complement (65871..66338)
FT CDS
FT /tag= s
FT /product= "Orf 12 protein (AAV58591)"
FT 66667..67137
FT CDS
FT /tag= t
FT /product= "Orf 13 protein (AAV58592)"
FT 67334..68251
FT CDS
FT /tag= u
FT /product= "Orf 14 protein (AAV58593)"
FT 68346..68750
FT CDS
FT /tag= v
FT /product= "Partial Orf 15 protein (AAV58594)"
FT /note= "No termination codon given in the specification"
XX
XX W09966028-A2.

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PD 23-DEC-1999.
XX
XX 16-JUN-1999; 99WO-EP04171.
PF
XX 18-JUN-1998; 98US-0099504.
PR 24-SEP-1998; 98US-0101631.
PR 05-FEB-1999; 99US-0118906.
XX
PA (NOVS ) NOVARTIS AG.
PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
XX Schupp T, Ligon JM, Molnar I, Zirkle R, Goerlach J, Cyr D;
XX WPI: 2000-097741/08.
DR P-PSDB: AAV58573, AAV58574, AAV58575, AAV58576, AAV58577, AAV58578,
DR AAV58579, AAV58580, AAV58581, AAV58582, AAV58583, AAV58584,
DR AAV58585, AAV58586, AAV58587, AAV58588, AAV58590, AAV58591,
DR AAV58592, AAV58593, AAV58594.
XX
XX New isolated epoethlione synthase genes, used for the recombinant
XX production of epoethlione for use in cancer therapy .
PT
PT Claim 14; Page 87-104; 174pp; English.
PS
XX
XX This sequence represents a 68.75 kb contig from Sorangium cellulosum
XX comprising 22 open reading frames (ORFs) and includes genes encoding
XX proteins involved in the biosynthesis of epoethliones. Epoethliones A and
XX B are 16-membered macrocyclic polyketides with an acylcysteine-derived
XX starter unit; polyketides being synthesised from two-carbon building
XX blocks, the beta-carbon of which always carries a keto group. Each round
XX of two-carbon addition is carried out by a complex of enzymes known as
XX the polyketide synthase in a manner similar to fatty acid biosynthesis.
XX EPOS A (AAV58573) and EPOS P (AAV58574) are involved in formation of
XX the thiazole ring formation of epoethliones, and EPOS B, EPOS C, EPOS D
XX and EPOS E (AAV58575-Y58578) are involved in polyketide backbone
XX formation. EPO F (AAV58579) is an epoethlione macrolactone oxidase, and
XX the proteins Orf 3 (AAV58582) and Orf14 (AAV58593) are thought to be
XX involved in transport. Epoethliones mimic the biological activity of
XX taxol, and may be substituted for taxol in cancer chemotherapeutic
XX compositions. Epoethliones exhibit a much lower drop in potency against a
XX multiply drug-resistant cell line compared with taxol, and are
XX considerably less efficiently exported from such cells by the multidrug
XX resistance protein (MDR, or P-glycoprotein). Despite the potential of
XX epoethliones as anticancer agents, they are problematical to produce on a
XX large scale. Epoethliones are too complex for industrial scale chemical
XX synthesis, and Sorangium cellulosum is difficult to ferment, producing
XX poor yields of epoethliones. The nucleic acids of the invention may be
XX used for the recombinant production of epoethliones in a heterologous host
XX that is more amenable to fermentation.
XX
XX Sequence 68750 BP; 9596 A; 22458 C; 25537 G; 11159 T; 0 other;
XX

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Query Match 3.0%; Score 18; DB 21; Length 68750;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 517 tegtccacagcgcg 534
DB 19020 TCGTCTCCACAGCGCG 19003
AAA29349/c
ID AAA29349 standard; DNA; 71989 BP.
AC AAA29349;
XX
XX 12-SEP-2000 (first entry)
XX Sorangium cellulosum epoethlione polyketide synthase operon genomic DNA.
XX DE Epoethlione; polyketide synthase; epoa; epob; epoc; epod; epoe; epof;
XX
XX W09966028-A2.

```

KW epou1, epok; P450 epoxidase; ORF\_A; ORF\_B; promoter; enhancer; anti-fungal;  
KW tubulin polymerization assay; anti-tumour; cytostatic; ds.  
OS Sorangium cellulosum.  
FH Key Location/Qualifiers  
FT CDS 3..992  
FT /\*tag- a  
FT /label= ORF\_A  
FT /product= transposase  
FT /note= "not part of the PKS"  
FT CDS 989..1501  
FT /\*tag- b  
FT /label= ORF\_B  
FT /product= transposase  
FT /note= "not part of the PKS"  
FT CDS 1998..6263  
FT /\*tag- c  
FT /label= epouA\_gene  
FT /note= "encodes the loading domain"  
FT misc\_RNA 2031..3548  
FT /\*tag- d  
FT /note= "encodes ketide synthase (KS-Y) of the loading domain"  
FT misc\_RNA 3621..4661  
FT /\*tag- e  
FT /note= "encodes acyl transferase (AT) of the loading domain"  
FT misc\_RNA 4917..5810  
FT /\*tag- f  
FT /note= "encodes enoyl reductase (ER) of the loading domain, potentially involved in formation of the thiazole moiety"  
FT misc\_RNA 5856..6155  
FT /\*tag- g  
FT /note= "encodes acyl carrier protein (ACP) of the loading domain"  
FT CDS 6260..10493  
FT /\*tag- h  
FT /label= epouB\_gene  
FT /note= "encodes module 1, the NRPS module"  
FT misc\_RNA 2031..3548  
FT /\*tag- i  
FT /note= "encodes condensation domain C2 of the NRPS module"  
FT misc\_RNA 2031..3548  
FT /\*tag- j  
FT /note= "encodes condensation domain C2 of the NRPS module"  
FT misc\_RNA 6861..6887  
FT /\*tag- k  
FT /note= "encodes heterocyclization signature sequence"  
FT misc\_RNA 6861..6887  
FT /\*tag- l  
FT /note= "encodes condensation domain C4 of the NRPS module"  
FT misc\_RNA 7358..7366  
FT /\*tag- m  
FT /note= "encodes condensation domain C7 (partial) of the NRPS module"  
FT misc\_RNA 7898..7921  
FT /\*tag- n  
FT /note= "encodes adenylation domain A1 of the NRPS module"  
FT misc\_RNA 7898..7921  
FT /\*tag- o  
FT /note= "encodes adenylation domain A1 of the NRPS module"  
FT misc\_RNA 8261..8308  
FT /\*tag- p  
FT /note= "encodes adenylation domain A3 of the NRPS module"  
FT misc\_RNA 8411..8422  
FT /\*tag- q  
FT /note= "encodes adenylation domain A4 of the NRPS module"  
FT misc\_RNA 8861..8905

FT /\*tag- r  
FT /note= "encodes adenylation domain A6 of the NRPS module"  
FT misc\_RNA 8966..8983  
FT /\*tag- s  
FT /note= "encodes adenylation domain A7 of the NRPS module"  
FT misc\_RNA 9090..9179  
FT /\*tag- t  
FT /note= "encodes adenylation domain A8 of the NRPS module"  
FT misc\_RNA 9183..9992  
FT /\*tag- u  
FT /note= "encodes oxidation region for forming thiazole"  
FT misc\_RNA 10121..10138  
FT /\*tag- v  
FT /note= "encodes adenylation domain A10 of the NRPS module"  
FT misc\_RNA 10261..10306  
FT /\*tag- w  
FT /note= "encodes thiolation domain (PCP) of the NRPS module"  
FT CDS 10639..16137  
FT /\*tag- x  
FT /label= epouC\_gene  
FT /note= "encodes module 2"  
FT misc\_RNA 10654..12033  
FT /\*tag- y  
FT /note= "encodes KS2, the KS domain of module 2"  
FT misc\_RNA 12250..13287  
FT /\*tag- z  
FT /note= "encodes AT2, the AT domain of module 2"  
FT misc\_RNA 13327..13899  
FT /\*tag- aa  
FT /note= "encodes dehydratase (DH) 2, the DH domain of module 2"  
FT misc\_RNA 14962..15756  
FT /\*tag- ab  
FT /note= "encodes ketoreductase (KR) 2, the KR domain of module 2"  
FT misc\_RNA 15763..16008  
FT /\*tag- ac  
FT /note= "encodes ACP2, the ACP domain of module 2"  
FT CDS 16134..37907  
FT /\*tag- ad  
FT /label= epouD\_gene  
FT /note= "encodes modules 3-6"  
FT misc\_RNA 16425..17606  
FT /\*tag- ae  
FT /note= "encodes KS3"  
FT misc\_RNA 17817..18857  
FT /\*tag- af  
FT /note= "encodes AT3"  
FT misc\_RNA 19581..20396  
FT /\*tag- ag  
FT /note= "encodes KR3"  
FT misc\_RNA 20424..20642  
FT /\*tag- ah  
FT /note= "encodes ACP3"  
FT misc\_RNA 20706..22082  
FT /\*tag- ai  
FT /note= "encodes KS4"  
FT misc\_RNA 22296..23336  
FT /\*tag- aj  
FT /note= "encodes AT4"  
FT misc\_RNA 24069..24647  
FT /\*tag- ak  
FT /note= "encodes KR4"  
FT misc\_RNA 24867..25151  
FT /\*tag- al  
FT /note= "encodes ACP4"  
FT misc\_RNA 25203..26576  
FT /\*tag- am  
FT /note= "encodes KS5"  
FT misc\_RNA 26793..27883  
FT /\*tag- an



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FT      misc_RNA      /note= "encodes AT5"
FT      27966..28574  /tag= ao
FT      /note= "encodes DH5"
FT      29433..30287  /tag= ap
FT      /note= "encodes ER5"
FT      30321..30869  /tag= aq
FT      /note= "encodes KR5"
FT      31077..31373  /tag= ar
FT      /note= "encodes ACP5"
FT      31440..32807  /tag= as
FT      /note= "encodes KS6"
FT      33018..34067  /tag= at
FT      /note= "encodes AT6"
FT      34107..34676  /tag= au
FT      /note= "encodes DH6"
FT      35760..36641  /tag= av
FT      /note= "encodes ER6"
FT      36705..37256  /tag= aw
FT      /note= "encodes KR6"
FT      37470..37769  /tag= ax
FT      /note= "encodes ACP6"
FT      37912..49308  /tag= ay
FT      /label= apoE.gene
FT      /note= "encodes modules 7 and 8"
FT      38014..39375  /tag= az
FT      /note= "encodes KS7"
FT      39589..40626  /tag= ba
FT      /note= "encodes AT7"
FT      41341..41922  /tag= bb
FT      /note= "encodes KR7"
FT      42181..42423  /tag= bc

Query Match      3.0%; Score 18; DB 21; Length 71989;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      517 tcgtctccacagcgcg 534
      |||
Db      13408 TCGTCTCCACAGCGCG 13391

RESULT 17
AAx84320
ID      AAx84320 standard; DNA: 198 BP.
XX
AC      AAx84320;
XX
DT      08-SEP-1999 (first entry)
XX
DE      Stealth virus nucleic acid clone, SEQ ID NO: 12.
XX
KW      Stealth virus; detection; diagnosis; infection; ss.
XX
OS      Stealth virus.
XX
PN      WO9934019-A1.
XX
PD      08-JUL-1999.
XX

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PF      30-DEC-1998; 98WO-US27744.
XX
PR      30-DEC-1997; 97US-0001184.
XX
PA      (MARTY) MARTIN W J.
XX
PI      Martin WJ;
XX
DR      WPI: 1999-405521/34.
XX
PT      Novel strains of stealth virus
XX
PS      Claim 19; Page 44; 95pp; English.
XX
CC      This sequence represents a Stealth virus nucleic acid clone. The
CC      invention relates to a method of detecting and characterizing a stealth
CC      virus by reacting a sample suspected of containing a stealth virus with a
CC      probe from a known stealth virus and sequencing the resultant isolated
CC      nucleotide. The method comprises the steps of: (a) isolating DNA or RNA
CC      from a sample suspected of containing a stealth virus, e.g. a culture of
CC      cells showing a viral cytopathic effect; (b) testing the reactivity of
CC      the isolated DNA or RNA with a molecular probe that contains at least 18
CC      or more contiguous nucleotides identical to sequence previously
CC      identified from a stealth virus; and, optionally (c) sequencing the
CC      isolated DNA or RNA molecules that react with the probe. The method is
CC      used to detect stealth virus in a biological product, food or in the
CC      environment. The method is also used to evaluate agents for their
CC      inhibitory or stimulatory effects on stealth virus replication and to
CC      determine capacity of the virus to recombine with and potentially alter
CC      the nucleic acid sequences of a cell or bacterium.
XX
SQ      Sequence 198 BP; 40 A; 71 C; 54 G; 33 T; 0 other;

```

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Query Match      2.9%; Score 17; DB 20; Length 198;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      395 cgacgaggtctacgcg 411
      |||
Db      177 cgacgaggtctacgcg 193

RESULT 18
AAC09227/C
ID      AAC09227 standard; CDNA: 353 BP.
XX
AC      AAC09227;
XX
DT      06-OCT-2000 (first entry)
XX
DE      Human secreted protein 5' EST, SEQ ID NO: 13302.
XX
KW      Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX      gene therapy; chromosome mapping; ss.
XX
OS      Homo sapiens.
XX
PN      EP1033401-A2.
XX
PD      06-SEP-2000.
XX
PE      21-FEB-2000; 2000EP-0200610.
XX
PR      26-FEB-1999; 99US-0122487.
XX
PA      (GEST ) GENSET.
XX
PI      Dumas Milne Edwards J, Duclert A, Giordano J;
XX
DR      WPI: 2000-500381/45.
XX
PT      New nucleic acid that is a 5' expressed sequence tag (5' EST) for

```

PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for  
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -  
XX  
PS Claim 1: SEQ ID 13302; 71bp + CD-ROM; English.  
XX  
CC The present sequence is one of a large number of 5' ESTs derived from  
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively  
CC identified within the present sequence. The 5' ESTs were prepared from  
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST  
CC sequences usually correspond mainly to the 3' untranslated region (UTR)  
CC of the mRNA because they are often obtained from oligo-dT primed cDNA  
CC libraries. Such ESTs are not well suited for isolating cDNA sequences  
CC derived from the 5' ends of mRNAs and even in those cases where longer  
CC cDNA sequences have been obtained, the full 5' UTR is rarely included.  
CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be  
CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used  
CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.  
CC They are used to obtain upstream regulatory sequences and to design  
CC expression and secretion vectors.  
XX  
SQ Sequence 353 BP; 94 A; 74 C; 57 G; 127 T; 1 other;

Query Match 2.9%; Score 17; DB 21; Length 353;  
Best Local Similarity 100.0%; Pred. No. 41;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 352 aatgtcaccccaaggag 368  
|||||  
DB 63 AATGTCAACCCCAAGAG 52

RESULT 19  
AAC01025  
ID AAC01025 standard; cDNA; 386 BP.  
XX  
AC AAC01025;  
XX  
DT 06-OCT-2000 (first entry)  
XX  
DE Human secreted protein 5' EST, SEQ ID NO: 1023.  
XX  
KM Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
KM gene therapy; chromosome mapping; ss.  
XX  
OS Homo sapiens.  
XX  
PN EP1033401-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 21-FEB-2000; 2000EP-0200610.  
XX  
PR 26-FEB-1999; 99US-0122487.  
XX  
PA (GEST ) GENSET.  
PI Dumas Milne Edwards J, Duclert A, Giordano J;  
PI MPI: 2000-500381/45.  
DR P-PSDB; AAC01019.  
XX  
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for  
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -  
XX  
PS Claim 1: SEQ ID 1023; 71bp + CD-ROM; English.  
XX  
CC The present sequence is one of a large number of 5' ESTs derived from  
CC mRNAs encoding secreted proteins. An ORF has been identified within the  
CC sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs  
CC derived from 30 different tissues. EST sequences usually correspond  
CC mainly to the 3' untranslated region (UTR) of the mRNA because they are

CC often obtained from oligo-dT primed cDNA libraries. Such ESTs are not  
CC well suited for isolating cDNA sequences derived from the 5' ends of  
CC mRNAs and even in those cases where longer cDNA sequences have been  
CC obtained, the full 5' UTR is rarely included. 5' ESTs are derived from  
CC mRNAs with intact 5' ends and can therefore be used to obtain full length  
CC cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,  
CC gene therapy and chromosome mapping procedures. They are used to obtain  
CC upstream regulatory sequences and to design expression and secretion  
CC vectors.  
XX  
SQ Sequence 386 BP; 125 A; 88 C; 102 G; 70 T; 1 other;

Query Match 2.9%; Score 17; DB 21; Length 386;  
Best Local Similarity 100.0%; Pred. No. 41;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 113 aacagcagccagcgcaa 129  
|||||  
DB 92 aacagcagccagcgcaa 108

RESULT 20  
AAC38084  
ID AAC38084 standard; DNA; 513 BP.  
XX  
AC AAC38084;  
XX  
DT 17-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 19733.  
XX  
KM Hybridisation assay; genetic mapping; gene expression control;  
KM protein identification; signal transduction pathway;  
KM metabolic pathway; promoter; termination sequence; ss.  
XX  
OS Arabidopsis thaliana.  
XX  
PN EP1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-0301439.  
XX  
PR 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130449.  
PR 23-APR-1999; 99US-0130510.  
PR 28-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
PR 30-APR-1999; 99US-0132407.  
PR 04-MAY-1999; 99US-0132484.  
PR 05-MAY-1999; 99US-0132485.  
PR 06-MAY-1999; 99US-0132486.  
PR 07-MAY-1999; 99US-0132487.  
PR 11-MAY-1999; 99US-0132863.  
PR 11-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134218.  
PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.

PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 17-JUN-1999; 99US-0139453.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
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PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.

PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 02-AUG-1999; 99US-0146389.  
PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.  
PR 09-AUG-1999; 99US-0147935.  
PR 10-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148319.  
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PR 17-AUG-1999; 99US-0149175.  
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PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151066.  
PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154018.  
PR 16-SEP-1999; 99US-0154039.  
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PR 24-SEP-1999; 99US-0155659.  
PR 28-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156596.  
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PR 07-OCT-1999; 99US-0158029.  
PR 08-OCT-1999; 99US-0158232.  
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PR 13-OCT-1999; 99US-0159293.  
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PR 21-OCT-1999; 99US-0160815.  
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PR 22-OCT-1999; 99US-0160989.  
PR 25-OCT-1999; 99US-0161404.  
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PR 25-OCT-1999; 99US-0161406.  
PR 26-OCT-1999; 99US-0161359.  
PR 26-OCT-1999; 99US-0161360.

PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161992.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.

Query Match 2.9%; Score 17; DB 21; Length 513;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 222 tgcgcacccctgcacat 238  
Db 481 tgcgcacccctgcacat 497

RESULT 21  
AAV16884  
ID AAV16884 standard; DNA; 673 BP.

AC AAV16884;  
XX  
XX 07-AUG-1998 (first entry)

DE Human prostate cancer marker UC Band #31.  
XX  
XX Prostate cancer; human; marker; diagnosis; treatment; probe; ss.

OS Homo sapiens.  
XX  
XX MO9804689-A1.

PD 05-FEB-1998.  
XX  
XX 31-JUL-1996; 96MO-US12516.

PR 31-JUL-1996; 96MO-US12516.  
XX  
XX (UROC-) UROCOR INC.

PI An G, O'hara SM, Ralph D, Veltre R;  
XX  
XX WPI; 1998-130681/12.

PT Human prostate cancer marker - useful for detection and treatment of  
XX human prostate cancer  
XX  
XX Claim 1; Page 135; 229pp; English.

XX This represents a marker sequence for human prostate cancer. Isolated  
CC nucleic acid segments shown in AAV16881 to AAV16885, AAV16890 to  
CC AAV16903, AAV26351 and AAV26352 which can act as human prostate cancer  
CC markers are provided in the specification. It also provides methods for  
CC identifying markers for human prostate cancer and for detection of  
CC prostate cancer cells. The markers can be identified by amplifying human  
CC prostate RNA to provide nucleic acid amplification products, separating  
CC the products and identifying those RNA that are differentially expressed  
CC between human prostate cancers versus normal or benign human prostate.  
CC Prostate cancer cells in a sample can be detected by detecting a nucleic  
CC acid in a sample, the nucleic acid being a prostate cancer marker.  
CC Primers and probes derived from this marker can be used for the detection  
CC of prostate cancer cells in a sample. Antibodies against the protein  
CC encoded by the marker nucleic acid fragments, inhibitors of the protein  
CC and oligonucleotides antisense to the markers can also be used in the  
CC treatment of prostate cancer. The antibodies can also be used for the  
CC diagnosis of human prostate cancer.

XX Sequence 673 BP; 222 A; 140 C; 145 G; 166 T; 0 other;

Query Match 2.9%; Score 17; DB 19; Length 673;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 537 gaaaccacagagaag 553  
Db 542 gaaaccacagagaag 558

RESULT 22  
AAZ26019  
ID AAZ26019 standard; DNA; 673 BP.

AC AAZ26019;  
XX  
XX 20-MAY-1999 (first entry)

DE Prostate disease marker gene fragment UC Band #31.  
XX  
XX Prostate cancer; benign prostatic hyperplasia; marker gene; tumour;  
XX differentiation; Reverse Transcription Polymerase Chain Reaction;  
XX diagnostic; progression; cancer; metastasis; human; RT-PCR; ss.

OS Homo sapiens.  
XX  
XX US5882864-A.

PN 16-MAR-1999.  
XX  
XX 31-JUL-1996; 96US-0692787.

PR 31-JUL-1995; 95US-0001655.  
PR 31-JUL-1996; 96US-0692787.

PA (UROC-) UROCOR INC.  
XX  
XX An G, O'hara SM, Ralph D, Veltre R;

PI WPI; 1999-214055/18.  
XX  
XX

PT Diagnosing prostate cancer and benign prostatic hyperplasia cells -  
XX using oligonucleotide probes specific for marker genes associated  
XX with tumor differentiation and progression in Reverse Transcription  
XX Polymerase Chain Reaction analysis

PS Claim 1; Columns 71-72; 74pp; English.  
XX  
XX

XX The invention relates to methods for diagnosing prostate cancer or benign  
CC prostatic hyperplasia cells in a biological sample. The method uses  
CC oligonucleotide probes specific for marker genes associated with tumour  
CC differentiation and progression in Reverse Transcription Polymerase Chain  
CC Reaction (RT-PCR) analysis. The methods are diagnostic techniques useful  
CC for detecting and monitoring the progression of benign prostatic  
CC hyperplasia and human prostate cancer (the most prevalent form of cancer  
CC and a major cause of death in males) prior to the tumor undergoing  
CC metastasis, therefore allowing the optimal method of treatment to be  
CC determined before the condition becomes life threatening. The present  
XX sequence represents a claimed marker gene fragment.

XX Sequence 673 BP; 222 A; 140 C; 145 G; 166 T; 0 other;

Query Match 2.9%; Score 17; DB 20; Length 673;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 537 gaaaccacagagaag 553  
Db 542 gaaaccacagagaag 558

RESULT 23  
AAZ87504  
ID AAZ87504 standard; cDNA; 673 BP.  
XX  
XX AAZ87504;  
AC

DT 19-APR-2000 (first entry)  
XX  
XX Prostate, breast and bladder cancers detecting biomarker UC Band #31.  
DE  
XX Nucleic acid marker; biomarker; tumour; prostate cancer; bladder cancer;  
XX benign prostatic hyperplasia; BPH; breast cancer; human; immunodetection;  
KM diagnosis; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX W09964631-A1.  
PM  
XX  
XX 16-DEC-1999.  
PD  
XX  
XX 11-JUN-1999; 99WO-US13151.  
PF  
XX  
XX 12-JUN-1998; 98US-0097199.  
PR  
XX  
XX (UNOC-) UNOCOR INC.  
PA  
XX  
XX An G, O'Hara SM, Ralph D, Veltri RM;  
PI  
XX  
XX WPI: 2000-116557/10.  
DR  
XX  
XX Novel RNA biomarkers for diagnosis, prognosis and management of  
PT prostate, breast and bladder cancer -  
XX  
XX  
XX Claim 1; Page 165; 191pp; English.  
PS  
XX  
XX The invention provides nucleic acid markers of prostate, breast and  
CC bladder cancer. The markers are indicators of malignant transformation of  
CC prostate, breast and bladder tissues and are diagnostic of the potential  
CC for metastatic spread of malignant prostate tumours. The nucleic acid can  
CC also be used as targets for therapeutic intervention in prostate cancer,  
CC benign prostatic hyperplasia (BPH), bladder cancer or breast cancer. The  
CC markers may be used to design specific probes and primers, for the rapid  
CC analysis of prostate, bladder or breast biopsy samples. The probes and  
CC primers may also be used for in situ hybridization or in situ PCR  
CC detection and diagnosis. They may also be used to identify and isolate  
CC full length gene sequences from various DNA libraries. Antibodies  
CC against the polypeptide products of the markers can be used to treat  
CC prostate cancer, bladder cancer or breast cancer. The encoded proteins  
CC may be used to detect antibodies. The proteins and antibodies can be  
CC used in immunodetection methods for detecting or quantifying the cancers,  
CC and for clinical diagnosis of these cancers. The antibodies may also be  
CC used for radioimaging to quantify and localize the encoded proteins.  
CC  
XX  
SQ Sequence 673 BP; 222 A; 140 C; 145 G; 166 T; 0 other;

Query Match 2.9%; Score 17; DB 21; Length 673;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 537 gaaccacagcaggaag 553  
|||||  
DB 542 gaaccacagcaggaag 558

RESULT 24  
AAZ33534  
ID AAZ33534 standard; cDNA: 697 BP.  
XX  
XX AAZ33534;  
AC  
XX  
XX 08-DEC-1999 (first entry)  
DT  
XX  
XX Human prostate cancer-associated EST 58.  
DE  
XX  
XX Expressed sequence tag: EST; prostate; tumor; treatment; gene therapy;  
KM cancer; tissue specificity; human; ss.  
XX  
OS Homo sapiens.

XX  
XX DE19811194-A1.  
PN  
XX  
XX 16-SEP-1999.  
PD  
XX  
XX 10-MAR-1998; 98DE-1011194.  
PF  
XX  
XX 10-MAR-1998; 98DE-1011194.  
PR  
XX  
XX (META-) METAGEN GES GENOMFORSCHUNG.MBH.  
PA  
XX  
XX Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E, Rosenthal A;  
PI  
XX  
XX WPI: 1999-519629/44.  
DR  
XX  
XX P-PSDB; AAV48440.  
DR  
XX  
XX New nucleic acid expressed at high level in normal prostatic tissue and  
PT encoded polypeptides, used to treat cancer and screen for therapeutic  
PT agents -  
XX  
XX  
XX Claim 1a; 119; 194pp; German.  
PS  
XX  
XX This invention describes novel nucleic acid sequences (A) that are  
CC expressed at high level in normal prostatic tissue. Polypeptides (1)  
CC encoded by (A) are used: (a) for identifying agents for treatment of  
CC prostatic cancer and (b) for therapy of prostate cancer, optionally  
CC where expressed by gene therapy methods. (A) is also used to isolate  
CC full-length genes (for gene therapy) and for recombinant production of  
CC (1), which can be used to raise specific antibodies. (A) are identified  
CC by assembly of ESTs (expressed sequence tags) before these are analyzed  
CC for expression pattern (tissue specificity). This approach eliminates  
CC many of the false results, as regards tissue specificity, associated  
CC with known methods that use single (usually short) ESTs. AA33477-233540  
CC represent expressed sequence tags described in the method of the  
CC invention.  
CC  
XX  
SQ Sequence 697 BP; 223 A; 140 C; 196 G; 138 T; 0 other;

Query Match 2.9%; Score 17; DB 20; Length 697;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 113 aacacagcagccca 129  
|||||  
DB 110 aacacagcagccca 126

RESULT 25  
AAC39218  
ID AAC39218 standard; DNA: 763 BP.  
XX  
XX AAC39218;  
AC  
XX  
XX 17-OCT-2000 (first entry)  
DT  
XX  
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 23810.  
DE  
XX  
XX Hybridisation assay; genetic mapping; gene expression control;  
KM protein identification; signal transduction pathway;  
KM metabolic pathway; promoter; termination sequence; ss.  
XX  
XX Arabidopsis thaliana.  
OS  
XX  
XX EP1033405-A2.  
PM  
XX  
XX 06-SEP-2000.  
PD  
XX  
XX 25-FEB-2000; 2000EP-0301439.  
PF  
XX  
XX 25-FEB-1999; 99US-0121825.  
PR  
XX  
XX 05-MAR-1999; 99US-0123180.  
PR  
XX  
XX 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130049.  
PR 23-APR-1999; 99US-0130510.  
PR 28-APR-1999; 99US-0130891.  
PR 30-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
PR 30-APR-1999; 99US-0132407.  
PR 04-MAY-1999; 99US-0132484.  
PR 05-MAY-1999; 99US-0132485.  
PR 06-MAY-1999; 99US-0132486.  
PR 07-MAY-1999; 99US-0132487.  
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PR 18-JUN-1999; 99US-0140695.  
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PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
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PR 14-JUL-1999; 99US-0143624.  
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PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
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PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
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PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
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PR 06-AUG-1999; 99US-0147416.  
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PR 24-SEP-1999; 99US-0155659.  
PR 28-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157753.  
PR 06-OCT-1999; 99US-0157865.

PR 07-OCT-1999; 99US-0158029.  
PR 08-OCT-1999; 99US-0158232.  
PR 12-OCT-1999; 99US-0158369.  
PR 13-OCT-1999; 99US-0159293.  
PR 13-OCT-1999; 99US-0159294.  
PR 13-OCT-1999; 99US-0159295.  
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PR 14-OCT-1999; 99US-0159330.  
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PR 14-OCT-1999; 99US-0159637.  
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PR 18-OCT-1999; 99US-0159584.  
PR 21-OCT-1999; 99US-0160741.  
PR 21-OCT-1999; 99US-0160767.  
PR 21-OCT-1999; 99US-0160768.  
PR 21-OCT-1999; 99US-0160770.  
PR 21-OCT-1999; 99US-0160814.  
PR 21-OCT-1999; 99US-0160815.  
PR 22-OCT-1999; 99US-0160980.  
PR 22-OCT-1999; 99US-0160981.  
PR 22-OCT-1999; 99US-0160989.  
PR 25-OCT-1999; 99US-0161404.  
PR 25-OCT-1999; 99US-0161405.  
PR 25-OCT-1999; 99US-0161406.  
PR 26-OCT-1999; 99US-0161359.  
PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161992.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.

Query Match 2.9%; Score 17; DB 21; Length 763;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 217 gccgctgctgcatccccc 233  
DB 204 gccgctgctgcatccccc 220

RESULT 26  
AAC99839/C  
ID AAC99839 standard; cDNA; 800 BP.

AC AAC99839;  
DT 13-MAR-2001 (first entry)  
XX

DE Human secreted protein gene 22 SEQ ID NO:32.

XX Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;  
KM antirheumatic; antiproliferative; cytostatic; cardiac; vasotropic;  
KM cerebroprotective; neuroprotective; antibacterial; virucide;  
KM fungicide; ophthalmological; gene therapy; pathological condition;  
KM autoimmune disease; rheumatoid arthritis; hyperproliferative disorder;  
KM neoplasm; cardiovascular disorder; cardiac arrest; cerebral ischaemia;  
KM cerebrovascular disorder; angiogenesis; nervous system disorder;  
KM Alzheimer's disease; infection; ocular disorder; corneal infection;  
KM wound healing; skin aging; food additive; preservative;  
KM chromosome 11; ss.

OS Homo sapiens.

PN WO20007042-A1.

PD 23-NOV-2000.

PF 11-MAY-2000; 2000WO-US12788.

PR 13-MAY-1999; 99US-0134068.

PA (HDMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM, Moore PA, Young PE, Komatsoulis GA, Birse CE;  
PI Duan RD, Florence KA, Soppet DR;  
XX WPT. 2000-679828/66.  
DR P-PSDB; AAB56098.  
XX  
PT Isolated nucleic acid molecule encoding a human secreted protein is  
PS used in preventing, treating or ameliorating a medical condition -  
XX Claim 1; Page 866; 1065pp; English.

The polynucleotide sequences given in AAC99818 to AAC99977 encode the human secreted proteins given in AAB56077 to AAB56362. Human secreted proteins have activities based on the tissues and cells the genes are expressed in. Examples of activities include: immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiac; vasotropic; cerebroprotective; neuroprotective; antibacterial; virucide; fungicide; and ophthalmological. The human secreted polynucleotides and proteins can be used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The proteins can also be used as a food additive or preservative to increase or decrease storage capabilities. AAC99809 to AAC99817 and AAB5076 represent sequences used in the exemplification of the present invention.

Sequence 800 BP; 154 A; 187 C; 154 G; 305 T; 0 other;

Query Match 2.9%; Score 17; DB 21; Length 800;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 aacagcagccagcccaa 129  
DB 743 AACAGCAGCCAGCCCAA 727

RESULT 27  
AAC42507  
ID AAC42507 standard; DNA; 1148 BP.

AC AAC42507;

DT 17-OCT-2000 (first entry)

XX Arabidopsis thaliana DNA fragment SEQ ID NO: 35818.  
DE Hybridisation assay; genetic mapping; gene expression control;  
KM protein identification; signal transduction pathway;  
KM metabolic pathway; promoter; termination sequence; ss.

XX Arabidopsis thaliana.

OS Arabidopsis thaliana.

PN EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

PR 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 9905-0123548.  
PR 23-MAR-1999; 9905-0125788.  
PR 25-MAR-1999; 9905-0126264.  
PR 29-MAR-1999; 9905-0126785.  
PR 01-APR-1999; 9905-0127462.  
PR 06-APR-1999; 9905-0128224.  
PR 08-APR-1999; 9905-0128714.  
PR 16-APR-1999; 9905-0129845.  
PR 19-APR-1999; 9905-0130077.  
PR 21-APR-1999; 9905-01300449.  
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PR 28-APR-1999; 9905-0131449.  
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PR 29-JUN-1999; 9905-0140991.  
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PR 04-AUG-1999; 9905-0147204.  
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PR 27-AUG-1999; 9905-0151080.  
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PR 31-AUG-1999; 9905-0151438.  
PR 01-SEP-1999; 9905-0151930.  
PR 07-SEP-1999; 9905-0152363.  
PR 10-SEP-1999; 9905-0153070.  
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PR 29-SEP-1999; 9905-0156596.  
PR 04-OCT-1999; 9905-0157117.  
PR 05-OCT-1999; 9905-0157753.



PR 06-OCT-1999; 99US-0157865.  
PR 07-OCT-1999; 99US-0156029.  
PR 08-OCT-1999; 99US-0156823.  
PR 12-OCT-1999; 99US-0156369.  
PR 13-OCT-1999; 99US-0159293.  
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PR 14-OCT-1999; 99US-0159637.  
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PR 25-OCT-1999; 99US-0161406.  
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PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161992.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.

Query Match 2.9%; Score 17; DB 21; Length 1148;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 222 tgcgcacccctgcacat 238  
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Db 593 tgcgcacccctgcacat 609

## RESULT 28

AAC49984  
ID AAC49984 standard; DNA: 1273 BP.

AC AAC49984;

DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 63167.

KW Hybridisation assay; genetic mapping; gene expression control;

KW Protein identification; signal transduction pathway;

KW Metabolic pathway; promoter; termination sequence; ss.

OS Arabidopsis thaliana.

PN EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

PR 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 23-MAR-1999; 99US-0123548.

PR 25-MAR-1999; 99US-0125788.

PR 29-MAR-1999; 99US-0126264.

PR 01-APR-1999; 99US-0126785.

PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130449.  
PR 23-APR-1999; 99US-0130510.  
PR 23-APR-1999; 99US-0130891.  
PR 28-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
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PR 06-MAY-1999; 99US-0132486.  
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PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
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PR 18-JUN-1999; 99US-0139460.  
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PR 30-JUN-1999; 99US-0141287.  
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PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
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Query Match 2.9%; Score 17; DB 21; Length 1273;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 222 tgcctgcctccctgcct 238  
Db 522 tgcctgcctccctgcct 538  
  
RESULT 29  
AAC37359 standard; DNA; 1277 BP.  
ID AAC37359;  
XX AAC37359;  
AC AAC37359;  
XX 17-OCT-2000 (first entry)  
DT 17-OCT-2000 (first entry)  
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 17090.  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 17090.  
XX Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway;  
KW metabolic pathway; promoter; termination sequence; ss.  
XX Arabidopsis thaliana.  
OS Arabidopsis thaliana.  
XX EP1033405-A2.  
XX EP1033405-A2.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
XX 06-SEP-2000.  
PF 25-FEB-2000; 2000EP-0301439.  
XX 25-FEB-2000; 2000EP-0301439.  
XX 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129645.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130449.  
PR 23-APR-1999; 99US-0130510.  
PR 23-APR-1999; 99US-0130891.  
PR 28-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.

PR 30-APR-1999; 99US-0132407.  
PR 04-MAY-1999; 99US-0132484.  
PR 05-MAY-1999; 99US-0132485.  
PR 06-MAY-1999; 99US-0132486.  
PR 06-MAY-1999; 99US-0132487.  
PR 07-MAY-1999; 99US-0132863.  
PR 11-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134218.  
PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 14-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0138452.  
PR 16-JUN-1999; 99US-0138453.  
PR 17-JUN-1999; 99US-0139492.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0138463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144632.  
PR 20-JUL-1999; 99US-0144884.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145085.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.  
PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 02-AUG-1999; 99US-0146389.  
PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.  
PR 09-AUG-1999; 99US-0147935.  
PR 10-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148319.  
PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148684.  
PR 16-AUG-1999; 99US-0149368.  
PR 17-AUG-1999; 99US-0149175.  
PR 18-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149722.  
PR 20-AUG-1999; 99US-0149723.  
PR 20-AUG-1999; 99US-0149929.  
PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149330.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151066.  
PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154018.  
PR 16-SEP-1999; 99US-0154039.  
PR 20-SEP-1999; 99US-0154779.  
PR 22-SEP-1999; 99US-0155139.  
PR 23-SEP-1999; 99US-0155486.  
PR 24-SEP-1999; 99US-0155659.  
PR 28-SEP-1999; 99US-0155658.  
PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157753.  
PR 06-OCT-1999; 99US-0157865.  
PR 07-OCT-1999; 99US-0158029.  
PR 08-OCT-1999; 99US-0158232.  
PR 12-OCT-1999; 99US-0158369.  
PR 13-OCT-1999; 99US-0158393.  
PR 13-OCT-1999; 99US-0159293.  
PR 13-OCT-1999; 99US-0159294.  
PR 13-OCT-1999; 99US-0159295.  
PR 14-OCT-1999; 99US-0159329.  
PR 14-OCT-1999; 99US-0159330.  
PR 14-OCT-1999; 99US-0159331.  
PR 14-OCT-1999; 99US-0159637.  
PR 14-OCT-1999; 99US-0159638.  
PR 18-OCT-1999; 99US-0159584.  
PR 21-OCT-1999; 99US-0160741.

PR 21-OCT-1999; 99US-0160767.  
PR 21-OCT-1999; 99US-0160768.  
PR 21-OCT-1999; 99US-0160770.  
PR 21-OCT-1999; 99US-0160814.  
PR 21-OCT-1999; 99US-0160815.  
PR 22-OCT-1999; 99US-0160980.  
PR 22-OCT-1999; 99US-0160981.  
PR 22-OCT-1999; 99US-0160989.  
PR 25-OCT-1999; 99US-0161404.  
PR 25-OCT-1999; 99US-0161405.  
PR 25-OCT-1999; 99US-0161406.  
PR 25-OCT-1999; 99US-0161359.  
PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161992.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.

Query Match 2.9%; Score 17; DB 21; Length 1277;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 222 tgctgcatccctgcgc 238  
|||||  
DB 524 tgctgcatccctgcgc 540

RESULT 30  
AAV64526/C  
ID AAV64526 standard; DNA: 1338 BP.  
XX  
AC AAV64526;

XX 27-JAN-1999 (first entry)

DE M. tuberculosis immunogenic polypeptide XP31 DNA.

XX Tuberculosis; immunogenic; soluble; antigen; protective immunity; TB;  
KM vaccine; pharmaceutical; infection; diagnosis; ss.

XX OS Mycobacterium tuberculosis.

XX PN W09816646-A2.

XX PD 23-APR-1998.

XX PF 07-OCT-1997; 97WO-US18293.

XX PR 13-MAR-1997; 97US-0818112.

XX PR 11-OCT-1996; 96US-0730510.

XX PA (CORI-) CORIXA CORP.

XX PI Campos-Neto A, Dillon DC, Houghton R, Lodes MJ;  
PI Reed SG, Skeiky YAW, Twardzik DR, Vedvick TS;

XX DR WPI; 1998-261042/23.

PT Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - used  
PT to develop products for the detection of M. tuberculosis infection  
PT and for diagnosis, treatment and prevention of tuberculosis  
XX Claim 31a; Page 162-163; 230pp; English.

XX This sequence encodes an immunogenic portion of a soluble Mycobacterium  
CC tuberculosis (MT) antigen which can be used in a method for inducing  
CC protective immunity against tuberculosis (TB). This sequence can be  
CC formulated into vaccines and/or pharmaceutical compositions for  
CC immunising against M. tuberculosis infection or may be used for the  
CC diagnosis of tuberculosis.

XX Sequence 1338 BP; 199 A; 432 C; 485 G; 222 T; 0 other;

Query Match 2.9%; Score 17; DB 19; Length 1338;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 505 gccagcgagcctgcgc 521  
|||||  
DB 1147 GCCAGCGGCGCTCGTC 1131

RESULT 31  
AAV44417/C  
ID AAV44417 standard; DNA: 1338 BP.  
XX  
AC AAV44417;

XX 09-NOV-1998 (first entry)

DE Mycobacterium tuberculosis antigen XP31 DNA.

XX Tuberculosis; infection; diagnosis; antigen; XP31; ss.

XX OS Mycobacterium tuberculosis strain Erdman.

XX PN W09816645-A2.

XX PD 23-APR-1998.

XX PF 07-OCT-1997; 97WO-US18214.

XX PR 13-MAR-1997; 97US-0818111.

XX PR 11-OCT-1996; 96US-0729622.

XX PA (CORI-) CORIXA CORP.

XX PI Campos-Neto A, Dillon DC, Houghton R, Lodes MJ;  
PI Reed SG, Skeiky YAW, Twardzik DR, Vedvick TS;

XX DR WPI; 1998-251292/22.

PT New isolated Mycobacterium tuberculosis polypeptides and DNA - used  
PT to develop products for the detection of M. tuberculosis infection  
PT and diagnosis of tuberculosis

XX Claim 11a; Page 171-172; 250pp; English.

XX This DNA sequence codes for a portion of Mycobacterium tuberculosis  
CC antigen XP31. It was isolated from a M. tuberculosis strain Erdman  
CC genomic DNA expression library using sera from patients having  
CC extrapulmonary tuberculosis. The clone bears some similarity to  
CC known sequences. The invention relates to compositions and methods  
CC for diagnosing tuberculosis. It provides polypeptides (see  
CC AAM64291-W64379) comprising an antigenic portion of a soluble M.  
CC tuberculosis antigen, or an immunogenic portion of an M.  
CC tuberculosis antigen, as well as DNA sequences encoding such  
CC polypeptides, recombinant expression vectors and transformed or  
CC transfected host cells. Also claimed are methods and diagnostic  
CC kits for detecting M. tuberculosis infection in a patient using  
CC these polypeptides, antibodies or oligonucleotide probes and  
CC primers.

XX Sequence 1338 BP; 199 A; 432 C; 485 G; 222 T; 0 other;

Query Match 2.9%; Score 17; DB 19; Length 1338;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 505 gccagcgagcctgcgc 521  
|||||  
DB 1147 GCCAGCGGCGCTCGTC 1131

```

RESULT 32
AA219327/C
ID AA219327 standard; DNA; 1338 BP.
XX
XX AA219327;
AC
XX 05-NOV-1999 (first entry)
DT
XX
XX M. tuberculosis antigen XP31 DNA sequence.
DE
XX
XX Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen;
KW immunotherapy; diagnosis; immunisation; vaccine; infection;
KM immune response; skin test; ss.
XX
XX Mycobacterium tuberculosis.
OS
XX WO9942076-A2.
PN
XX 26-AUG-1999.
PD
XX
XX 17-FEB-1999; 99WO-US03268.
PE
XX
XX 05-MAY-1998; 98US-0072967.
PR
XX 18-FEB-1998; 98US-0025197.
PA
XX (CORI-) CORIXA CORP.
XX
XX Campos-Neto A, Dillon DC, Hendrickson RC, Houghton R;
PI Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR, Vedvick TS;
XX
XX WPI; 1999-527409/44.
DR
XX
XX New antigens from Mycobacterium tuberculosis useful in diagnostic
PT skin tests and protective or therapeutic vaccines or compositions
PS
XX Claim 11; Page 157-158; 299pp; English.
PS
XX
XX The present invention describes polypeptides comprising an immunogenic
CC part of a Mycobacterium tuberculosis antigen (Ag). Also described
CC are vaccines and fusion protein containing M. tuberculosis Ag's.
CC M. tuberculosis Ag's, DNAs encoding them, derived fusion proteins and
CC other polypeptides fragments, can be used in pharmaceutical compositions
CC or vaccines to generate a protective or therapeutic immune response to
CC M. tuberculosis and as reagents in skin tests for diagnosis of
CC tuberculosis. Ag can induce proliferation of, or cytokine secretion
CC by, T, B or natural killer cells and/or macrophages in
CC tuberculosis-immune subjects. AA219249 to AA219460 and AAY39083 to
CC AAY39325 are used in the exemplification of the present invention.
XX
XX Sequence 1338 BP; 199 A; 432 C; 485 G; 222 T; 0 other;
SQ

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Query Match 2.9%; Score 17; DB 20; Length 1338;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 505 gccagcgagcctgctc 521
    |||||||||||||||
Db 1147 GCCAGCGGCGCTCGTC 1131

```

```

RESULT 33
AA219115/C
ID AA219115 standard; DNA; 1338 BP.
XX
XX AA219115;
AC
XX 05-NOV-1999 (first entry)
DT
XX
XX M. tuberculosis recombinant antigen DNA encoding XP31.
DE
XX
XX Antigen; diagnosis; detection; infection; antibody; immunisation;
KW

```

```

KW vaccine; immunity; ss.
XX
XX Mycobacterium tuberculosis.
OS
XX WO9942118-A2.
PN
XX 26-AUG-1999.
PD
XX
XX 17-FEB-1999; 99WO-US03265.
PE
XX
XX 05-MAY-1998; 98US-0072596.
PR
XX 18-FEB-1998; 98US-0024753.
PA
XX (CORI-) CORIXA CORP.
XX
XX Campos-Neto A, Dillon DC, Hendrickson RC, Houghton R;
PI Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR, Vedvick TS;
XX
XX WPI; 1999-527416/44.
DR
XX
XX New polypeptide comprising antigenic portions of M. tuberculosis
PT
XX
XX Claim 11a; Page 202-203; 323pp; English.
PS
XX
XX This invention describes novel recombinant antigens and their encoding
CC nucleic acids derived from Mycobacterium tuberculosis. The novel
CC polypeptides are useful for detecting M. tuberculosis infection in a
CC biological sample by detecting antibodies which bind with the
CC polypeptides, and are useful as vaccines for immunizing against
CC M. tuberculosis infection. The new detection methods are needed as
CC current vaccination strategies do not provide 100% immunity.
XX
XX Sequence 1338 BP; 199 A; 432 C; 485 G; 222 T; 0 other;
SQ

```

```

Query Match 2.9%; Score 17; DB 20; Length 1338;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 505 gccagcgagcctgctc 521
    |||||||||||||||
Db 1147 GCCAGCGGCGCTCGTC 1131

```

## RESULT 34

AACT9935  
ID AACT9935 standard; cDNA; 1647 BP.

AC AACT9935;

DT 12-FEB-2001 (first entry)

DE Human secreted protein encoding cDNA for gene 38.

KW Secreted protein; human; immunosuppressive; antiarthritic; antirheumatic;  
KW antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;  
KW neurotropic; neuroprotective; antibacterial; virucide; fungicide;  
KW ophthalmological; gene therapy; treatment; autoimmune disease; infection;  
KW cardiovascular disorder; nervous system disorder; ocular disorder;  
KW wound healing; epithelial cell proliferation; skin aging; mental state;  
KW transplantation; metabolism modulation; ss.

OS Homo sapiens.

PN WO200055200-A1.

PD 21-SEP-2000.

PE 09-MAR-2000; 2000WO-US06042.

PR 12-MAR-1999; 99US-0124143.

PR 03-DEC-1999; 99US-0168663.

PA (HUMA-) HUMAN GENOME SCI INC.  
 XX Rosen CA, Ruben SM, Komatsoulis G;  
 XX WPI: 2000-656008/63.  
 DR P-PSDB; AAB44954.  
 XX  
 XX Isolated human secretory proteins, nucleic acids encoding them and  
 PT antibodies directed against them, useful for diagnosing and treating  
 PT disorders related to the proteins such as cancer, Alzheimer's disease  
 PT and Parkinsons -  
 XX  
 PS Claim 1a; Page 370-371; 453pp; English.  
 XX  
 CC This invention describes a novel isolated polypeptide (I) and its  
 CC encoding nucleic acid molecule (II) which have immunosuppressive,  
 CC antiarthritic, antirheumatic, antiproliferative, cyostatic, cardiac,  
 CC vasotropic, cerebroprotective, neurotropic, neuroprotective, antibacterial,  
 CC virucide, fungicide and ophthalmological activity and which can be used  
 CC for gene therapy. (I) and (II) are used to prevent, treat or ameliorate  
 CC a medical condition in e.g. humans, mice, rabbits, goats, horses, cats,  
 CC dogs, chickens or sheep. (I) and (II) are also used in diagnosing a  
 CC pathological condition or susceptibility to a pathological condition. The  
 CC antibodies to (II) can also be used in alleviating symptoms associated  
 CC with the disorders and in diagnostic immunoassays e.g. radioimmunoassays  
 CC or enzyme linked immunosorbent assays (ELISA). Disorders which are  
 CC diagnosed or treated include autoimmune diseases e.g. Rheumatoid  
 CC arthritis, hyperproliferative disorders e.g. neoplasms of the breast or  
 CC liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular  
 CC disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders  
 CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and  
 CC fungi and ocular disorders e.g. corneal infection. The polypeptides can  
 CC also be used to aid wound healing and epithelial cell proliferation, to  
 CC prevent skin aging due to sunburn, to maintain organs before  
 CC transplantation, for supporting cell culture of primary tissues, to  
 CC regenerate tissues and in chemotaxis. The polypeptides are used to  
 CC modulate mammalian metabolism, to change mammal's mental state or  
 CC physical state by influencing biorhythms circadian rhythms, depression  
 CC tendency for violence tolerance for-pain, reproductive capabilities,  
 CC hormonal or endocrine levels, appetite, libido, memory, stress or other  
 CC cognitive qualities, as a food additive or preservative, such as to  
 CC increase or decrease storage capabilities, fat content, lipid, protein,  
 CC carbohydrates, vitamins, minerals, cofactors or other nutritional  
 CC components.  
 CC  
 SQ Sequence 1647 BP; 425 A; 301 C; 329 G; 583 T; 9 other;  
 XX  
 XX  
 Query Match 2.9%; Score 17; DB 21; Length 1647;  
 Best Local Similarity 100.0%; Pred. No. 39;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 485 tggtagcagctaatagt 501  
 ||||||||||||||||  
 DB 1018 tggtagcagctaatagt 1034  
 RESULT 35  
 AAT34620  
 ID AAT34620 standard; DNA; 3337 BP.  
 XX  
 AC AAT34620;  
 XX  
 XX 12-NOV-1996 (first entry)  
 XX  
 DE P. vivax ESP-1 blood stage antigen coding sequence.  
 XX  
 KM ESP-1; blood stage antigen; diagnosis; malaria; infection;  
 KW causative agent; antibody; monoclonal; polyclonal; assay; ds.  
 OS Plasmodium vivax (clone PvMB3.3.1).  
 XX  
 XX  
 FH Key Location/Qualifiers

FT Exon 1..91  
 FT /\*tag- a  
 FT /note= "encodes initial (N-terminal) sequence of  
 FT hydrophobic amino acids"  
 FT  
 FT Intron 92..230  
 FT /\*tag- b  
 FT /note= "contains typical malaria intervening  
 FT sequence splice sites splice sites"  
 FT 231..3197  
 FT /\*tag- c  
 FT  
 PN US5532133-A.  
 XX  
 XX  
 PD 02-JUL-1996.  
 XX  
 PF 02-JUN-1993; 93US-0072610.  
 XX  
 PR 02-JUN-1993; 93US-0072610.  
 XX  
 PA (UYNX ) UNIV NEW YORK STATE.  
 XX  
 PI Barnwell JW;  
 XX  
 XX WPI: 1996-321110/32.  
 DR P-PSDB; AAR9747.  
 XX  
 PT Antibodies to Plasmodium vivax blood stage antigens - used to  
 PT diagnose malaria and to determine whether P. vivax is the species  
 PT responsible for infection  
 XX  
 XX Example 4; Column 15-20; 22pp; English.  
 PS  
 XX The present sequence encodes a species-specific Plasmodium vivax  
 CC malarial antigen, PvESP-1. The gene appears to be missing a small  
 CC portion of its 5' end. This protein is secreted into the plasma of  
 CC a susceptible mammalian host after infection. Monoclonal/polyclonal  
 CC antibodies can be utilized in assays used to diagnose malaria, as well  
 CC as to determine whether P. vivax is the species responsible for the  
 CC infection.  
 CC  
 SQ Sequence 3337 BP; 1304 A; 467 C; 875 G; 691 T; 0 other;  
 XX  
 XX  
 Query Match 2.9%; Score 17; DB 17; Length 3337;  
 Best Local Similarity 100.0%; Pred. No. 38;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 539 aaccaacagagaaga 555  
 ||||||||||||||||  
 DB 2029 aaccaacagagaaga 2045  
 RESULT 36  
 AAX15174  
 ID AAX15174 standard; DNA; 3337 BP.  
 XX  
 AC AAX15174;  
 XX  
 XX 28-APR-1999 (first entry)  
 XX  
 DE DNA encoding a secreted blood-stage protein called PvESP-1.  
 XX  
 KM Erythrocyte secreted protein-1; PvESP-1; malarial antigen;  
 KW blood-stage protein; malaria; monoclonal antibody 1D11G10; ds.  
 XX  
 OS Plasmodium vivax.  
 XX  
 XX  
 FH Key Location/Qualifiers  
 FH CDS 1..3197  
 FT /\*tag- a  
 FT /note= "contains 1 intron"  
 FT 1..91  
 FT exon /\*tag- b

FT /number= 1  
 FT 92..230  
 FT /\*tag= c  
 FT /number= 1  
 FT exon 231..3194  
 FT /\*tag= d  
 FT /number= 2  
 PN US5874527-A.  
 XX 23-FEB-1999.  
 PD 30-SEP-1996; 96US-0719822.  
 PE 02-JUN-1993; 93US-0072610.  
 PR 07-JUN-1995; 95US-0478417.  
 PR 30-SEP-1996; 96US-0719822.  
 XX (UYNV ) UNIV NEW YORK STATE.  
 PA Barnwell JM;  
 XX WPI, 1999-180063/15.  
 DR P-PSDB; AAW97039.  
 DR P-PSDB; AAW97039.  
 PT Plasmodium vivax peptide antigen - for diagnosis of malaria caused  
 PT by Plasmodium vivax  
 XX Example 4; Fig 5A-C; 23pp; English.  
 PS The present sequence encodes a C-terminal erythrocyte secreted  
 CC protein-1 (PvESP-1) of Plasmodium vivax. PvESP-1 is a malarial  
 CC antigen which is a secreted blood-stage protein present in detectable  
 CC amounts in biological samples from individuals infected with P. vivax.  
 CC The protein comprises an epitope not present in other Plasmodium species  
 CC that cause malaria in humans, and is bound by monoclonal antibody  
 CC 1D1G10. The peptide antigen can be used in immunoassays for diagnosis  
 CC of malaria caused by P. vivax and/or can be used to produce antibodies  
 CC for use in such immunoassays.  
 CC XX  
 SQ Sequence 3337 BP; 1304 A; 467 C; 875 G; 691 T; 0 other;  
 OY 539 aaccaacagagaaga 555  
 ||||||||||||||||  
 Db 2029 aaccaacagagaaga 2045  
 RESULT 37  
 AAC74895  
 ID AAC74895 standard; cDNA; 6171 BP.  
 AC AAC74895;  
 XX 08-FEB-2001 (first entry)  
 DE Human ORF450 polynucleotide sequence SEQ ID NO:899.  
 XX Human; open reading frame: ORF; detection: cytosolic; hepatotropic;  
 KW vulnary; antiparasitic; antiparkinsonian; neurotropic; neuroprotective;  
 KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;  
 KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;  
 KW hypotensive; dermatological; immunosuppressive; antiinflammatory;  
 KW antiviral; antibacterial; antifungal; antineumatic; antithyroid;  
 KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;  
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;  
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;  
 KW cholesterol ester storage; systemic lupus erythematosus; infection;  
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;

KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;  
 KW bone damage; cartilage damage; antiinflammatory disease; coagulation;  
 KW thrombosis; contraceptive; ss.  
 XX Homo sapiens.  
 XX WO200058473-A2.  
 XX 05-OCT-2000.  
 PD 31-MAR-2000; 2000WO-US08621.  
 PE 31-MAR-1999; 99US-0127607.  
 PR 02-APR-1999; 99US-0127636.  
 PR 05-APR-1999; 99US-0127728.  
 PR 30-MAR-2000; 2000US-0540763.  
 XX (CURA-) CURAGEN CORP.  
 PA Shimkets RA, Leach M;  
 XX WPI, 2000-602362/57.  
 DR P-PSDB; AAB40686.  
 DR Novel nucleic acids and peptides derived from open reading frame X,  
 PT useful for treating e.g. cancers, proliferative disorders,  
 PT neurodegenerative disorders and cardiovascular disease -  
 XX Claim 5; Page 910-914; 5507pp; English.  
 PS AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,  
 CC which represent the human ORF open reading frames 1 to 3161. The ORF  
 CC sequences have activities such as: cytosolic; hepatotropic; vulnary;  
 CC osteopathic; antiparkinsonian; neurotropic; neuroprotective;  
 CC anticonvulsant; cardiant; thrombolytic; coagulant; vasotropic;  
 CC immunostimulant; antidiabetic; dermatological; immunosuppressive;  
 CC antidiabetic; hypotensive; dermatological; immunosuppressive;  
 CC antineumatic; antiviral; antithyroid; antineumatic;  
 CC antithyroid; and antianaemic. The sequences can be used for determining  
 CC the presence of or predisposition to, or preventing or treating  
 CC pathological conditions associated with an ORF-associated disorder. The  
 CC nucleic acids can be used to express ORF proteins in gene therapy  
 CC vectors. The proteins and nucleic acids may be used to treat cancers,  
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,  
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,  
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus  
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,  
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,  
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,  
 CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance  
 CC coagulation; to inhibit thrombosis; and as a contraceptive.  
 CC XX  
 SQ Sequence 6171 BP; 1659 A; 1317 C; 1436 G; 1759 T; 0 other;  
 OY 245 ctgttcacgcgcacgc 261  
 ||||||||||||||||  
 Db 1615 ctgttcacgcgcacgc 1631  
 RESULT 38  
 AAA58762  
 ID AAA58762 standard; DNA; 11212 BP.  
 AC AAA58762;  
 XX 20-OCT-2000 (first entry)  
 DE DNA encoding a cyclohexadepsipeptide synthetase.

| XX | Cyclohexadepsipeptide synthetase; filamentous fungal cell;          |
|----|---------------------------------------------------------------------|
| KW | cyclohexadepsipeptide; antibiotic, ss.                              |
| OS | Fusarium venenatum.                                                 |
| XX |                                                                     |
| FH | Key                                                                 |
| FT | 270..9659                                                           |
| FT | /*tag= a                                                            |
| FT | /product= "cyclohexadepsipeptide synthetase"                        |
| XX |                                                                     |
| PN | WO200042203-A2.                                                     |
| XX |                                                                     |
| PD | 20-JUL-2000.                                                        |
| XX |                                                                     |
| PE | 13-JAN-2000; 2000WO-US00913.                                        |
| XX |                                                                     |
| PR | 13-JAN-1999; 99US-0229862.                                          |
| XX |                                                                     |
| PA | (NOVO ) NOVO NORDISK BIOTECH INC.                                   |
| XX |                                                                     |
| PI | Berka RM, Rey MW, Yoder WT;                                         |
| XX |                                                                     |
| DR | WPI: 2000-482833/42.                                                |
| DR | P-PSDB: AAB07427.                                                   |
| XX |                                                                     |
| PT | Producing a heterologous polypeptide for production of antibiotics  |
| PT | comprises cultivating a mutant of a parent filamentous fungal cell  |
| PT | comprising a nucleic acid sequence encoding cyclohexadepsipeptide - |
| XX |                                                                     |
| PS | Claim 55; Fig 1A-I; 76pp; English.                                  |
| XX |                                                                     |
| CC | The present sequence encodes a cyclohexadepsipeptide synthetase     |
| CC | polypeptide. The specification describes a method for producing a   |
| CC | heterologous polypeptide. The method comprises cultivating a        |
| CC | mutant of a parent filamentous fungal cell, which produces less     |
| CC | cyclohexadepsipeptide than the parent filamentous fungal cell when  |
| CC | cultured under the same conditions. The method if used for the      |
| CC | production of biologically active compounds e.g. antibiotics.       |
| XX |                                                                     |
| SQ | Sequence 11212 BP; 2808 A; 2844 C; 2658 G; 2901 T; 1 other;         |

|                       |                                                                          |                                                                           |                                                          |
|-----------------------|--------------------------------------------------------------------------|---------------------------------------------------------------------------|----------------------------------------------------------|
| FT                    | XX                                                                       | WO200029596-A1.                                                           | /product= "Escherichia coli AMPA acyltransferase (AAT)"  |
| FT                    | XX                                                                       |                                                                           | /function= "transfers acyl group from an acylcarrier     |
| FT                    | XX                                                                       |                                                                           | (CoA) to the free amino group of aminomethylphosphonate" |
| PD                    | XX                                                                       | 25-MAY-2000.                                                              |                                                          |
| PF                    | XX                                                                       | 16-NOV-1999;                                                              | 99WO-US27152.                                            |
| PR                    | XX                                                                       | 17-NOV-1998;                                                              | 98US-0108763.                                            |
| PA                    | XX                                                                       | (MONS ) MONSANTO CO.                                                      |                                                          |
| PI                    | XX                                                                       | Barry GF;                                                                 |                                                          |
| DR                    | XX                                                                       | WPI: 2000-387806/33.                                                      |                                                          |
| DR                    | XX                                                                       | P-PSDB; AAY71250.                                                         |                                                          |
| PT                    | XX                                                                       | Enhancing phosphonate herbicide tolerance in corn, tobacco, wheat,        |                                                          |
| PT                    | XX                                                                       | cotton, canola and rice plants involves transforming plants with          |                                                          |
| PT                    | XX                                                                       | phosphonate metabolizing genes encoding acyltransferase enzyme -          |                                                          |
| PS                    | XX                                                                       | Disclosure; Page 143-150; 179pp; English.                                 |                                                          |
| CC                    | XX                                                                       | The patent discloses a method for selectively enhancing the phosphonate   |                                                          |
| CC                    | XX                                                                       | herbicide tolerance in recombinant corn, tobacco, wheat, cotton, canola   |                                                          |
| CC                    | XX                                                                       | and rice plants, by transforming the plants with an expression cassette.  |                                                          |
| CC                    | XX                                                                       | It comprises of a structural DNA sequence, that encodes an aminomethyl    |                                                          |
| CC                    | XX                                                                       | phosphonic acid (AMPA) acyltransferase or transacylase (AAT), capable of  |                                                          |
| CC                    | XX                                                                       | N-acylation of AMPA. This sequence has an amino terminal chloroplast      |                                                          |
| CC                    | XX                                                                       | transit peptide (CTP), that targets AAT to the chloroplast. Co-expression |                                                          |
| CC                    | XX                                                                       | of glyphosate oxidase (GOX) gene, encoding glyphosate oxidoreductase,     |                                                          |
| CC                    | XX                                                                       | along with AAT provides the transformed plants with higher resistance to  |                                                          |
| CC                    | XX                                                                       | phosphonate herbicides. This method is useful for enhancing phosphonate   |                                                          |
| CC                    | XX                                                                       | herbicides such as glyphosate and AMPA tolerance, in recombinant plants   |                                                          |
| CC                    | XX                                                                       | and to prevent self-fertilisation and enhance hetero-fertilisation.       |                                                          |
| CC                    | XX                                                                       | The present DNA sequence is the Escherichia coli phn operon sequence #2,  |                                                          |
| CC                    | XX                                                                       | comprising the pmo gene, encoding AMPA acyltransferase enzyme (AAT).      |                                                          |
| SO                    | XX                                                                       | Sequence 11672 BP; 2448 A; 3590 C; 3379 G; 2255 T; 0 other;               |                                                          |
| Query Match           |                                                                          | 2.9%; Score 17; DB 21; Length 11672;                                      |                                                          |
| Best Local Similarity |                                                                          | 100.0%; Pred. NO. 37;                                                     |                                                          |
| Matches               | 17; Conservative                                                         | 0; Mismatches                                                             | 0; Indels                                                |
|                       |                                                                          |                                                                           | 0; Gaps                                                  |
| QY                    | 244                                                                      | ccgtgttcacgcacacg 260                                                     |                                                          |
|                       |                                                                          |                                                                           |                                                          |
| DB                    | 4799                                                                     | cctgtttcagccgcacg 4783                                                    |                                                          |
| RESULT                | 40                                                                       |                                                                           |                                                          |
| AAD01008/C            |                                                                          |                                                                           |                                                          |
| ID                    | AAD01008                                                                 | standard; DNA; 15611 BP.                                                  |                                                          |
| AC                    | AAD01008;                                                                |                                                                           |                                                          |
| DT                    | 21-SEP-2000                                                              | (first entry)                                                             |                                                          |
| DE                    | Escherichia coli phn operon sequence #1.                                 |                                                                           |                                                          |
| KW                    | Phosphonate herbicide tolerance; aminomethyl phosphonic acid; AMPA; AAT; |                                                                           |                                                          |
| KW                    | acyltransferase; transacylase; recombinant plant; expression cassette;   |                                                                           |                                                          |
| KW                    | corn; tobacco; wheat; cotton; canola; rice; chloroplast transit peptide; |                                                                           |                                                          |
| KW                    | CTP; glyphosate oxidase; GOX; glyphosate oxidoreductase; phn operon;     |                                                                           |                                                          |
| KW                    | self-fertilisation; hetero-fertilisation; ds.                            |                                                                           |                                                          |
| OS                    | Escherichia coli.                                                        |                                                                           |                                                          |
| Key                   | Location/Qualifiers                                                      |                                                                           |                                                          |
| CDS                   | 13962..14396                                                             |                                                                           |                                                          |
| FT                    | /*tag= a                                                                 |                                                                           |                                                          |



FT /product= "Escherichia coli AMPA acyltransferase (AAT)"  
 FT /function= "Transfers acyl group from an acylcarrier  
 FT (CoA) to the free amino group of aminomethylphosphonate"  
 XX  
 XX WO200029596-A1.  
 XX  
 XX 25-MAY-2000.  
 XX  
 XX 16-NOV-1999; 99WO-US27152.  
 XX  
 XX 17-NOV-1998; 98US-0108763.  
 XX  
 XX (MONS ) MONSANTO CO.  
 PA  
 XX Barry GF;  
 XX  
 XX WPI: 2000-387806/33.  
 DR P-PSDB; AAF71250.  
 XX  
 XX Enhancing phosphonate herbicide tolerance in corn, tobacco, wheat,  
 PT cotton, canola and rice plants involves transforming plants with  
 PT phosphonate metabolizing genes encoding acyltransferase enzyme -  
 XX  
 XX PS Disclosure: Page 134-143; 179pp; English.  
 XX  
 CC The patent discloses a method for selectively enhancing the phosphonate  
 CC herbicide tolerance in recombinant corn, tobacco, wheat, cotton, canola  
 CC and rice plants, by transforming the plants with an expression cassette.  
 CC It comprises of a structural DNA sequence, that encodes an aminomethyl  
 CC phosphonic acid (AMPA) acyltransferase or transacylase (AAT), capable of  
 CC N-acylation of AMPA. This sequence has an amino terminal chloroplast  
 CC transit peptide (CTP), that targets AAT to the chloroplast. Co-expression  
 CC of glyphosate oxidase (GOX) gene, encoding glyphosate oxidoreductase,  
 CC along with AAT provides the transformed plants with higher resistance to  
 CC phosphonate herbicides. This method is useful for enhancing phosphonate  
 CC herbicides such as glyphosate and AMPA tolerance, in recombinant plants  
 CC and to prevent self-fertilisation and enhance hetero-fertilisation.  
 CC The present DNA sequence is the Escherichia coli phn operon sequence #1,  
 CC comprising the phnO gene, encoding AMPA acyltransferase enzyme (AAT).  
 XX  
 XX Sequence 15611 BP; 3466 A; 4625 C; 4306 G; 3214 T; 0 other;  
 SQ

Query Match 2.9%; Score 17; DB 21; Length 15611;  
 Best Local Similarity 100.0%; Pred. No. 36;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 244 cctgttcagcgccagc 260  
 ||||||||||||||||  
 DB 9035 CCTGTTTCAGCGCCAGC 9019

RESULT 41  
 AAF24497  
 ID AAF24497 standard; cDNA; 240825 BP.  
 XX  
 AC AAF24497;  
 XX  
 DT 23-MAY-2001 (first entry)  
 XX  
 DE Human PG-3 gene.  
 XX  
 KW Human; PG-3; cancer; BRCA1; chromosome 8p23; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH 1..2000  
 FT misc\_feature  
 FT /tag= a  
 FT /note= "5' regulatory region"  
 FT primer\_bind 1823..1840  
 FT /tag= b  
 FT primer\_bind 1980..1998

FT misc\_binding  
 FT /tag= c  
 FT 1987..2011  
 FT /tag= d  
 FT /note= "binds probe"  
 FT replace(199,C)  
 FT /tag= e  
 FT primer\_bind complement(2000..2018)  
 FT /tag= f  
 FT CDS 2001..238825  
 FT /tag= g  
 FT /product= "Pg-3"  
 FT /note= "this sequence contains introns"  
 FT 2001..2079  
 FT /tag= h  
 FT /label= "A"  
 FT 2108..2125  
 FT /tag= i  
 FT primer\_bind 4559..4577  
 FT /tag= j  
 FT primer\_bind 4582..4600  
 FT /tag= k  
 FT misc\_binding 4589..4613  
 FT /tag= l  
 FT /note= "binds probe"  
 FT replace(4601,G)  
 FT /tag= m  
 FT primer\_bind complement(4602..4620)  
 FT /tag= n  
 FT exon 4627..4718  
 FT /tag= o  
 FT /label= "B"  
 FT 4891..4908  
 FT /tag= p  
 FT primer\_bind 10007..10025  
 FT /tag= q  
 FT exon 10115..10233  
 FT /tag= r  
 FT /label= "C"  
 FT 10209..10227  
 FT /tag= s  
 FT primer\_bind 10216..10240  
 FT /tag= t  
 FT /note= "binds probe"  
 FT replace(10228,T)  
 FT /tag= u  
 FT allele complement(10229..10247)  
 FT /tag= v  
 FT primer\_bind 10267..10285  
 FT /tag= w  
 FT misc\_binding 10274..10298  
 FT /tag= x  
 FT /note= "binds probe"  
 FT replace(10286,T)  
 FT /tag= y  
 FT primer\_bind complement(10287..10305)  
 FT /tag= z  
 FT allele replace(10370,)  
 FT /tag= aa  
 FT primer\_bind 10411..10430  
 FT /tag= ab  
 FT exon 26810..26897  
 FT /tag= ac  
 FT /label= "D"  
 FT 31357..31471  
 FT /tag= ad  
 FT /label= "E"  
 FT exon 34261..34404  
 FT /tag= ae  
 FT /label= "F"  
 FT exon 37377..37466  
 FT /tag= af  
 FT /label= "S"  
 FT exon 39704..40858

```

FT      /*tag- ag
FT      /label- "T"
FT      primer_bind
FT      39556..39574
FT      /*tag- ah
FT      primer_bind
FT      39877..39896
FT      /*tag- ai
FT      primer_bind
FT      39925..39943
FT      /*tag- aj
FT      primer_bind
FT      39932..39956
FT      /*tag- ak
FT      /note- "binds probe"
FT      replace(39944,T)
FT      allele
FT      /*tag- al
FT      primer_bind
FT      complement(39945..39963)
FT      /*tag- am
FT      primer_bind
FT      39953..39970
FT      /*tag- an
FT      primer_bind
FT      39954..39972
FT      /*tag- ao
FT      primer_bind
FT      39961..39985
FT      /*tag- ap
FT      /note- "binds probe"
FT      replace(39973,C)
FT      allele
FT      /*tag- aq
FT      primer_bind
FT      complement(39974..39992)
FT      /*tag- ar
FT      primer_bind
FT      40242..40259
FT      /*tag- as
FT      primer_bind
FT      41137..41154
FT      /*tag- at
FT      primer_bind
FT      41366..41384
FT      /*tag- au
FT      primer_bind
FT      41373..71397
FT      /*tag- av
FT      /note- "binds probe"
FT      replace(41385,C)
FT      allele
FT      /*tag- aw
FT      primer_bind
FT      41385..41403
FT      /*tag- ax
FT      primer_bind
FT      complement(41386..41404)
FT      /*tag- ay
FT      primer_bind
FT      41392..41416
FT      /*tag- az
FT      /note- "binds probe"
FT      replace(41404,C)
FT      allele
FT      /*tag- ba
FT      primer_bind
FT      complement(41405..41423)
FT      /*tag- bb
FT      primer_bind
FT      41564..41581
FT      /*tag- bc
FT      primer_bind
FT      42122..42141
FT      /*tag- bd
FT      primer_bind
FT      42213..42231
FT      /*tag- be
FT      primer_bind
FT      42220..42244
FT      /*tag- bf
FT      /note- "binds probe"
FT      replace(42232,C)
FT      allele
FT      /*tag- bg
FT      primer_bind
FT      complement(42233..42251)
FT      /*tag- bh
FT      primer_bind
FT      42526..42543
FT      /*tag- bi
FT      exon
FT      50436..50545
FT      /*tag- bj
FT      /label- "G"
FT      primer_bind
FT      67289..67309
FT      /*tag- bk
FT      primer_bind
FT      67456..67474
FT      /*tag- bl
FT      primer_bind
FT      67463..67487
FT      /*tag- bm
FT      /note- "binds probe"

```

```

FT      allele
FT      replace(67475,G)
FT      /*tag- bn
FT      primer_bind
FT      complement(67476..67494)
FT      /*tag- bo
FT      primer_bind
FT      67724..67741
FT      /*tag- bp
FT      primer_bind
FT      69182..69200
FT      /*tag- bq
FT      primer_bind
FT      69502..69520
FT      /*tag- br
FT      primer_bind
FT      69509..69533
FT      /*tag- bs
FT      /note- "binds probe"
FT      allele
FT      /*tag- bt
FT      primer_bind
FT      replace(69521,G)
FT      /*tag- bu
FT      primer_bind
FT      complement(69522..69540)
FT      /*tag- bv
FT      primer_bind
FT      69609..69626
FT      /*tag- bv
FT      primer_bind
FT      72698..72715
FT      /*tag- bw
FT      primer_bind
FT      72819..72837
FT      /*tag- bx
FT      primer_bind
FT      72826..72850
FT      /*tag- by
FT      /note- "binds probe"
FT      allele
FT      /*tag- bz
FT      primer_bind
FT      replace(72838,T)
FT      /*tag- ca
FT      primer_bind
FT      complement(72839..72857)
FT      /*tag- cb
FT      primer_bind
FT      72881..72918
FT      /*tag- cb
FT      /label- "H"
FT      primer_bind
FT      73099..73117
FT      /*tag- cc

```

```

Query Match      2.98; Score 17; DB 22; Length 240825;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      254 cgcagccaagcagcgc 270
Db      23840 cgcagccaagcagcgc 23856

```

```

RESULT 42
AA036842/c
ID AA036842 standard; DNA: 41 BP.
XX
AC AA036842;
XX
DT 16-JUN-1993 (first entry)
XX
DE Adaptor-primer.
XX
KW Cyclophilin C; bone marrow; stromal cell line; AC 6; ss.
XX
OS Synthetic.
XX
PN WO9303050-A.
XX
PD 18-FEB-1993.
XX
PE 05-AUG-1992; 92WO-US06462.
XX
PR 05-AUG-1991; 91US-0740375.
XX
PA (STRD ) UNIV LEIAND STANFORD JUNIOR.
XX
PI Friedman JS, Weissman IL;
XX
DR WPI; 1993-076431/09.
XX

```

PT Cyclophilin C polypeptide and nucleic acid encoding it - useful  
 PT for screening a tissue-specific immunosuppressive agent

PS Example 1; Page 30; 63pp; English.

CC In the cDNA cloning and library construction described in Example  
 CC 1, total RNA was prep'd. from murine bone marrow derived stromal cell  
 CC line AC 6. cDNA synthesis was performed using an adaptor-primer  
 CC method (Rubenstein J. et al., (1990) Nuc. Acids Res. 18, 4833-4842)  
 CC with slight modifications. The adaptor-primer used, having the  
 CC sequence below, was the kind gift of Dr. Dan Denney.

XX Sequence 41 BP; 2 A; 9 C; 11 G; 19 T; 0 other;

Query Match 2.7%; Score 16; DB 14; Length 41;

Best Local Similarity 100.0%; Pred. No. 1.4e+02; Mismatches 0; Indels 0; Gaps 0;

OY 554 aaagagcctcgcgcgc 569  
 |||||||  
 DB 27 AAAAGCCTCCGCGC 12

RESULT 43

AAO73710 ID AAO73710 standard; DNA; 222 BP.

XX AAO73710;

DT 18-JUL-1995 (first entry)

XX Retrotransposon probe Tos1-1, cloned from Oryza sativa.

XX Retrotransposon; probe; rice; plant; identification; genetic uniformity;

KM pure line; Inbred parent line; near-isogenic line; ss.

XX Oryza sativa.

OS Location/Qualifiers

Key 17..161

FT Misc\_feature /tag= a

FT /note= "probe sequence"

XX JP06277063-A.

XX 04-OCT-1994.

XX 08-OCT-1992; 92JP-0309167.

XX 08-OCT-1992; 92JP-0309167.

XX (NORI-) NORIN SUISANSO NOGYO SEIBUTSU SHIGEN.

PA (TAKE) TAKEDA CHEM IND LTD.

DR WPI; 1994-353746/44.

XX Identification of plants at the DNA level - using retrotransposon

PT sequences as probes

XX Claim 6; Page 5; 41pp; Japanese.

XX The nucleotide sequence of the retrotransposon probe Tos1-1 cloned from

CC the rice plant Oryza sativa. The probes may be used for the analysis of

CC plant genes to secure the efficient identification of plants and genetic

CC uniformity for the production of pure lines, Inbred parent lines and

XX near-isogenic lines.

SQ Sequence 222 BP; 54 A; 48 C; 63 G; 57 T; 0 other;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 321 catgtctaactagtc 336  
 |||||||  
 DB 34 catgtctaactagtc 49

RESULT 44

AAAX25170 ID AAAX25170 standard; DNA; 334 BP.

XX AAAX25170;

DT 19-JUL-1999 (first entry)

XX HIV-1 group O isolate 533 gp41 antigen DNA.

XX HIV-1 group O; Outlier strain; gp41; envelope protein; antigen;

KW vaccine; diagnosis; AIDS; ss.

XX Human immunodeficiency virus type 1.

PN WO9904011-A2.

XX 28-JAN-1999.

XX 20-JUL-1998; 98MO-EP04522.

XX 18-JUL-1997; 97EP-0870110.

XX (INNO-) INNOGENETICS NV.

XX Delaporte E, Peeters M, Saman E, Vanden Haesevelde M;

DR WPI; 1999-132255/11.

DR P-PSDB; AAY05562.

XX New isolated HIV-1 group O strains - used to produce

PT polynucleotides, antigens and antibodies for use in diagnosis and in

PT vaccines for prevention of HIV-1 infection

XX Claim 4; Fig 6; 162pp; English.

XX This DNA sequence codes for an antigen (see AAY05562) of the gp41

CC protein of HIV-1 group O (Outlier) strain 533, an isolate from

CC Gabon. The invention relates to new HIV-1 group O antigens (see

CC AAY05562-625), and the use of these antigens, or nucleic acids

CC encoding them (see AAX25154-80), in the diagnosis and prophylaxis of

CC AIDS. They can be used as reagents for detecting HIV-1 group O

CC infection and for differentiating different types of HIV-1 group O

CC infection. Vaccines that provide protective immunity against

CC HIV-1 infection, in particular against HIV-1 group O infection,

CC comprise at least one HIV-1 type O antigen, a nucleic acid encoding

CC such an antigen, a virus-like particle comprising such an antigen,

CC or an attenuated form of an HIV-1 type O strain. The invention also

CC relates to new HIV-1 group O strains, mostly from patients from

XX Cameroon and its neighbouring countries.

SQ Sequence 334 BP; 124 A; 64 C; 77 G; 69 T; 0 other;

Query Match 2.7%; Score 16; DB 20; Length 334;

Best Local Similarity 100.0%; Pred. No. 1.3e+02; Mismatches 0; Indels 0; Gaps 0;

OY 540 accaacaagagaagaa 555  
 |||||||  
 DB 290 accaacaagagaagaa 305

RESULT 45

AAAX21399/C ID AAAX21399 standard; DNA; 371 BP.

```

XX AAX21399;
XX
XX 21-MAY-1999 (first entry)
XX
XX 3' fragment of AbsA operon from S.coelicolor.
XX
XX AbsA; operon: open reading frame; histidine kinase; response regulator;
XX mutation; insertion; antibiotic; actinorhodin; undecylprodigiosin; ss.
XX
XX Streptomyces coelicolor.
XX
XX Key Location/Qualifiers
XX CDS 1..371
XX /*tag= a
XX FT /note= "3' end of D9 coding sequence: no start codon
XX FT given at 5' end of sequence"
XX
XX US5876987-A.
XX
XX 02-MAR-1999.
XX
XX 06-FEB-1997; 96US-0796414.
XX
XX 07-FEB-1996; 96US-0011286.
XX 06-FEB-1997; 97US-0796414.
XX
XX (UNMS ) UNIV MICHIGAN STATE.
XX
XX PI Anderson TB, Brian P, Champness WC;
XX
XX WPI; 1999-189640/16.
XX
XX P-PSDB; AAW78494.
XX
XX
XX Recombinant Streptomyces species - useful for the production of
XX recombinant proteins and the hyper-expression of antibiotics,
XX particularly actinorhodin and undecylprodigiosin
XX
XX Claim 10; Fig 4; 30pp; English.
XX
XX The sequences AAX21397-X21399 represent overlapping sequences from the
XX AbsA operon of Streptomyces coelicolor. This sequence corresponds to
XX the downstream (3') fragment and contains a fragment of the D9 open
XX reading frame on the complementary strand to the Abs1 and Abs2 genes.
XX The Abs1 gene encodes a histidine kinase and the Abs2 gene encodes a
XX response regulator for the Abs1 gene. Inactivation of the Abs1 gene
XX either by mutation or insertion of heterologous DNA into the Abs1 gene
XX results in a Streptomyces organism which can hyperproduce heterologous
XX proteins or antibiotics, especially actinorhodin and undecylprodigiosin.
XX
XX Sequence 371 BP; 55 A; 141 C; 130 G; 45 T; 0 other;
XX
XX
XX Query Match 2.7%; Score 16; DB 20; Length 371;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 506 ccagcgcgccctc 521
XX |||||||
XX Db 202 CCAAGCGCGCCTC 187
XX
XX RESULT 46
XX AAC01286/c
XX ID AAC01286 standard; cDNA; 398 BP.
XX
XX AAC01286;
XX
XX 06-OCT-2000 (first entry)
XX
XX Human secreted protein 5' EST, SEQ ID NO: 1284.
XX
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX

```

```

KW gene therapy; chromosome mapping; ss.
XX
XX Homo sapiens.
XX
XX EPI033401-A2.
XX
XX 06-SEP-2000.
XX
XX 21-FEB-2000; 2000EP-0200610.
XX
XX 26-FEB-1999; 99US-0122487.
XX
XX (GEST ) GENSET.
XX
XX Dumas Milne Edwards J, Duclert A, Giordano J;
XX
XX WPI; 2000-500381/45.
XX
XX P-PSDB; AAG01280.
XX
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
XX diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
XX Claim 1; SEQ ID 1284; 71pp + CD-ROM; English.
XX
XX The present sequence is one of a large number of 5' ESTs derived from
XX mRNAs encoding secreted proteins. An ORF has been identified within the
XX sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
XX derived from 30 different tissues. EST sequences usually correspond
XX mainly to the 3' untranslated region (UTR) of the mRNA because they are
XX often obtained from oligo-dT primed cDNA libraries. Such ESTs are not
XX well suited for isolating cDNA sequences derived from the 5' ends of
XX mRNAs and even in those cases where longer cDNA sequences have been
XX obtained, the full 5' UTR is rarely included. 5' ESTs are derived from
XX cDNAs with intact 5' ends and can therefore be used to obtain full length
XX cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
XX gene therapy and chromosome mapping procedures. They are used to obtain
XX upstream regulatory sequences and to design expression and secretion
XX vectors.
XX
XX Sequence 398 BP; 86 A; 118 C; 110 G; 84 T; 0 other;
XX
XX
XX Query Match 2.7%; Score 16; DB 21; Length 398;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 378 cactgagcgccgcc 393
XX |||||||
XX Db 207 CACTGAGCGCGCC 192
XX
XX RESULT 47
XX AAA79394/c
XX ID AAA79394 standard; cDNA; 413 BP.
XX
XX AAA79394;
XX
XX 27-NOV-2000 (first entry)
XX
XX Eucaalyptus grandis cell signalling involved polynucleotide SEQ ID NO:195.
XX
XX Eucaalyptus grandis; Pinus radiata; Monterey pine; plant; modification;
XX plant cell signalling; modulation; transgenic plant; pathogen; growth;
XX environmental change; development; cell proliferation; differentiation;
XX elongation; survival; disease resistance; nutrient metabolism; ss.
XX
XX Eucaalyptus grandis.
XX
XX WO200042171-A1.
XX
XX 20-JUL-2000.
XX

```

PF 11-JAN-2000; 2000WO-US00724.  
XX  
XX 12-JAN-1999; 99US-0228986.  
PR 01-NOV-1999; 99US-0162866.  
XX  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PI Strabala TJ, Nieuwenhuizen NJ;  
XX  
XX WPI: 2000-476052/41.  
DR  
XX  
XX Isolated polynucleotide encoding a polypeptide involved in cell  
PT signaling used for generating transgenic plants with modified responses  
PR to external signals -  
XX  
XX  
PS Claim 1: Page 124; 527pp; English.  
XX  
XX AAA79263 to AAA79736 and AAB25100 to AAB25570 represent polynucleotide  
CC and protein sequences isolated from eucalyptus (Eucalyptus grandis) or  
CC pine (Pinus radiata also known as Monterey pine). The protein sequences  
CC are involved in cell signalling. The polynucleotide and protein  
CC sequences can be used to modify the response of plant cells to external  
CC signals e.g. environmental changes or pathogens during the growth and  
CC development of a plant. They can be used to modify cell proliferation,  
CC differentiation, elongation and survival, resistance to disease and  
CC nutrient metabolism. Examples of modifications which can be produced are  
CC altered fruit ripening and senescence of leaves and flowers e.g. to  
CC delay senescence and prolong the life of cut flowers or enhance  
CC senescence of reproductive organs to engineer sterile plants. Other  
CC modifications can be used to delay senescence in selected cell types or  
CC organs providing fruit and vegetables which have a longer shelf life  
CC between harvest and consumption, or to decrease branching frequency in  
CC forest tree species giving long stretches of valuable knot-free clear  
CC wood which can be used in solid timber furniture and veneers.  
XX  
SQ Sequence 413 BP; 101 A; 86 C; 118 G; 108 T; 0 other;

Query Match 2.7%; Score 16; DB 21; Length 413;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 114 acagcagccagcaca 129  
DB 99 ACAGCAGCCAGCCCAA 84

RESULT 48  
AAC01726  
ID AAC01726 standard; cDNA; 489 BP.  
XX  
AC AAC01726;  
XX  
DT 06-OCT-2000 (first entry)  
XX  
DE Human secreted protein 5' EST, SEQ ID NO: 1724.  
XX  
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
KM gene therapy; chromosome mapping; ss.  
XX  
OS Homo sapiens.  
XX  
XX EP1033401-A2.  
PN  
XX  
XX 06-SEP-2000.  
PD  
XX  
XX 21-FEB-2000; 2000EP-0200610.  
PF  
XX  
XX 26-FEB-1999; 99US-0122487.  
PR  
XX  
XX (GENST ) GENSET.  
PA  
XX  
PI Dunas Milne Edwards J, Duclert A, Giordano J;

XX  
DR WPI: 2000-500381/45.  
DR P-PSDB; AAG01720.  
XX  
XX  
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for  
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -  
XX  
XX  
PS Claim 1: SEQ ID 1724; 71pp + CD-ROM; English.  
XX  
XX The present sequence is one of a large number of 5' ESTs derived from  
CC mRNAs encoding secreted proteins. An ORF has been identified within the  
CC sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs  
CC derived from 30 different tissues. EST sequences usually correspond  
CC mainly to the 3' untranslated region (UTR) of the mRNA because they are  
CC often obtained from oligo-dT primed cDNA libraries. Such ESTs are not  
CC well suited for isolating cDNA sequences derived from the 5' ends of  
CC mRNAs and even in those cases where longer cDNA sequences have been  
CC obtained, the full 5' UTR is rarely included. 5' ESTs are derived from  
CC mRNAs with intact 5' ends and can therefore be used to obtain full length  
CC cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,  
CC gene therapy and chromosome mapping procedures. They are used to obtain  
CC upstream regulatory sequences and to design expression and secretion  
CC vectors.  
XX  
SQ Sequence 489 BP; 146 A; 104 C; 146 G; 91 T; 2 other;

Query Match 2.7%; Score 16; DB 21; Length 489;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 542 caccaggaagaaga 557  
DB 351 caacaggaagaaga 366

RESULT 49  
AAT76907/C  
ID AAT76907 standard; DNA; 541 BP.  
XX  
XX AAT76907;  
XX  
DT 02-JUL-1998 (first entry)  
XX  
XX  
DE S. glaucescens Hstre DNA fragment.  
XX  
XX Acarbose biosynthesis: acbA gene; acbB gene; acbC gene; acbD gene;  
KM acbE gene; acbF gene; enzyme; alpha-amylase inhibitor; treatment;  
KW diabetes; Hstre gene; ss.  
XX  
XX Streptomyces glaucescens.  
OS  
XX  
XX DEL19622783-A1.  
PN  
XX  
XX 11-DEC-1997.  
PD  
XX  
XX 07-JUN-1996; 96DE-1022783.  
PF  
XX  
XX 07-JUN-1996; 96DE-1022783.  
PR  
XX  
XX (FARH ) HOECHST AG.  
PA  
XX  
XX Decker H;  
PI  
XX  
XX WPI: 1998-033827/04.  
DR  
XX  
XX Recombinant DNA molecule comprising genes for biosynthesis of  
PT acarbose - an alpha-amylase inhibitor useful in treatment of  
PT diabetes  
XX  
XX  
XX Example 2; Page 8; 35pp; German.

CC This sequence encodes a fragment of the *Streptomyces glaucescens* GLA.O  
CC *hstre* gene which has been generated via PCR. This gene is used in a  
CC method to identify the *acbd* gene which is involved in the acetate  
CC biosynthesis pathway. *acbd* and other acetate biosynthesis genes such  
CC as those represented in AAT75903 are useful for producing acetate.  
CC which is an alpha-amylase inhibitor useful in the treatment of  
CC diabetes.  
XX  
SQ Sequence 541 BP; 72 A; 173 C; 221 G; 75 T; 0 other;

Query Match 2.7%; Score 16; DB 19; Length 541;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 395 CGACGAGTCTACGCG 410  
|||  
DB 187 CGACGAGTCTACGCG 172

RESULT 50  
AAT84039  
ID AAT84039 standard; DNA: 624 BP.  
XX  
AC AAT84039;  
XX  
DT 01-SEP-1998 (first entry)  
XX  
DE DNA encoding a *Staphylococcus aureus* protein of unknown function.  
XX  
KM *Staphylococcus aureus* protein; ribozyme; antisense sequence; control;  
KM *Staphylococcal* gene; regulatory element; bacterial gene expression;  
KM vaccine; *Staphylococcal* infection; food poisoning; scaled skin syndrome;  
KM toxic shock syndrome; ss.  
XX  
OS *Staphylococcus aureus*.  
XX  
FH Key Location/Qualifiers  
FT CDS 187..477  
FT /\*tag= a  
XX  
PN WC9730070-A1.  
XX  
PD 21-AUG-1997.  
XX  
PF 19-FEB-1997; 97MO-US02318.  
XX  
PR 20-FEB-1996; 96US-0011888.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
XX  
PI Black MT, Burnham MK, Hodgson JE, Knowles DJC, Nicholas RO;  
PI Pratt JM, Reichard RW, Rosenberg M, Ward JM;  
XX  
DR P-PSDB; AAM28105.  
XX  
PT Novel polypeptide(s) from *Staphylococcus aureus* strain WC9730070 - used  
PT to isolate antimicrobial compounds, and in vaccines against *S.*  
PT *aureus* infection  
XX  
PS Claim 9; Page 837; 989pp; English.  
XX  
XX The present sequence encodes a *Staphylococcus aureus* protein of  
CC unknown function. The present sequence was isolated from a  
CC library of clones of *S. aureus* WC9730070 in *Escherichia coli*. The DNA  
CC sequence can be used in the construction of ribozymes and antisense  
CC sequences to control the expression of *Staphylococcal* genes. The DNA  
CC sequence is also useful as a source of regulatory elements for the  
CC control of bacterial gene expression. The encoded protein may be used  
CC to produce vaccines to enable a host to produce specific antibodies  
CC with antibacterial action. These vaccines and antibodies would protect  
CC a host against invasion by *S. aureus*, and conditions relating to

CC *Staphylococcal* infection, e.g. *Staphylococcal* food poisoning, scaled  
CC skin syndrome, and toxic shock syndrome.  
XX

SQ Sequence 624 BP; 248 A; 72 C; 123 G; 171 T; 10 other;

Query Match 2.7%; Score 16; DB 18; Length 624;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 GGTAGTGGCGAGCG 153  
|||  
DB 53 GGTAGTGGCGAGCG 68

Search completed: September 21, 2001, 16:24:34  
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REFERENCE 1 (bases 1 to 523)  
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.  
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome  
JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)  
MEDLINE 99380589  
COMMENT Contact: Mahairas GG, Wallace JC, Hood L  
High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: jwallace@u.washington.edu  
Clones may be purchased from Research Genetics (info@resgen.com).  
BAC end Web Server: <http://www.htsc.washington.edu>  
Plate: 593 row: K column: 4  
Seq primer: T7  
Class: BAC ends  
High quality sequence stop: 523.  
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/cell\_type="lymphocytes"  
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BASE COUNT 183 a 151 c 125 g 58 t 6 others  
ORIGIN

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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 347 ggattaatgcacccaag 365  
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Db 151 GGATTATGTCACCAAG 169

RESULT 2  
LOCUS AZ497878 656 bp DNA GSS 05-OCT-2000  
DEFINITION 1M0334G34R Mouse 10kb plasmid UNGC1M library Mus musculus genomic  
ACCESSION clone UNGC1M0334G24 R, DNA sequence.  
VERSION AZ497878 GI:10675204  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 656)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00

Plate: 0334 row: G column: 24  
Seq primer: CACACAGAAACAGTATGACC  
Class: plasmid ends  
High quality sequence stop: 656.  
Location/Qualifiers  
1..656  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UNGCM0334G24"  
/clone\_lib="Mouse 10kb plasmid UNGC1M library"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g114732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."  
BASE COUNT 155 a 176 c 132 g 192 t 1 others  
ORIGIN

Query Match 3.28; Score 19; DB 245; Length 656;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 537 gaaccacagggagagaa 555  
|||||  
Db 110 GAACCAACAGAGAGAA 92

RESULT 3  
LOCUS AO938059 657 bp DNA GSS 23-AUG-2000  
DEFINITION NB6-808R Human NotI clones Homo sapiens genomic, DNA sequence.  
ACCESSION AO938059  
VERSION AO938059.1 GI:7214437  
KEYWORDS GSS.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 657)  
Zabarovskiy,E.R., Gizekulin,R., Podowski,R.M., Zabarovska,V.V., Xie L., Muravenko,O.V., Kozirev,S., Petrenko,L., Skobeleva,N., Li,J., Protolopov,A., Kashub,V., Ernborg,I., Winberg,G. and Wahlstedt,C.  
TITLE NotI clones in the analysis of the human genome  
JOURNAL Nucleic Acids Res. 28 (7), 1635-1639 (2000)  
MEDLINE 20175728  
COMMENT Contact: Podowski RM  
Center for Genomics Research  
Karolinska Institute  
17177 Stockholm, Sweden  
Tel: +46-8-728-6372  
Fax: +46-8-337983  
Email: Raf.Podowski@cgr.ki.se  
Class: NotI site.  
Location/Qualifiers  
1..657





RESULT 8  
AA358477/c  
LOCUS AA358477 261 bp mRNA EST 21-APR-1997  
DEFINITION EST67411 Fetal Lung III Homo sapiens cDNA 5' end, mRNA sequence.  
ACCESSION AA358477  
VERSION AA358477.1 GI:2010845  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 261)  
AUTHORS Adams M.D., Soares M.B., Kerlavage A.R., Fields C. and Venter J.C.  
TITLE Rapid cDNA sequencing (expressed sequence tags) from a  
directionally cloned human infant brain cDNA library  
JOURNAL Nature Genet. 4, 373-380 (1993)  
MEDLINE 94004965  
COMMENT Contact: Kerlavage, AR  
Bioinformatics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850 USA  
Tel: 3018699056  
Fax: 3018699423  
Email: arkerlav@tigr.org  
For clone availability, additional sequence and expression  
information related to this EST, please check the TIGR Human Gene  
Index (<http://www.tigr.org/tdb/hgl/hgl.html>)  
Seq primer: M13 Reverse.  
Location/Qualifiers  
1..261  
/organism="Homo sapiens"  
/db\_xref="ATCC (inhost):162671"  
/db\_xref="taxon:9606"  
/clone\_lib="Fetal Lung III"  
/dev\_stage="fetus"  
/note="Organ: Lung; Vector: pBluescript SK-; Site\_1: EcoRI  
; Site\_2: XhoI"  
BASE COUNT 47 a 77 c 85 g 48 t 4 others  
ORIGIN

Query Match 3.0%; Score 18; DB 6; Length 261;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 44 gtactgcgtccctgctg 61  
|||||  
DB 18 GTAGCTGCGCTCGCTG 1

RESULT 9  
AM896020 327 bp mRNA EST 24-MAY-2000  
LOCUS AM896020  
DEFINITION QYA-NN0039-110500-204-a03 NN0039 Homo sapiens cDNA, mRNA sequence.  
ACCESSION AM896020  
VERSION AM896020.1 GI:8060225  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 327)  
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,  
Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,  
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare  
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
Simpson, A.J.  
TITLE Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
MEDLINE 20202663

COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?l1=et2-QYA-NN0039-110500-204-a03&t3=2000-05-11&t4=1>)  
Seq primer: puc 18 forward  
High quality sequence start: 9  
High quality sequence stop: 132.  
Location/Qualifiers  
1..327  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="NN0039"  
/dev\_stage="Adult"  
/note="Organ: nervous\_normal; Vector: puc18; Site\_1: SmaI;  
Site\_2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the puc 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."  
BASE COUNT 107 a 65 c 98 g 57 t  
ORIGIN

Query Match 3.0%; Score 18; DB 122; Length 327;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 544 acagagagaagaagcc 561  
|||||  
DB 140 ACAGCAGAGAGAAAGGCC 157

RESULT 10  
AI991901/c 334 bp mRNA EST 08-MAR-2000  
LOCUS AI991901/c  
DEFINITION ws42b06.x1 NCI-CGAP\_Brn25 Homo sapiens cDNA clone IMAGE:2498827 3'  
similar to contains element MSRI repetitive element ;, mRNA  
sequence.  
ACCESSION AI991901  
VERSION AI991901  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 334)  
AUTHORS NCI/NIHDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute / National Institute of Neurological  
Disorders and Stroke, Brain Tumor Genome Anatomy Project  
(CGAP/BRGAP), Tumor Gene Index  
Unpublished (1998)  
Contact: Robert Strausberg, Ph.D.  
Email: cgsbbs-remail.nih.gov  
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,  
Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.  
DNA Library Arrayed by: Greg Lennon, Ph.D.  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
[www.bio.lnl.gov/bbrp/image/image.html](http://www.bio.lnl.gov/bbrp/image/image.html)  
Insert length: 555 Std Error: 0.00  
Seq primer: -40UP from Gibco



MEDLINE  
COMMENT 99380589  
Contact: Mahairas GG, Wallace JC, Hood L  
High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: jwallace@u.washington.edu  
Sequence Tagged Connector  
Plate: 2227 row: M column: 8  
Class: BAC ends  
High quality sequence stop: 392.  
Location/Qualifiers  
1. .392

FEATURES  
source  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="CIT Approved Human Genomic Sperm Library D"  
/sex="male"  
/note="Organ: sperm; Vector: pBelBAC11; BAC Clones in E-Coli DH10B"

BASE COUNT 94 a 101 c 67 g 129 t 1 others  
ORIGIN

Query Match 3.0%; Score 18; DB 226; Length 392;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 489 ggcagctaatagtgtgac 506  
|||||  
Db 154 GGCAGCTAATAGTGTCTC 137

RESULT 14  
AI991951/c 463 bp mRNA EST 08-MAR-2000  
LOCUS ws43a04.x1 NCI-CGAP\_Brn25 Homo sapiens cDNA clone IMAGE:2499918 3'  
DEFINITION similar to contains element MSRI repetitive element ;, mRNA  
sequence.  
ACCESSION AI991951 GI:5838856  
VERSION AI991951  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
TITLE 1 (bases 1 to 463)  
NCI/INNS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute / National Institute of Neurological  
Disorders and Stroke, Brain Tumor Genome Anatomy Project  
(CGAP/BRGAP), Tumor Gene Index  
Unpublished (1998)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: cgaps-r@mail.nih.gov  
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,  
Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonafido, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/dbp/image/image.html  
Insert length: 566 Std Error: 0.00  
Seq primer: -400P from Gidco.  
Location/Qualifiers  
1. .463

FEATURES  
source  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="IMAGE:2499918"  
/clone\_lib="NCI-CGAP\_Brn25"  
/tissue\_type="anaplastic oligodendroglioma"

/lab\_host="DH10B"  
/note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a  
modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer (5'  
TGTTCACCAATCGAAGTGGAGCGCCGATAGCTTTTCTTTTCTTTT  
T 3'); double-stranded cDNA was ligated to Eco RI  
adaptors (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of the modified pT73 vector.  
Library is normalized, and was constructed by Bento  
Soares and M. Fatima Bonafido."

BASE COUNT 99 a 102 c 132 g 129 t 1 others  
ORIGIN

Query Match 3.0%; Score 18; DB 104; Length 463;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 230 cccctgcacacccccctg 247  
|||||  
Db 151 CCCCTGCATCACCCCTG 134

RESULT 15  
BF612300 463 bp mRNA EST 14-DEC-2000  
LOCUS dba17a11.y1 NICHD XGC Lul Xenopus laevis cDNA clone IMAGE:4056476  
DEFINITION 5' similar to SW:CSF.FORCA P56101 CYSTEINE STRING PROTEIN ;, mRNA  
sequence.  
ACCESSION BF612300 GI:11782798  
VERSION BF612300  
KEYWORDS EST.  
SOURCE <African clawed frog.  
ORGANISM Xenopus laevis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
Xenopodinae; Xenopus.  
REFERENCE 1 (bases 1 to 463)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: cgaps-r@mail.nih.gov  
Tissue Procurement: Martha Redbert, Steven L. Klein, Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
clone distribution: Xenopus clones from this library are available  
through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov  
Seq primer: -40RP from Gidco  
High quality sequence stop: 439.  
Location/Qualifiers  
1. .463

FEATURES  
source  
/organism="Xenopus laevis"  
/db\_xref="taxon:8355"  
/clone\_lib="IMAGE:4056476"  
/clone\_lib="NICHD XGC Lul"  
/dev\_stage="adult"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: lung; Vector: pCMV-Sport6; Site\_1: NotI;  
Site\_2: SalI; Cloned unidirectionally. Primer: oligo dT.  
Average insert size 2.6 kb. Constructed by Life  
Technologies. Note: This is a Xenopus gene Collection (XGC  
Library.)"

BASE COUNT 108 a 111 c 138 g 106 t  
ORIGIN

Query Match 3.0%; Score 18; DB 151; Length 463;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 453 cgggcaaatgcccagc 470  
 DB 30 CCGGCACAAATGGCCGACC 47

RESULT 16  
 BE811867 465 bp mRNA EST 21-SEP-2000  
 LOCUS PM0-AN0032-110700-001-a12 AN0032 Homo sapiens cDNA, mRNA sequence.  
 DEFINITION BE811867  
 VERSION BE811867.1 GI:10244101  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 (bases 1 to 465)  
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Britones, M.R., Nagai, M.A., da Silva, M. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.  
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 COMMENT 20202663  
 CONTACT: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the PAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=6t2-PM0-AN0032-110700-001-a12&t3=2000-07-11&t4=1)  
 Seq primer: puc 18 forward  
 High quality sequence stop: 266.  
 Location/Qualifiers  
 1. 465  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="AN0032"  
 /dev\_stage="Adult"  
 /note="Organ: amnion, normal; Vector: puc18; Site: 1: Smal; Site: 2: Sma1; A mini-library was made by cloning products derived from ORESSES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."  
 BASE COUNT 111 a 160 c 92 g 102 t  
 ORIGIN

Query Match 3.0%; Score 18; DB 140; Length 465;  
 Best Local Similarity 100.0%; Pred. No. 76;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 230 cccctgcatacccccctg 247  
 DB 138 CCCCTGCATCACCCTCG 155

RESULT 17  
 A2462258 474 bp DNA GSS 04-OCT-2000  
 LOCUS IM0269023f Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0269023 F, DNA sequence.  
 DEFINITION A2462258  
 ACCESSION

VERSION A2462258.1 GI:10620383  
 KEYWORDS GSS.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 474)  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A. and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 Unpublished (2000)  
 CONTACT: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 1000 Std Error: 0.00  
 Plate: 0269 row: 0 column: 23  
 Seq primer: CGTTGTAAACGACGCGCAGT  
 Class: plasmid ends  
 High quality sequence stop: 474.  
 Location/Qualifiers  
 1. 474  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0269023"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g147321141g147129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."  
 BASE COUNT 85 a 132 c 135 g 122 t  
 ORIGIN

Query Match 3.0%; Score 18; DB 244; Length 474;  
 Best Local Similarity 100.0%; Pred. No. 77;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 265 gcagccgcgcctcctgccc 282  
 DB 219 GCAGCCGCGCCTCTCC 236

RESULT 18  
 A1466074 476 bp mRNA EST 09-MAR-1999  
 LOCUS VW39b02.y1 Soares mammary gland NDMG Mus musculus cDNA clone IMAGE:1246155 5' similar to gb:U17574 mouse mRNA for



|                          |                                                                                                                                                                                        |                                                                                                                                      |
|--------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------|
| ACCESSION                | A166074                                                                                                                                                                                | procrasin-binding protein (MOUSE).; mRNA sequence.                                                                                   |
| VERSION                  | A166074.1                                                                                                                                                                              | GI:4320104                                                                                                                           |
| KEYWORDS                 | EST.                                                                                                                                                                                   |                                                                                                                                      |
| SOURCE                   | house mouse.                                                                                                                                                                           |                                                                                                                                      |
| ORGANISM                 | Mus musculus                                                                                                                                                                           | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. |
| REFERENCE                | NCl-CGAP                                                                                                                                                                               | http://www.ncbi.nlm.nih.gov/ncicgap.                                                                                                 |
| AUTHORS                  | Tumor Gene Index                                                                                                                                                                       | National Cancer Institute, Cancer Genome Anatomy Project (CGAP),                                                                     |
| TITLE                    | Unpublished (1997)                                                                                                                                                                     |                                                                                                                                      |
| JOURNAL                  | Contact: Robert Strausberg, Ph.D.                                                                                                                                                      | Email: cgapbs-rt@mail.nih.gov                                                                                                        |
| COMMENT                  | This clone is available royalty-free through LNL ; contact the IMAGE Consortium (infoimage.llnl.gov) for further information.                                                          | MCI:659843                                                                                                                           |
| FEATURES                 | This read is a RESSEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in the correct orientation)                               | Seq primer: -40RP from Gldco High quality sequence stop: 317.                                                                        |
| SOURCE                   | Location/Qualifiers                                                                                                                                                                    | 1..476                                                                                                                               |
|                          | /organism="Mus musculus"                                                                                                                                                               |                                                                                                                                      |
|                          | /strain="C57BL/6J"                                                                                                                                                                     |                                                                                                                                      |
|                          | /db_xref="taxon:10090"                                                                                                                                                                 |                                                                                                                                      |
|                          | /clone="IMAGE:1246155"                                                                                                                                                                 |                                                                                                                                      |
|                          | /clone_lib="Soares_mammary_gland_NBMWG"                                                                                                                                                |                                                                                                                                      |
|                          | /sex="male"                                                                                                                                                                            |                                                                                                                                      |
|                          | /tissue_type="mammary gland"                                                                                                                                                           |                                                                                                                                      |
|                          | /dev_stage="4 weeks"                                                                                                                                                                   |                                                                                                                                      |
|                          | /lab_host="DH10B"                                                                                                                                                                      |                                                                                                                                      |
|                          | /note="Organ: mammary gland; Vector: pT7T3D-Pac (pharmacia ) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dt) primer [5' |                                                                                                                                      |
|                          | GTGTACCATCTGTAAGTGAGCGCCGCCGAATGGTTTTTTTTTTTTTTTTTT TTTT                                                                                                                               |                                                                                                                                      |
|                          | T 3']; double-stranded cDNA was ligated to Eco RI                                                                                                                                      |                                                                                                                                      |
|                          | adaptors (Pharmacia), digested with Not I and cloned into                                                                                                                              |                                                                                                                                      |
|                          | the Not I and Eco RI sites of the modified pT7T3 vector.                                                                                                                               |                                                                                                                                      |
|                          | cRNA provided by Dr. Minoru Ko, Wayne State Univ. library                                                                                                                              |                                                                                                                                      |
|                          | constructed and normalized by Bento Soares and W.Falima                                                                                                                                |                                                                                                                                      |
|                          | Bernaldo."                                                                                                                                                                             |                                                                                                                                      |
| BASE COUNT               | 104 a 132 c 134 g 106 t                                                                                                                                                                |                                                                                                                                      |
| ORIGIN                   |                                                                                                                                                                                        |                                                                                                                                      |
| Query Match              | 3.0%; Score 18;                                                                                                                                                                        | DB 20; Length 476;                                                                                                                   |
| Best Local Similarity    | 100.0%; Pred. No. 77;                                                                                                                                                                  |                                                                                                                                      |
| Matches 18; Conservative | 0; Mismatches                                                                                                                                                                          | 0; Indels 0; Gaps 0;                                                                                                                 |
| QY                       | 265 gcagcgcgacctccggcc 282                                                                                                                                                             |                                                                                                                                      |
| Db                       | 380 GCAGCGCGCCTCTGC 397                                                                                                                                                                |                                                                                                                                      |
|                          |                                                                                                                                                                                        |                                                                                                                                      |
| RESULT 19                |                                                                                                                                                                                        |                                                                                                                                      |
| BE215806/c               |                                                                                                                                                                                        |                                                                                                                                      |
| LOCUS                    | BE215806                                                                                                                                                                               | 493 bp mRNA EST 09-MAR-2001                                                                                                          |
| DEFINITION               | HV.CE50008I16f Hordeum vulgare seedling green leaf EST library                                                                                                                         |                                                                                                                                      |
|                          | HVCDNA0005 (Erysipale infected & control) Hordeum vulgare cDNA clone                                                                                                                   |                                                                                                                                      |
|                          | HV.CE50008I16f, mRNA sequence.                                                                                                                                                         |                                                                                                                                      |
| ACCESSION                | BE215806                                                                                                                                                                               |                                                                                                                                      |
| VERSION                  | BE215806.1                                                                                                                                                                             | GI:8903418                                                                                                                           |
| KEYWORDS                 | EST.                                                                                                                                                                                   |                                                                                                                                      |
| SOURCE                   | Barley.                                                                                                                                                                                |                                                                                                                                      |
| ORGANISM                 | Hordeum vulgare                                                                                                                                                                        | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;                                                                   |
|                          | Eruyotia; Tridiplantae; Streptophyta; Embryophyta; Tracheophyta;                                                                                                                       |                                                                                                                                      |
|                          | Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae                                                                                                                    |                                                                                                                                      |
|                          | ; Triticeae; Hordeum.                                                                                                                                                                  |                                                                                                                                      |
| REFERENCE                | 1 (bases 1 to 493)                                                                                                                                                                     |                                                                                                                                      |

|                          |     |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |     |  |  |  |  |  |  |  |  |
|--------------------------|-----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|--|--|--|--|--|--|--|--|
| AUTHORS                  |     | Wing,R., Close,T.J., Kleinbols,A., Wise,R., Begum,D., Fisch,D., Y<br>'V., Anderson,H., Dale,J., Henry,D., Kennode,S., Palmer,M., Rambo<br>'T., Saski,C., Schwartzbeck,U., Simmons,J., Choi,D.W., Main,D. and<br>Wood,J.                                                                                                                                                                                                                                                                                                  |     |  |  |  |  |  |  |  |  |
| TITLE                    |     | Development of a genetically and physically anchored EST resource<br>for barley genomics                                                                                                                                                                                                                                                                                                                                                                                                                                 |     |  |  |  |  |  |  |  |  |
| JOURNAL                  |     | Unpublished (2000)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |     |  |  |  |  |  |  |  |  |
| COMMENT                  |     | Contact: Wing RA<br>Clemson University Genomics Institute<br>Clemson University<br>100 Jordan Hall, Clemson, SC 29634, USA<br>Tel: 864 656 7288<br>Fax: 864 656 4293<br>Email: rwing@clemson.edu<br>Seq primer: AATTACCTCCTCAATAAGG<br>High quality sequence stop: 486.                                                                                                                                                                                                                                                  |     |  |  |  |  |  |  |  |  |
| FEATURES                 |     | Location/Qualifiers                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |     |  |  |  |  |  |  |  |  |
| source                   |     | 1..493                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |     |  |  |  |  |  |  |  |  |
|                          |     | /organism="Hordeum vulgare"<br>/cultivar="C116151 (M1a6)"<br>/db_xref="taxon:4513"<br>/clone="HV_CEP0008116f"<br>/clone_lib="Hordeum vulgare seedling green leaf EST<br>library HVCN00005 (Erysiphe infected & control)"<br>/tissue_type="Seedling green leaf"<br>/lab_host="SOLR"<br>/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI"                                                                                                                                                                             |     |  |  |  |  |  |  |  |  |
| BASE COUNT               |     | 55 a 213 c 151 g 74 t                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |     |  |  |  |  |  |  |  |  |
| ORIGIN                   |     |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |     |  |  |  |  |  |  |  |  |
| Query Match              |     | 3.0%, Score 18; DB 164; Length 493;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |     |  |  |  |  |  |  |  |  |
| Best Local Similarity    |     | 100.0%; Pred. No. 77;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |     |  |  |  |  |  |  |  |  |
| Matches 18; Conservative |     | 0; Mismatches 0; Indels 0; Gaps 0;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |     |  |  |  |  |  |  |  |  |
| Oy                       | 385 | gcgcggccacgacgag                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 402 |  |  |  |  |  |  |  |  |
|                          |     |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |     |  |  |  |  |  |  |  |  |
| Db                       | 73  | gcgcggccacgacgag                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 56  |  |  |  |  |  |  |  |  |
| RESULT 20                |     |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |     |  |  |  |  |  |  |  |  |
| LOCUS                    |     | BE487307 498 bp mRNA EST 28-AUG-2000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |     |  |  |  |  |  |  |  |  |
| DEFINITION               |     | 175980 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |     |  |  |  |  |  |  |  |  |
| ACCESSION                |     | BE487307                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |     |  |  |  |  |  |  |  |  |
| VERSION                  |     | BE487307.1 GI:9606840                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |     |  |  |  |  |  |  |  |  |
| KEYWORDS                 |     | EST.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |     |  |  |  |  |  |  |  |  |
| SOURCE                   |     | cow.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |     |  |  |  |  |  |  |  |  |
| ORGANISM                 |     | Bos taurus                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |     |  |  |  |  |  |  |  |  |
|                          |     | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;<br>Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;<br>Bovidae; Bovinae; Bos.                                                                                                                                                                                                                                                                                                                                                         |     |  |  |  |  |  |  |  |  |
| REFERENCE                |     | 1 (bases 1 to 498)<br>Sonstegard,T.S., Capuco,A.V., Van Tassel,C.P., Ashwell,M.S. and<br>Wells,K.D.                                                                                                                                                                                                                                                                                                                                                                                                                      |     |  |  |  |  |  |  |  |  |
| AUTHORS                  |     | Mapping of Expressed Sequence Tags from a normalized bovine mammary<br>gland cDNA library                                                                                                                                                                                                                                                                                                                                                                                                                                |     |  |  |  |  |  |  |  |  |
| TITLE                    |     | Unpublished (2000)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |     |  |  |  |  |  |  |  |  |
| JOURNAL                  |     | Contact: Sonstegard TS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |     |  |  |  |  |  |  |  |  |
| COMMENT                  |     | USA, ARS, Beltsville Agricultural Research Center<br>Bldg. 200 Km 2A, Beltsville, MD 20705, USA<br>Tel: 301 504 8416<br>Fax: 301 504 8414<br>Email: tads@psl.barc.usda.gov<br>Single pass sequencing. Bases called and alt trimmed with phred<br>v0.980904.e. Vector identified by cross_match with the -minscore 18<br>and -mismatch 12 options.<br>PCR primers<br>FORWARD: AGCAACAGCTATGACCAT<br>BACKWARD: GTTTCACAGTCAGCAG<br>Plate: 123 row: K column: 2<br>Seq primer: ATTTAGGTGACACTATATAC.<br>Location/Qualifiers |     |  |  |  |  |  |  |  |  |
| FEATURES                 |     |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |     |  |  |  |  |  |  |  |  |

source  
1. 498  
/organism="Bos taurus"  
/db\_xref="taxon:9913"  
/clone.lib="BARC SBOV"  
/tissue.type="pooled"  
/lab.host="DH10B"  
/note="Vector: PCMV SPORT6; Site\_1: XbaI; Site\_2: XhoI;  
Library made from pooled mRNA isolated from mammary  
tissues at eight physiological, developmental, and disease  
states."

BASE COUNT  
87 a 181 c 125 g 105 t

ORIGIN

Query Match 3.0%; Score 18; DB 136; Length 498;  
Best Local Similarity 100.0%; Pred. No. 77;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 514 gccgtctccacagcc 531  
|||||  
DB 27 GCCTCGTCTCCACAGCC 44

RESULT 21  
BE215810/c 512 bp mRNA EST 09-MAR-2001  
LOCUS  
DEFINITION  
HV.CEBD008120f Hordeum vulgare seedling green leaf EST library  
HVCNDA0005 (Erysiphe infected & control) Hordeum vulgare cDNA clone  
HV.CEBD008120f, mRNA sequence.  
BE215810  
ACCESSION BE215810.1 GI:8903422  
KEYWORDS EST.  
SOURCE  
ORGANISM  
Hordeum vulgare  
barley.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae  
; Triticeae; Hordeum.  
1 (bases 1 to 512)  
Wing, R., Close, T. J., Kleinbofs, A., Wise, R., Begum, D., Frisch, D., Yu  
, T., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo  
, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D. W., Main, D. and  
Wood, T.  
Development of a genetically and physically anchored EST resource  
for barley genomics  
Unpublished (2000)  
CONTACT: Wing RA  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Tel: 864 656 7288  
Fax: 864 656 4293  
Email: rtwing@clemson.edu  
Seq primer: AATTAACCTCCTCAAGG  
High quality sequence start: 2  
High quality sequence stop: 233.  
Location/Qualifiers  
1. 512  
/organism="Hordeum vulgare"  
/cultivar="C116151 (Mia6)"  
/db\_xref="taxon:4513"  
/clone.lib="HV\_CEBD008120f"  
/clone.lib="Hordeum vulgare seedling green leaf EST  
library HVCNDA0005 (Erysiphe infected & control)"  
/tissue.type="seedling green leaf"  
/lab.host="SOLR"  
/note="Vector: lambdaZAP; Site\_1: EcoRI; Site\_2: XhoI"

BASE COUNT  
114 a 167 c 127 g 104 t

ORIGIN

Query Match 3.0%; Score 18; DB 164; Length 512;  
Best Local Similarity 100.0%; Pred. No. 77;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 385 gccgcgcgcacagagc 402  
|||||  
DB 75 GCCCGCGCCACGACGAGC 58

RESULT 22  
AQ399589 512 bp DNA GSS 06-MAR-1999  
LOCUS  
DEFINITION  
mqxb0018E01f CUGI Rice Blast BAC Library Magnaporthe grisea genomic  
clone mqxb0018E01f, DNA sequence.  
AQ399589  
ACCESSION AQ399589.1 GI:4370616  
KEYWORDS GSS.  
SOURCE  
ORGANISM  
Magnaporthe grisea.  
Magnaporthe grisea  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetes Incertae sedis; Magnaporthaceae; Magnaporthe.  
1 (bases 1 to 512)  
Yu, Y., Zhu, H., Boyd, C. A., Gaudette, B., Gayle, A., Kingsbury, R.,  
Phillips, K., Sasinowski, M., Wing, R. A. and Dean, R. A.  
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea  
Genome  
Unpublished (1998)  
CONTACT: Dean RA  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson University, Clemson, SC 29634  
Tel: 864 656 5737  
Fax: 864 656 4293  
Email: rdeane@clemson.edu  
Seq primer: TAATGACTCCTACTATAGCG  
Class: BAC ends  
High quality sequence stop: 354.  
Location/Qualifiers  
1. 512  
/organism="Magnaporthe grisea"  
/strain="70-15"  
/db\_xref="taxon:148305"  
/clone.lib="mqxb0018E01f"  
/clone.lib="CUGI Rice Blast BAC Library"  
/tissue.type="protoplasts"  
/lab.host="E. coli DH10B"  
/note="Vector: pBACWICH; Site\_1: HindIII; Site\_2: HindIII;  
Rice blast is one of the most devastating fungal diseases  
of rice world wide. It is a filamentous ascomycete with  
a haploid genome (n=7) of approximately 40 Mbp. Rice  
blast is an important model fungal pathogen for studying  
numerous aspects of the fungal-host interaction. In  
order to facilitate genome wide analysis, a BAC library  
containing 9216 clones with an average insert size of 130  
kbp was constructed. This library represents greater  
than 25x genome coverage. High density colony filters  
are available upon request."

BASE COUNT  
102 a 167 c 131 g 112 t

ORIGIN

Query Match 3.0%; Score 18; DB 228; Length 512;  
Best Local Similarity 100.0%; Pred. No. 77;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 271 gccgcctcgcgcgcgcgc 288  
|||||  
DB 239 GCCCGCTCTGCCGCGCGC 222

RESULT 23  
AM168137 527 bp mRNA EST 12-NOV-1999  
LOCUS  
DEFINITION  
xg60d04.x1 NCL\_CGAP\_Ut4 Homo sapiens cDNA clone IMAGE:2632711 3',  
mRNA sequence.  
ACCESSION AM168137

VERSION AM168137.1 GI:6399662  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 527)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bdrr/image/image.html](http://www-bio.llnl.gov/bdrr/image/image.html)

FEATURES  
source  
Possible reversed clone: polyT not found  
Seq primer: -40UP from Gibco  
High quality sequence stop: 306.  
Location/Qualifiers  
1..527  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2632711"  
/clone\_1id="NCI CGAP\_U44"  
/tissue\_type="serous papillary carcinoma, high grade, 2  
pooled tumors"  
/lab\_host="DH10B"  
/note="Organ: uterus; Vector: PCMV-SPORT6; Site\_1: SalI;  
Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.48 kb. Life Technologies catalog #:  
11542-016"

BASE COUNT 151 a 152 c 162 g 61 t 1 others  
ORIGIN

Query Match 3.0%; Score 18; DB 112; Length 527;  
Best Local Similarity 100.0%; Pred. No. 77;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 160 ggggtgtgtctctcgggc 177  
|||||  
Db 469 GGGGTGTGTCTCTCGGC 486

RESULT 24  
A1158964/c 536 bp mRNA EST 02-OCT-1998  
DEFINITION u142905.x1 Sugano mouse embryo mewa Mus musculus cDNA clone  
IMAGE:1885112.3' similar to WP:FL3B12.1 C505599 ;, mRNA sequence.  
ACCESSION A1158964  
VERSION A1158964.1 GI:3692146  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 536)  
AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,  
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,  
Reising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
Waterston, R.  
TITLE The Mashu-HMI Mouse EST Project  
JOURNAL Unpublished (1996)  
COMMENT Contact: Marra M/Mouse EST Project  
Mashu-HMI Mouse EST Project

Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: [mouseest@wustl.edu](mailto:mouseest@wustl.edu)  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
MGI:969436

FEATURES  
source  
Possible reversed clone: similarity on wrong strand  
Seq primer: custom primer used  
High quality sequence stop: 409.  
Location/Qualifiers  
1..536  
/organism="Mus musculus"  
/strain="C57BL"  
/db\_xref="taxon:10090"  
/clone="IMAGE:1885112"  
/clone\_1id="Sugano mouse embryo mewa"  
/dev\_stage="embryo, 14 dpc"  
/lab\_host="DH10B"  
/note="Vector: pME18S-FL3; Site\_1: DraIII (CACTGTGTG);  
Site\_2: DraIII (CACCATGTG); 1st strand cDNA was primed  
with an oligo(dT) primer [ATGTGGCTTTTCTTTTCTTTT];  
double-stranded cDNA was ligated to a DraIII adaptor  
[TGTGGCTTCTGTG], digested and cloned into distinct DraIII  
sites of the pME18S-FL3 vector (5' site CACCATGTG, 3' site  
CACCATGTG). XhoI should be used to isolate the cDNA  
insert. Size selection was performed to exclude fragments  
<1.5kb. Library constructed by Dr. Sumio Sugano  
(University of Tokyo Institute of Medical Science).  
Custom primers for sequencing: 5' end primer  
CTTCTGCTCTAAAGCTGCG and 3' end primer  
CGACCTGCAGCTCAGCACA."

BASE COUNT 138 a 120 c 99 g 179 t  
ORIGIN

Query Match 3.0%; Score 18; DB 16; Length 536;  
Best Local Similarity 100.0%; Pred. No. 77;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 543 aacagagaaagaaagc 560  
|||||  
Db 516 AACAGAGAAAGAAAGC 499

RESULT 25  
BG147743 556 bp mRNA EST 01-FEB-2001  
BG147743  
DEFINITION mab53h05.x1 Soares.NMBA\_brachial\_arch Mus musculus cDNA clone  
IMAGE:3974241.3' similar to TR:075462 075462 CYTOKINE-LIKE FACTOR-1  
PRECUSOR. [1] ;, mRNA sequence.  
ACCESSION BG147743  
VERSION BG147743.1 GI:12651151  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 556)  
AUTHORS Other\_ESTs: mab53h05.y1  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo,  
Ph.D.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:

image.llnl.gov/image/html/iresources.shtml

MG1:1474273

Possible reversed clone: similarity on wrong strand

Possible reversed clone: polyT not found

High quality sequence stop: 463.

#### FEATURES

source

Location/Qualifiers

1..556  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/clone="IMAGE:3974241"  
/clone\_lib="Soares NMEBA branchial arch"  
/tissue\_type="branchial arches"  
/dev\_stage="embryo, 10.5 dpc"  
/lab\_host="DH10B (phage resistant)"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker. Site 1: NotI; Site 2: EcoRI; 1st strand cDNA  
was primed with a Not I - oligo(dT) primer [5'  
TGTTCACATCTGAGATGGAGCGCGCCGATCATTTTCTTTTCTTTT  
3']; double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not  
I and Eco RI sites of the modified pT73 vector. Library  
constructed and normalized by Bento Soares and M. Fatima  
Bonaldo."  
BASE COUNT 101 a 183 c 162 g 110 t  
ORIGIN

#### Query Match

Best Local Similarity 100.0%; Score 18; DB 174; Length 556;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 159 ggggtgtgtgtcctcg 176

|||||

Db 32 GGGGTGTGTCTCTCGG 49

#### RESULT 26

AUI64787

LOCUS

DEFINITION

AUI64787 570 bp mRNA EST 20-NOV-2000  
AUI64787 Rice cDNA from immature leaf including apical meristem  
(under short day condition) Oryza sativa cDNA clone E61272, mRNA  
sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

EST.

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Eriaraloideae; Oryzaceae; Oryza.

1 (bases 1 to 570)

Sasaki, T. and Yamamoto, K.

Rice cDNA from immature leaf including apical meristem (2000)

Unpublished (2000)

Contact: Takuji Sasaki

National Institute of Agrobiological Resources

Rice Genome Research Program

2-1-2 Kannondai, Tsukuba

Ibaraki,

Japan 305

Tel: 0298-38-7441

Fax: 0298-38-7468

Email: tsasaki@abr.affrc.go.jp

PROJECT "RGP"

E61272\_22.

Location/Qualifiers

1..570

/organism="Oryza sativa"

/strain="Nipponbare"

/db\_xref="taxon:4530"

/clone="E61272"

/clone\_lib="Rice cDNA from immature leaf including apical

meristem (under short day condition)"  
/dev\_stage="Immature leaf including apical meristem (under  
short day condition)"  
BASE COUNT 123 a 186 c 132 g 126 t 3 others  
ORIGIN

#### Query Match

Best Local Similarity 100.0%; Score 18; DB 108; Length 570;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 394 acgacgaggtctacggc 411

|||||

Db 243 ACGACGAGGTCTACGGC 260

#### RESULT 27

BF620011

LOCUS

DEFINITION

BF620011 598 bp mRNA EST 22-FEB-2001  
HVSMEC000924f Hordeum vulgare seedling shoot EST library  
HVCNDA0003 (Etiolated and unstressed) Hordeum vulgare cDNA clone  
HVSMEC000924f, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

EST.

Hordeum vulgare

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae  
Triticeae; Hordeum.

1 (bases 1 to 598)

Wing, R., Close, T.J., Kleinbols, A., Wise, R., Begum, D., Frisch, D., Yu

, Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo

, T., Sasaki, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and

Wood, T.

Development of a genetically and physically anchored EST resource

for barley genomics

Unpublished (2000)

On Dec 18, 2000 this sequence version replaced gi:11883745.

Contact: Wing RA

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: rwing@clemson.edu

Seq primer: AATTACCTCACTAAGCG

High quality sequence stop: 592.

Location/Qualifiers

1..598

/organism="Hordeum vulgare"

/cultivar="Morex"

/db\_xref="taxon:4513"

/clone="HVSMEC000924f"

/clone\_lib="Hordeum vulgare seedling shoot EST library

HVCNDA0003 (Etiolated and unstressed)"

/tissue\_type="Seedling shoot"

/lab\_host="TUC121"

/note="Vector: lambdaZAP; Site 1: EcoRI; Site 2: XhoI"

BASE COUNT 120 a 167 c 195 g 116 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 18; DB 151; Length 598;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 416 cgtcacgactaccgcc 433

|||||

Db 254 CGTCACGACTACCGCC 271

|||||

RESULT 28

AU101340  
 LOCUS AU101340 618 bp mRNA EST 22-AUG-2000  
 DEFINITION AU101340 Rice panicle at ripening stage Oryza sativa cDNA clone  
 E1131, mRNA sequence.  
 ACCESSION AU101340  
 VERSION AU101340.1 GI:9865590  
 KEYWORDS EST.  
 SOURCE Oryza sativa.  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 618)  
 Sasaki, T. and Yamamoto, K.  
 Rice cDNA from panicle at ripening stage (2000)  
 Unpublished (2000)  
 Contact: Takuji Sasaki  
 National Institute of Agrobiological Resources  
 Rice Genome Research Program  
 2-1-2 Kannondai, Tsukuba  
 Ibaraki,  
 Japan 305  
 Tel: 0298-38-7441  
 Fax: 0298-38-7468  
 Email: tsasaki@abrr.affrc.go.jp  
 PROJECT = 'RGP'.  
 E1131\_42.

FEATURES  
 source  
 1..618  
 /organism="Oryza sativa"  
 /strain="Nipponbare"  
 /db\_xref="taxon:4530"  
 /clone="E1131"  
 /clone\_lib="Rice panicle at ripening stage"  
 /dev\_stage="ripening stage"  
 /note="Organ: panicle; Rice cDNA from panicle at ripening stage"

BASE COUNT 151 a 166 c 145 g 155 t 1 others  
 ORIGIN

Query Match 3.0%; Score 18; DB 107; Length 618;  
 Best Local Similarity 100.0%; Pred. No. 77;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 394 acgacgaggtctacggcg 411  
 ||||||||||||||||  
 Db 190 acgacgaggtctacggcg 207

RESULT 29  
 BE291467 682 bp mRNA EST 13-JUL-2000  
 LOCUS BE291467  
 DEFINITION 601085211F1 NCI\_CGAP\_Mam6 Mus musculus cDNA clone IMAGE:349371 5',  
 mRNA sequence.  
 ACCESSION BE291467  
 VERSION BE291467.1 GI:9173211  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 682)  
 NIH-MGC http://mgc.nci.nih.gov/  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs@email.nih.gov  
 Tissue Procurement: Jeffrey Green M.D.  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

found through the I.M.A.G.E. Consortium/LNLN at:  
 http://image.llnl.gov  
 Plate: L1AM8556 row: e Column: 04  
 High quality sequence stop: 577.  
 Location/Qualifiers  
 1..682  
 /organism="Mus musculus"  
 /strain="FVB/N"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:349371"  
 /clone\_lib="NCI\_CGAP\_Mam6"  
 /sex="female, virgin"  
 /tissue\_type="infiltrating ductal carcinoma"  
 /dev\_stage="5 months"  
 /lab\_host="DH10B"  
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site\_1: SalI;  
 Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
 Library constructed by Life Technologies, Inc. Investigator  
 providing samples: Jeffrey Green, M.D., NIH"

BASE COUNT 215 a 150 c 179 g 138 t  
 ORIGIN

Query Match 3.0%; Score 18; DB 165; Length 682;  
 Best Local Similarity 100.0%; Pred. No. 77;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 543 aacagagagaagaagc 560  
 ||||||||||||||||  
 Db 337 AACAGAGAGAGAAAGGC 354

RESULT 30  
 BG323623 707 bp mRNA EST 27-FEB-2001  
 LOCUS BG323623  
 DEFINITION 602422094F1 NIH\_MGC\_14 Homo sapiens cDNA clone IMAGE:4560167 5',  
 mRNA sequence.  
 ACCESSION BG323623  
 VERSION BG323623.1 GI:13130060  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 707)  
 NIH-MGC http://mgc.nci.nih.gov/  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs@email.nih.gov  
 Tissue Procurement: DCTD/DRP  
 CDNA Library Preparation: Ling Hong/Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNLN at:  
 http://image.llnl.gov  
 Plate: L1CM1268 row: 1 Column: 24  
 High quality sequence stop: 656.  
 Location/Qualifiers  
 1..707  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4560167"  
 /clone\_lib="NIH\_MGC\_14"  
 /tissue\_type="renal cell adenocarcinoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: kidney; Vector: pORF7; Site\_1: XhoI; Site\_2:  
 EcoRI; CDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGCACGAG(G). Size-selected >500bp for average  
 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of

FEATURES  
 source

BASE COUNT 182 a 199 c 163 g 162 t 1 others  
 ORIGIN California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 3.0%; Score 18; DB 152; Length 707;  
 Best Local Similarity 100.0%; Pred. No. 77;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 230 cccctgcatcccccctg 247  
 ||||||||||||||||  
 Db 194 CCCCTGATCCCCCTG 211

RESULT 31  
 LOCUS A2631126 711 bp DNA GSS 13-DEC-2000  
 DEFINITION IM0485G09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 ACCESSION A2631126  
 VERSION A2631126.1 GI:11753316  
 KEYWORDS GSS.  
 SOURCE house mouse.  
 ORGANISM Mus musculus

REFERENCE  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamli, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0485 row: G column: 09  
 Seq primer: CGTTGTAACGACGCGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 711.  
 Location/Qualifiers

FEATURES  
 source 1. .711  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0485G09"  
 /clone\_1lb="Mouse 10kb plasmid UUGC1M library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1147321149b/AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to

BASE COUNT 210 a 180 c 118 g 203 t  
 ORIGIN adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 3.0%; Score 18; DB 247; Length 711;  
 Best Local Similarity 100.0%; Pred. No. 77;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 547 ggaagaagaaggctcc 564  
 ||||||||||||||||  
 Db 146 GGAGAAGAAAAGCCTCC 163

RESULT 32  
 LOCUS A2867529/c 712 bp DNA GSS 21-FEB-2001  
 DEFINITION 2M0178H23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 ACCESSION A2867529  
 VERSION A2867529.1 GI:13069921  
 KEYWORDS GSS.  
 SOURCE house mouse.  
 ORGANISM Mus musculus

REFERENCE  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamli, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0178 row: H column: 23  
 Seq primer: CGTTGTAACGACGCGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 712.  
 Location/Qualifiers

FEATURES  
 source 1. .712  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0178H23"  
 /clone\_1lb="Mouse 10kb plasmid UUGC1M library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1147321149b/AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

BASE COUNT 191 a 213 c 141 g 166 t 1 others

ORIGIN

Query Match 3.0%; Score 18; DB 251; Length 712;

Best Local Similarity 100.0%; Pred. No. 77; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 297 tgaagccgacgctggagg 314  
|||||  
Db 525 TGAGCCGACGTCGGGAG 508

RESULT 33

BE892353

LOCUS 722 bp mRNA EST 20-OCT-2000  
DEFINITION 601433812P1 NIH\_MGC\_72 Homo sapiens cDNA clone IMAGE:3919130 5', mRNA sequence.

ACCESSION BE892353

VERSION BE892353.1 GI:10352576

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 722)

AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
Tissue Procurement: ATCC/DCTP/DRP  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:  
<http://image.llnl.gov>  
Plate: LLM9748 row: 9 column: 03  
High quality sequence stop: 709.

Location/Qualifiers

1..722  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3919130"  
/clone\_lib="NIH\_MGC\_72"  
/tissue\_type="melanotic melanoma"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: skin; Vector: pCMV-Sport6; Site\_1: NotI; Site\_2: SalI; Cloned unidirectionally. Primer: oligo dt. Average insert size 2 kb. Library constructed by Life Technologies."

BASE COUNT 197 a 198 c 161 g 166 t

ORIGIN

Query Match 3.0%; Score 18; DB 141; Length 722;

Best Local Similarity 100.0%; Pred. No. 77; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 230 cccctgcacacccctg 247  
|||||  
Db 337 CCCTGCATCACCCCTG 354

RESULT 34

BF267443/c

LOCUS 862 bp mRNA EST 09-MAR-2001  
DEFINITION HV\_CEA0017P07f Hordeum vulgare seedling green leaf EST library

HVCDNA0004 (Erysiphe infected & control) Hordeum vulgare cDNA clone HV\_CEA0017P07f, mRNA sequence.

ACCESSION BF267443  
VERSION BF267443.2 GI:13263387  
KEYWORDS EST.

SOURCE barley.

ORGANISM Hordeum vulgare

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Hordeum.

REFERENCE 1 (bases 1 to 862)

Wing, R., Close, T.J., Kleinholz, A., Wise, R., Begum, D., Frisch, D., Yu, Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and Wood, T.

Development of a genetically and physically anchored EST resource for barley genomics

JOURNAL Unpublished (2000)

COMMENT On Nov 17, 2000 this sequence version replaced gi:11198438.

CONTACT: Wing RA

Clemson University Genomics Institute

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: [rwing@clemson.edu](mailto:rwing@clemson.edu)

Seq primer: AATTAACCTCCTAAGG

High quality sequence stop: 741.

Location/Qualifiers

1..862

/organism="Hordeum vulgare"

/cultivar="C116155 (M1a13)"

/db\_xref="taxon:4513"

/clone="HV\_CEA0017P07f"

/clone\_lib="Hordeum vulgare seedling green leaf EST library HVCDNA0004 (Erysiphe infected & control)"

/tissue\_type="seedling green leaf"

/lab\_host="TJ10121"

/note="Vector: lambdaZAP; Site\_1: EcoRI; Site\_2: XhoI"

BASE COUNT 193 a 380 c 206 g 80 t 3 others

ORIGIN

Query Match 3.0%; Score 18; DB 146; Length 862;

Best Local Similarity 100.0%; Pred. No. 78; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 385 ggcgcgcacgacgag 402  
|||||  
Db 52 GCGCGCGCAGCAGAG 35

RESULT 35

AQ901727/c

LOCUS 898 bp DNA GSS 10-NOV-1999

DEFINITION HS\_2019\_A2\_E01\_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate-2019 Col-2 Row-I, DNA sequence.

ACCESSION AQ901727

VERSION AQ901727.1 GI:6357917

KEYWORDS GSS.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 898)

AUTHORS Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.

Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome

Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)

CONTACT: Mahairas GG, Wallace JC, Hood L

JOURNAL MEDLINE

99380589

COMMENT

High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: jwallace@u.washington.edu

Clones may be purchased from Research Genetics (info@resgen.com).  
BAC end Web Server: <http://www.htsc.washington.edu>  
Plate: 2019 row: 1 column: 2  
Seq primer: T7  
Class: BAC ends  
High quality sequence stop: 898.

## FEATURES

source

1. .898

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="Plate=2019 Col=2 Row=1"

/clone\_lib="CIT Approved Human Genomic Sperm Library D"

/sex="male"

/note="Organ: sperm; Vector: pBelobAC11; BAC Clones in E-Coli DH10B"

## BASE COUNT

154 a 251 c 168 g 322 t 3 others

## ORIGIN

Query Match 3.0%; Score 18; DB 235; Length 898;  
Best Local Similarity 100.0%; Pred. No. 78;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 542 caacagagagagagagagag 559  
|||||  
DB 881 CACACGACGACGACGACG 864

## RESULT 36

CNS01XEF 909 bp DNA GSS 12-MAY-2000  
LOCUS Tetraodon nigroviridis genome survey sequence PUC-Or1 end of clone  
DEFINITION 202608 of library G from Tetraodon nigroviridis, genomic survey  
sequence.

ACCESSION AL171604.1 GI:7809661  
VERSION GSS: genome survey sequence.  
KEYWORDS Tetraodon nigroviridis.  
SOURCE Tetraodon nigroviridis  
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
Tetraodontidae; Tetraodon.

## REFERENCE

1 (bases 1 to 909)  
Roest-Crollius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C.,  
Bonneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and

## TITLE

Characterization and repeat analysis of the compact genome of the  
freshwater pufferfish Tetraodon nigroviridis

## JOURNAL

Unpublished  
2 (bases 1 to 909)

## AUTHORS

Roest-Crollius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C.,  
Bernot,A., Fizames,C., Wincker,P., Brothier,P., Quetier,F.,  
Saurin,W. and Weissenbach,J.

## JOURNAL

Submitted (12-Apr-2000) to the EMBL/GenBank/DBJ databases  
Genoscope.

## TITLE

Human gene number estimate provided by genome wide analysis using  
Tetraodon nigroviridis DNA sequence

## COMMENT

Unpublished  
3 (bases 1 to 909)

## FEATURES

location/Qualifiers  
1. .909

/organism="Tetraodon nigroviridis"

/db\_xref="taxon:99883"

/clone="202608"

/clone\_lib="G"

/note="Genoscope sequence ID : C0AG202BD04SP1-end :  
PUC-Or1"

BASE COUNT 192 a 228 c 218 g 258 t 13 others

## ORIGIN

Query Match 3.0%; Score 18; DB 220; Length 909;  
Best Local Similarity 100.0%; Pred. No. 78;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 114 acagcagcagcagcagcagc 131  
|||||  
DB 524 ACACGACGACGACGACG 507

## RESULT 37

CNS030F7 919 bp DNA GSS 17-MAY-2000  
LOCUS Tetraodon nigroviridis genome survey sequence T7 end of clone  
DEFINITION 047614 of library G from Tetraodon nigroviridis, genomic survey  
sequence.

ACCESSION AL255868.1 GI:7976880  
VERSION GSS: genome survey sequence.  
KEYWORDS Tetraodon nigroviridis.  
SOURCE Tetraodon nigroviridis  
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
Tetraodontidae; Tetraodon.

## REFERENCE

1 (bases 1 to 919)  
Roest-Crollius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C.,  
Bonneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and

## TITLE

Characterization and repeat analysis of the compact genome of the  
freshwater pufferfish Tetraodon nigroviridis

## JOURNAL

Unpublished  
2 (bases 1 to 919)

## AUTHORS

Roest-Crollius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C.,  
Bernot,A., Fizames,C., Wincker,P., Brothier,P., Quetier,F.,  
Saurin,W. and Weissenbach,J.

## JOURNAL

Submitted (12-Apr-2000) to the EMBL/GenBank/DBJ databases  
Genoscope.

## TITLE

Human gene number estimate provided by genome wide analysis using  
Tetraodon nigroviridis DNA sequence

## COMMENT

Unpublished  
3 (bases 1 to 919)

## FEATURES

location/Qualifiers  
1. .919

BASE COUNT 170 a 312 c 280 g 148 t 9 others

## ORIGIN

Query Match 3.0%; Score 18; DB 221; Length 919;  
Best Local Similarity 100.0%; Pred. No. 78;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 268 gccgcgcctcctgcgcgcg 285  
|||||



Db 575 GCCGCCCTCTCTGCCGCG 592

RESULT 38  
LOCUS CNS05JPS/ 952 bp DNA GSS 26-MAY-2000  
DEFINITION Tetraodon nigroviridis genome survey sequence T3 end of clone 028E23 of library A from Tetraodon nigroviridis, genomic survey sequence.

ACCESSION AL340489  
VERSION AL340489.1 GI:8234247  
KEYWORDS GSS; genome survey sequence.  
SOURCE Tetraodon nigroviridis.  
ORGANISM Tetraodon nigroviridis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorphi; Acanthopterygii; Percomorphi; Tetraodontiformes; Tetraodontidae; Tetraodon.

REFERENCE 1 (bases 1 to 952)  
AUTHORS Roest-Crollius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.  
TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 952)  
AUTHORS Roest-Crollius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brothier,P., Quetier,F., Saurin,W. and Weissenbach,J.  
TITLE Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence  
JOURNAL Unpublished  
REFERENCE 3 (bases 1 to 952)  
AUTHORS Genoscope.  
TITLE Direct Submission  
JOURNAL Submitted (12-APR-2000) to the EMBL/Genbank/DBJ databases  
COMMENT This sequence is a single read and was generated as part of a large scale clone-and-sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.

FEATURES  
source  
1..952  
/organism="Tetraodon nigroviridis"  
/db\_xref="taxon:99883"  
/clone="028E23"  
/clone\_1lb="A"  
/note="Genoscope sequence ID : C0AA028AC12A2-end : T3"

BASE COUNT 239 a 231 c 236 g 236 t 10 others

ORIGIN

Query Match 3.0%; Score 18; DB 222; Length 952;  
Best Local Similarity 100.0%; Pred. No. 78;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 114 acagcagccagggccaaa 131  
|||||  
Db 137 ACAGCAGCCAGGCCAANA 120

RESULT 39  
LOCUS BE741337 968 bp mRNA EST 15-SEP-2000  
DEFINITION 601594184F1 NIH\_MGC\_9 Homo sapiens cDNA clone IMAGE:3947972 5', mRNA sequence.  
ACCESSION BE741337  
VERSION BE741337.1 GI:10155329  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 968)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: DCTD/DRP  
cDNA Library Preparation: Ling Hong/Rubln Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [image.llnl.gov](http://image.llnl.gov)  
Plate: LRCM810 row: h column: 21  
High quality sequence stop: 697.

FEATURES  
source  
1..968  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3947972"  
/clone\_1lb="NIH\_MGC.9"  
/tissue\_type="adenocarcinoma cell line"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: ovary; Vector: pOTB7; site\_1: XhoI; site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACAGC(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using 2AP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 253 a 275 c 237 g 203 t

ORIGIN

Query Match 3.0%; Score 18; DB 139; Length 968;  
Best Local Similarity 100.0%; Pred. No. 78;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 230 cccctgacaccacctg 247  
|||||  
Db 277 CCCCTGCATCACCCTCG 294

RESULT 40  
LOCUS CNS035RQ 966 bp DNA GSS 15-MAY-2000  
DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone 214B05 of library G from Tetraodon nigroviridis, genomic survey sequence.

ACCESSION AL229103  
VERSION AL229103.1 GI:7888098  
KEYWORDS GSS; genome survey sequence.  
SOURCE Tetraodon nigroviridis.  
ORGANISM Tetraodon nigroviridis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorphi; Acanthopterygii; Percomorphi; Tetraodontiformes; Tetraodontidae; Tetraodon.

REFERENCE 1 (bases 1 to 966)  
AUTHORS Roest-Crollius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.  
TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 966)  
AUTHORS Roest-Crollius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brothier,P., Quetier,F., Saurin,W. and Weissenbach,J.  
TITLE Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence  
JOURNAL Unpublished  
REFERENCE 3 (bases 1 to 966)  
AUTHORS Genoscope.

TITLE Direct Submission  
JOURNAL Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases  
COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.

FEATURES  
source  
1. 986  
/organism="Tetraodon nigroviridis"  
/db\_xref="taxon:99883"  
/clone\_1lb="G"  
/note="Genoscope sequence ID : COAG214CA03LPI-end : T7"  
BASE COUNT 180 a 329 c 318 g 154 t 5 others  
ORIGIN

Query Match 3.0%; Score 18; DB 220; Length 986;  
Best Local Similarity 100.0%; Pred. No. 78;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 268 gccgcgcctcctgcgcgcg 285  
|||||  
Db 572 GCCGCGCCTCCTCGCGG 589

RESULT 41  
CNS0305J 1009 bp DNA GSS 17-MAY-2000  
LOCUS Tetraodon nigroviridis genome survey sequence T7 end of clone  
DEFINITION 046L1 of library G from Tetraodon nigroviridis, genomic survey sequence.  
ACCESSION AL255520.1 GI:7976532  
VERSION AL255520.1  
KEYWORDS GSS; genome survey sequence.  
SOURCE Tetraodon nigroviridis.  
ORGANISM Tetraodon nigroviridis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.  
1 (bases 1 to 1009)  
Roest-Crollius, H., Jallion, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.  
Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis  
Unpublished  
2 (bases 1 to 1009)  
Roest-Crollius, H., Jallion, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brothier, P., Quetier, F., Saurin, W. and Weissenbach, J.  
Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence  
Unpublished  
3 (bases 1 to 1009)  
Genoscope.  
Direct Submission  
Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases  
JOURNAL This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.  
COMMENT

FEATURES  
source  
1. 1009  
/organism="Tetraodon nigroviridis"  
/db\_xref="taxon:99883"  
/clone\_1lb="G"  
/note="Genoscope sequence ID : COB046CF06LPI-end : T7"  
BASE COUNT 211 a 263 c 238 g 294 t 3 others  
ORIGIN

Query Match 3.0%; Score 18; DB 221; Length 1009;  
Best Local Similarity 100.0%; Pred. No. 78;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 acagcagccagcgccaana 131  
|||||  
Db 736 ACAGCAGCCAGCGCCAAA 719

RESULT 42  
CNS05EAA 1056 bp DNA GSS 26-MAY-2000  
LOCUS Tetraodon nigroviridis genome survey sequence T3 end of clone  
DEFINITION 028A19 of library A from Tetraodon nigroviridis, genomic survey sequence.  
ACCESSION AL333451 GI:8227209  
VERSION AL333451  
KEYWORDS GSS; genome survey sequence.  
SOURCE Tetraodon nigroviridis.  
ORGANISM Tetraodon nigroviridis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.  
1 (bases 1 to 1056)  
Roest-Crollius, H., Jallion, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.  
Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis  
Unpublished  
2 (bases 1 to 1056)  
Roest-Crollius, H., Jallion, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brothier, P., Quetier, F., Saurin, W. and Weissenbach, J.  
Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence  
Unpublished  
3 (bases 1 to 1056)  
Genoscope.  
Direct Submission  
Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases  
JOURNAL This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.  
COMMENT

FEATURES  
source  
1. 1056  
/organism="Tetraodon nigroviridis"  
/db\_xref="taxon:99883"  
/clone\_1lb="A"  
/note="Genoscope sequence ID : COA028A10A1-end : T3"  
BASE COUNT 223 a 246 c 262 g 278 t 47 others  
ORIGIN

Query Match 3.0%; Score 18; DB 222; Length 1056;  
Best Local Similarity 100.0%; Pred. No. 78;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 acagcagccagcgccaana 131  
|||||  
Db 148 ACAGCAGCCAGCGCCAAA 131

RESULT 43  
AL543701 1078 bp mRNA EST 16-FEB-2001  
LOCUS AL543701 L7L NFE006\_P12 Homo sapiens cDNA clone CS0D1006YNI0 5  
DEFINITION prime, mRNA sequence.  
ACCESSION AL543701

|                       |                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |                                    |
|-----------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------|
| VERSION               | AL543701.1                                                                                                                                                                                                                                                                                                                                                                                                                                                            | GI:12876180                        |
| KEYWORDS              | EST.                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |                                    |
| SOURCE                | human.                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                    |
| ORGANISM              | Homo sapiens                                                                                                                                                                                                                                                                                                                                                                                                                                                          |                                    |
| REFERENCE             | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.                                                                                                                                                                                                                                                                                                                                           |                                    |
| AUTHORS               | 1 (bases 1 to 1078)                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                    |
| TITLE                 | L1.W.B., Gruber,C., Jesse,J. and Polayes,D.                                                                                                                                                                                                                                                                                                                                                                                                                           |                                    |
| JOURNAL               | Full-length cDNA libraries and normalization                                                                                                                                                                                                                                                                                                                                                                                                                          |                                    |
| COMMENT               | Unpublished (2001)                                                                                                                                                                                                                                                                                                                                                                                                                                                    |                                    |
| FEATURES              | Contact: Genoscope                                                                                                                                                                                                                                                                                                                                                                                                                                                    |                                    |
| source                | Genoscope - Centre National de Sequencage                                                                                                                                                                                                                                                                                                                                                                                                                             |                                    |
|                       | Bp 191 91006 EVRY cedex - France                                                                                                                                                                                                                                                                                                                                                                                                                                      |                                    |
|                       | Email: <a href="mailto:seq@genoscope.cns.fr">seq@genoscope.cns.fr</a> , Web : <a href="http://www.genoscope.cns.fr">www.genoscope.cns.fr</a> .                                                                                                                                                                                                                                                                                                                        |                                    |
|                       | location/Qualifiers                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                    |
|                       | 1..1078                                                                                                                                                                                                                                                                                                                                                                                                                                                               |                                    |
|                       | /organism="Homo sapiens"                                                                                                                                                                                                                                                                                                                                                                                                                                              |                                    |
|                       | /db_xref="taxon:9606"                                                                                                                                                                                                                                                                                                                                                                                                                                                 |                                    |
|                       | /clone="CS0D1006YN10"                                                                                                                                                                                                                                                                                                                                                                                                                                                 |                                    |
|                       | /clone_id="L1.NFL006.PL2"                                                                                                                                                                                                                                                                                                                                                                                                                                             |                                    |
|                       | /tissue_type="Placenta"                                                                                                                                                                                                                                                                                                                                                                                                                                               |                                    |
|                       | /note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 |                                    |
|                       | Email: <a href="mailto:liang@lifetech.com">liang@lifetech.com</a> URL :                                                                                                                                                                                                                                                                                                                                                                                               |                                    |
|                       | <a href="http://fulllength.invitrogen.com">http://fulllength.invitrogen.com</a> "                                                                                                                                                                                                                                                                                                                                                                                     |                                    |
| BASE COUNT            | 246 a                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 287 c 329 g 201 t 15 others        |
| ORIGIN                |                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |                                    |
| Query Match           | 3.0%                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Score 18; DB 106; Length 1078;     |
| Best Local Similarity | 100.0%                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Prod. No. 78;                      |
| Matches               | 18; Conservative                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 0; Mismatches 0; Indels 0; Gaps 0; |
| Oy                    | 230                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | ccccgcacacccccct 247               |
|                       |                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |                                    |
| Db                    | 683                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | CCCCGCATCACCCCTG 700               |
| RESULT 44             |                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |                                    |
| CNS054X1/c            |                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |                                    |
| LOCUS                 | CNS054X1                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 1081 bp DNA GSS 26-JUL-2000        |
| DEFINITION            | Tetradon nigroviridis genome survey sequence T7 end of clone 046L22 of library A from Tetradon nigroviridis, genomic survey sequence.                                                                                                                                                                                                                                                                                                                                 |                                    |
| ACCESSION             | AL321310                                                                                                                                                                                                                                                                                                                                                                                                                                                              | GI:9554194                         |
| VERSION               | AL321310                                                                                                                                                                                                                                                                                                                                                                                                                                                              |                                    |
| KEYWORDS              | GSS: genome survey sequence.                                                                                                                                                                                                                                                                                                                                                                                                                                          |                                    |
| SOURCE                | Tetradon nigroviridis.                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                    |
| ORGANISM              | Tetradon nigroviridis                                                                                                                                                                                                                                                                                                                                                                                                                                                 |                                    |
|                       | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetradon.                                                                                                                                                                                                                                        |                                    |
| REFERENCE             | 1 (bases 1 to 1081)                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                    |
| AUTHORS               | Roest Crolius,H., Jallou,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Winkler,P., Brotlier,P., Quetier,F., Saurin,W. and Weissbach,J.                                                                                                                                                                                                                                                                                                                |                                    |
| TITLE                 | Estimate of human gene number provided by genome-wide analysis using Tetradon nigroviridis DNA sequence                                                                                                                                                                                                                                                                                                                                                               |                                    |
| JOURNAL               | Nat. Genet. 25 (2), 235-238 (2000)                                                                                                                                                                                                                                                                                                                                                                                                                                    |                                    |
| MEDLINE               | 20296633                                                                                                                                                                                                                                                                                                                                                                                                                                                              |                                    |
| REFERENCE             | 2 (bases 1 to 1081)                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                    |
| AUTHORS               | Fischer,C., Bouneau,L., Ballault,A., Quetier,F., Saurin,W., Bernot,A. and Weissbach,J.                                                                                                                                                                                                                                                                                                                                                                                |                                    |
| TITLE                 | Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradon nigroviridis                                                                                                                                                                                                                                                                                                                                                         |                                    |

| FEATURES                                                                  | SOURCE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
|---------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| JOURNAL<br>MEDLINE<br>REFERENCE<br>AUTHORS<br>TITLE<br>JOURNAL<br>COMMENT | Genome Res. 10 (7), 939-949 (2000)<br>20359837<br>3 (bases 1 to 1081)<br>Genoscope.<br>Direct Submission<br>Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases<br>This sequence is a single read and was generated as part of a large<br>scale clone-end and sequencing project of the Tetraodon nigroviridis<br>genome. For more information, please take a look at<br><a href="http://www.genoscope.cns.fr/tetraodon">http://www.genoscope.cns.fr/tetraodon</a> .                                                                                                                                                                          |
| FEATURES                                                                  | location/Qualifiers                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| SOURCE                                                                    | 1..1081<br>/organism="Tetraodon nigroviridis"<br>/db_xref="taxon:99883"<br>/clone="046L22"<br>/clone_lib="A"<br>/note="Genoscope sequence ID : C0NA046P1C1-end : T7"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| BASE COUNT                                                                | 269 a 256 c 267 g 282 t 7 others                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| ORIGIN                                                                    |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| Query Match                                                               | 3.0%; Score 18; DB 222; Length 1081;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| Best Local Similarity                                                     | 100.0%; Prod. No. 78;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| Matches                                                                   | 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| QY                                                                        | 114 acagcagccagcccaaa 131<br>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| Db                                                                        | 123 ACAGCAGCCAGCCCAAA 106                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| RESULT 45                                                                 |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| AK006925                                                                  | AK006925 1101 bp mRNA HTC 08-FEB-2001                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| LOCUS                                                                     | Mus musculus adult male testis cDNA, RIKEN full-length enriched                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| DEFINITION                                                                | library, clone:1700069015, full insert sequence.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| ACCESSION                                                                 | AK006925                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| VERSION                                                                   | AK006925.1 GI:12840231                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| KEYWORDS                                                                  | CAP trapper.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| SOURCE                                                                    | Mus musculus (strain:C57BL/6J) adult male testis cDNA to mRNA,<br>clone.lib:RIKEN full-length enriched mouse cDNA library<br>clone:1700069015.<br>Mus musculus<br>Mus musculus<br>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;<br>Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.                                                                                                                                                                                                                                                                                                                           |
| ORGANISM                                                                  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| REFERENCE                                                                 | 1 (sites)<br>Carninci,P. and Hayashizaki,Y.<br>High-efficiency full-length cDNA cloning<br>Methods Enzymol. 303, 19-44 (1999)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| AUTHORS                                                                   | 2 (sites)<br>Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,<br>Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.<br>Normalization and subtraction of cap-trapper-selected cDNAs to<br>prepare full-length cDNA libraries for rapid discovery of new genes<br>Genome Res. 10 (10), 1617-1630 (2000)                                                                                                                                                                                                                                                                                                                       |
| TITLE                                                                     |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| JOURNAL                                                                   | 3 (sites)<br>20499374                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| MEDLINE                                                                   |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| REFERENCE                                                                 |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| AUTHORS                                                                   | Shibata,K., Itoh,M., Atzawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,<br>Kono,H., Akiyama,Y., Nishi,K., Kitsuana,T., Tashiro,H., Itoh,M.,<br>Kikuchi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T.,<br>Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T.,<br>Kashiwagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,<br>Matsuhira,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,<br>Matsura,S., Okazaki,Y., Muramatsu,M., Inoue,Y. and Hayashizaki,Y.<br>RIKEN integrated sequence analysis (RISA) system--384-format<br>sequencing pipeline with 384 multicapillary sequencer<br>Genome Res. 10 (11), 1757-1771 (2000) |
| JOURNAL                                                                   | 4 (sites)<br>20530913                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| MEDLINE                                                                   |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| REFERENCE                                                                 |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| AUTHORS                                                                   | FANTOM Consortium.<br>The RIKEN Genome Exploration Research Group Phase II Team and<br>Functional annotation of a full-length mouse cDNA collection-<br>Nature 409, 685-690 (2001)<br>5 (bases 1 to 1101)                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| TITLE                                                                     |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| JOURNAL                                                                   |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| MEDLINE                                                                   |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| REFERENCE                                                                 |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| AUTHORS                                                                   |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |



Tissue Procurement: ATCC  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM10289 row: j column: 10  
 High quality sequence stop: 28.  
 Location/Qualifiers

## FEATURES

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1. 1481  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4471017"  
 /clone\_1ib="NIH\_MGC\_90"  
 /tissue\_type="adenocarcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: liver; Vector: PCMV-SPORT6; Site: 1: NotI;  
 Site: 2: SalI; Cloned unidirectionally; oligo-dT primed.  
 Average insert size 1.7 kb. Library enriched for  
 full-length clones and constructed by Life Technologies.  
 Note: this is a NIH-MGC Library."  
 BASE COUNT 460 a 355 c 326 g 340 t  
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OY 539 aaccacagagagaagaa 556  
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 DB 1371 AACCAACAGACAGAGAA 1388

## RESULT 48

A1701300/c

LOCUS

DEFINITION

A1701300 164 bp mRNA EST 17-DEC-1999  
 w659h07.x1 NCI CGAP Panl Homo sapiens cDNA clone IMAGE:2322973 3'  
 similar to gb:M1606 PHOSPHORYLASE B KINASE GAMMA CATALYTIC CHAIN,  
 TESTIS (HOMAN);, mRNA sequence.

ACCESSION

A1701300

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT

Email

Life Technologies catalog #

DNA Sequencing by

found through the

www-bio.llnl.gov/bbrp/image/image.html

Insert Length

Std Error

Seq primer

High quality sequence stop

Location/Qualifiers

1. 164

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:2322973"

/clone\_1ib="NCI CGAP Panl"

/tissue\_type="adenocarcinoma"

/lab\_host="DH10B"

/note="Organ: pancreas; Vector: PCMV-SPORT6; Site: 1: SalI;  
 Site: 2: NotI; Cloned unidirectionally. Primer: Oligo dT."

Average insert size 1.72 kb. Life Technologies catalog #:  
 11548-013"  
 BASE COUNT 34 a 40 c 53 g 36 t 1 others  
 ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 222 tgcgtacccctgcacat 238  
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 DB 43 TCGTCATCCCTGCAT 27

## RESULT 49

AA002343

LOCUS

DEFINITION

AA002343 165 bp mRNA EST 19-JUL-1996  
 mg42a03.r1 Soares mouse embryo NBME13.5 14.5 Mus musculus cDNA  
 clone IMAGE:426412 5', mRNA sequence.

ACCESSION

AA002343

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.

1 (bases 1 to 165)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Gelsel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and

Waterston, R.

The WashU-HM Mouse EST Project

Unpublished (1996)

Contact: Maria M/Mouse EST Project

WashU-HM Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@wustl.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:260964

Seq primer: mob.REGA+ET

High quality sequence stop: 156.

Location/Qualifiers

1. 165

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="IMAGE:426412"

/clone\_1ib="Soares mouse embryo NBME13.5 14.5"

/sex="unknown"

/tissue\_type="embryo"

/dev\_stage="13.5-14.5dpc total fetus"

/lab\_host="DH10B"

/note="Vector: pRT3D-Pac (Pharmacia) with a modified

polylinker; Site: 1: Not I; Site: 2: Eco RI; 1st strand cDNA

was primed with a Not I - oligo(dT) primer 15'

TGTTCACATCTGAGAGCGGCGCGCGGAAATTTT

T 3'1, on equal amounts of mRNA from 2 13.5dpc and 2

14.5dpc embryos (total RNA provided by Minoru Ko, Wayne

State Univ., from 2 j; double-stranded cDNA was ligated to

Eco RI adaptors (Pharmacia), digested with Not I and

cloned into the Not I and Eco RI sites of the modified

pRT3 vector. Library went through one round of

normalization, and was constructed by Bento Soares and

M. Fatima Bonaldo.

BASE COUNT 52 a 38 c 47 g 28 t

ORIGIN

Query Match 2.9%; Score 17; DB 1; Length 165;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 aacagcagccagcccaa 129  
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 Db 50 AACAGCAGCCAGCCCAA 66

QY 113 aacagcagccagcccaa 129  
 |||  
 Db 115 AACAGCAGCCAGCCCAA 131

Search completed: September 21, 2001, 03:16:32  
 Job time: 9108 sec

## RESULT 50

AA042040

LOCUS AA042040 206 bp mRNA EST 03-SEP-1996  
 DEFINITION mJ06a07.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA  
 clone IMAGE:475284 5', mRNA sequence.

ACCESSION AA042040

VERSION AA042040.1 GI:1520230

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;  
 1 (bases 1 to 206)  
 Mairra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
 Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,  
 Schellenberg, K., Stepien, M., Tan, F., Underwood, K., Moore, B.,  
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
 Waterston, R.

TITLE The WashU-HHMI Mouse EST Project  
 JOURNAL Unpublished (1996)  
 COMMENT Contact: Marra M/Mouse EST Project  
 WashU-HHMI Mouse EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810

Email: mouseest@wustl.edu  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 MGI:286028  
 Seq primer: -28M13 rev2 from Amersham  
 High quality sequence stop: 151.

## FEATURES

Location/Qualifiers

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 /strain="C57Bl/6J"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:475284"  
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 /sex="unknown"  
 /tissue\_type="embryo"  
 /dev\_stage="13.5-14.5dpc total fetus"  
 /lab\_host="DH10B"  
 /note="Vector: pT73D-PAC (Pharmacia) with a modified  
 polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA  
 was primed with a Not I - 01190(dt) primer [5'  
 TGTTCACATCGAAGCGAGCGCGCGGCAATTTTTTTTTTTTTTTT  
 T 3']; on equal amounts of RNA from 2 13.5dpc and 2  
 14.5dpc embryos [total RNA provided by Minoru Ko, Wayne  
 State Univ., from 2 ]; double-stranded cDNA was ligated to  
 Eco RI adaptors (Pharmacia), digested with Not I and  
 cloned into the Not I and Eco RI sites of the modified  
 pT73 vector. Library went through one round of  
 normalization, and was constructed by Bento Soares and  
 M. Fatima Bonaldo."

BASE COUNT 52 a 47 c 68 g 39 t  
 ORIGIN

Query Match 2.9%; Score 17; DB 1; Length 206;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|       |    |     |      |   |                   |                   |       |    |     |      |   |                    |                   |
|-------|----|-----|------|---|-------------------|-------------------|-------|----|-----|------|---|--------------------|-------------------|
| 831   | 13 | 2.2 | 2070 | 1 | US-08-028-463-13  | Sequence 13, Appl | c 904 | 13 | 2.2 | 2395 | 4 | US-08-446-935-7    | Sequence 7, Appl  |
| 832   | 13 | 2.2 | 2070 | 1 | US-08-461-836-13  | Sequence 13, Appl | 905   | 13 | 2.2 | 2400 | 1 | US-07-648-796A-15  | Sequence 15, Appl |
| 833   | 13 | 2.2 | 2070 | 1 | US-08-463-470-7   | Sequence 7, Appl  | 906   | 13 | 2.2 | 2400 | 1 | US-08-486-013-69   | Sequence 69, Appl |
| 834   | 13 | 2.2 | 2074 | 1 | US-08-414-685-1   | Sequence 1, Appl  | 907   | 13 | 2.2 | 2408 | 2 | US-08-482-279-69   | Sequence 69, Appl |
| 835   | 13 | 2.2 | 2081 | 2 | US-09-096-982-7   | Sequence 7, Appl  | 908   | 13 | 2.2 | 2408 | 2 | US-08-342-268-69   | Sequence 69, Appl |
| 836   | 13 | 2.2 | 2081 | 2 | US-08-653-650A-7  | Sequence 7, Appl  | 909   | 13 | 2.2 | 2408 | 3 | US-09-015-968-69   | Sequence 69, Appl |
| c 837 | 13 | 2.2 | 2092 | 4 | US-09-318-978-1   | Sequence 1, Appl  | 910   | 13 | 2.2 | 2420 | 2 | US-08-330-123A-3   | Sequence 3, Appl  |
| 838   | 13 | 2.2 | 2096 | 5 | PCT-US94-08119-9  | Sequence 9, Appl  | c 911 | 13 | 2.2 | 2427 | 2 | US-08-678-0139A-39 | Sequence 39, Appl |
| 839   | 13 | 2.2 | 2096 | 5 | PCT-US94-12913A-9 | Sequence 9, Appl  | c 912 | 13 | 2.2 | 2434 | 1 | US-08-630-592-3    | Sequence 3, Appl  |
| 840   | 13 | 2.2 | 2096 | 5 | PCT-US94-12913A-9 | Sequence 9, Appl  | c 913 | 13 | 2.2 | 2434 | 1 | US-08-714-991-3    | Sequence 3, Appl  |
| 841   | 13 | 2.2 | 2099 | 1 | US-08-094-533B-9  | Sequence 9, Appl  | c 914 | 13 | 2.2 | 2434 | 3 | US-09-032-365A-3   | Sequence 3, Appl  |
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| 843   | 13 | 2.2 | 2099 | 1 | US-08-444-393-9   | Sequence 9, Appl  | 916   | 13 | 2.2 | 2464 | 2 | US-07-863-169A-4   | Sequence 4, Appl  |
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| 845   | 13 | 2.2 | 2099 | 2 | US-08-799-913-9   | Sequence 9, Appl  | 918   | 13 | 2.2 | 2464 | 3 | US-07-935-087-4    | Sequence 4, Appl  |
| 846   | 13 | 2.2 | 2099 | 2 | US-08-711-893-9   | Sequence 9, Appl  | 919   | 13 | 2.2 | 2464 | 5 | PCT-US93-08062-4   | Sequence 4, Appl  |
| c 847 | 13 | 2.2 | 2099 | 2 | US-08-142-368A-25 | Sequence 25, Appl | 920   | 13 | 2.2 | 2472 | 1 | US-08-221-750A-2   | Sequence 2, Appl  |
| 848   | 13 | 2.2 | 2099 | 2 | US-09-150-200-9   | Sequence 9, Appl  | c 921 | 13 | 2.2 | 2472 | 1 | US-08-221-750A-2   | Sequence 2, Appl  |
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| c 850 | 13 | 2.2 | 2099 | 3 | US-08-967-727-25  | Sequence 25, Appl | c 923 | 13 | 2.2 | 2483 | 2 | US-08-687-706-1    | Sequence 1, Appl  |
| 851   | 13 | 2.2 | 2099 | 4 | US-09-452-370-9   | Sequence 9, Appl  | 924   | 13 | 2.2 | 2487 | 1 | US-08-377-292-1    | Sequence 1, Appl  |
| c 852 | 13 | 2.2 | 2099 | 4 | US-08-037-230D-25 | Sequence 25, Appl | 925   | 13 | 2.2 | 2496 | 1 | US-08-073-384C-2   | Sequence 2, Appl  |
| 853   | 13 | 2.2 | 2101 | 4 | US-09-276-531-21  | Sequence 21, Appl | 926   | 13 | 2.2 | 2496 | 1 | US-08-254-359A-2   | Sequence 2, Appl  |
| c 854 | 13 | 2.2 | 2103 | 3 | US-08-931-952-1   | Sequence 1, Appl  | 927   | 13 | 2.2 | 2496 | 1 | US-08-483-043-2    | Sequence 2, Appl  |
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| c 856 | 13 | 2.2 | 2103 | 3 | PCT-US95-08560-1  | Sequence 1, Appl  | 929   | 13 | 2.2 | 2496 | 2 | US-08-471-066B-2   | Sequence 2, Appl  |
| c 857 | 13 | 2.2 | 2122 | 5 | US-08-738-168B-4  | Sequence 4, Appl  | 930   | 13 | 2.2 | 2496 | 2 | US-08-484-956-2    | Sequence 2, Appl  |
| c 858 | 13 | 2.2 | 2150 | 1 | US-08-299-849B-24 | Sequence 24, Appl | 931   | 13 | 2.2 | 2496 | 2 | US-08-757-653-2    | Sequence 2, Appl  |
| c 859 | 13 | 2.2 | 2150 | 2 | US-08-142-368A-24 | Sequence 24, Appl | 932   | 13 | 2.2 | 2496 | 2 | US-08-599-491-2    | Sequence 2, Appl  |
| c 860 | 13 | 2.2 | 215  |   |                   |                   |       |    |     |      |   |                    |                   |







CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Berridge, William P.  
REGISTRATION NUMBER: 30,024  
REFERENCE/DOCKET NUMBER: WPB 36400  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6400  
TELEFAX: 703-836-2787  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-480-917-9

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OY 35 cagccgacgtagctgcgtcct 56  
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Db 1 CAGCCGACGCTAGCTGCTGCT 22

RESULT 3  
US-08-970-269A-32/c  
Sequence 32, Application US/08970269A  
Patent No. 5976803  
GENERAL INFORMATION:  
APPLICANT: Kathryn Meek  
TITLE OF INVENTION: Genetic Test For Equine Severe  
TITLE OF INVENTION: Combined Immunodeficiency Disease  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dr. Benjamin A. Adler  
STREET: 8011 Candle Lane  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple  
OPERATING SYSTEM: Macintosh  
SOFTWARE: Microsoft Word for Macintosh  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/970/269A  
FILING DATE: No. 5976803ember 14, 1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Adler Ph.D., Benjamin A.  
REGISTRATION NUMBER: 35,423  
REFERENCE/DOCKET NUMBER: D5860  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713-777-2321  
TELEFAX: 713-777-6908  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11873 bp  
TYPE: nucleic acid  
STRANDEDNESS: double stranded  
TOPOLOGY: linear  
MOLECULE TYPE:  
DESCRIPTION: other nucleic acid  
HYPOTHETICAL: no  
ANTI-SENSE: no  
ORIGINAL SOURCE:  
FEATURE:  
US-08-970-269A-32

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Db 6446 ACTCTGCCGCTGCTGCAT 6428

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Patent No. 5976803  
GENERAL INFORMATION:  
APPLICANT: Kathryn Meek  
TITLE OF INVENTION: Genetic Test For Equine Severe  
TITLE OF INVENTION: Combined Immunodeficiency Disease  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dr. Benjamin A. Adler  
STREET: 8011 Candle Lane  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple  
OPERATING SYSTEM: Macintosh  
SOFTWARE: Microsoft Word for Macintosh  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/970/269A  
FILING DATE: No. 5976803ember 14, 1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Adler Ph.D., Benjamin A.  
REGISTRATION NUMBER: 35,423  
REFERENCE/DOCKET NUMBER: D5860  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713-777-2321  
TELEFAX: 713-777-6908  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11878 bp  
TYPE: nucleic acid  
STRANDEDNESS: double stranded  
TOPOLOGY: linear  
MOLECULE TYPE:  
DESCRIPTION: other nucleic acid  
HYPOTHETICAL: no  
ANTI-SENSE: no  
ORIGINAL SOURCE:  
FEATURE:  
US-08-970-269A-31

Query Match 3.2%; Score 19; DB 2; Length 11878;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 211 actctgcgcgtgcgtcat 229  
|||||  
Db 6446 ACTCTGCCGCTGCTGCAT 6428

RESULT 5  
US-08-970-269A-28/c  
Sequence 28, Application US/08970269A  
Patent No. 5976803  
GENERAL INFORMATION:  
APPLICANT: Kathryn Meek  
TITLE OF INVENTION: Genetic Test For Equine Severe

```

; TITLE OF INVENTION: Combined Immunodeficiency Disease
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dr. Benjamin A. Adler
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/970,269A
; FILING DATE: No. 5976803ember 14, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler Ph.D., Benjamin A.
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D5860
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-777-2321
; TELEFAX: 713-777-6508
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11883 bp
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: other nucleic acid
; HYPOHETICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; US-08-970-269A-28

Query Match      3.2%; Score 19; DB 2; Length 11883;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 211 actctgcgcgtctgcacat 229
|||||
Db 6449 ACTCTGCCGCTGCTGCAT 6431

RESULT 6
US-08-480-917-5
; Sequence 5, Application US/08480917
; Patent No. 5820864
; GENERAL INFORMATION:
; APPLICANT: PARANHOS-BACCALA, Glaucia
; APPLICANT: LESSENECHAL, Mylene
; APPLICANT: JOLIVET, Michel
; TITLE OF INVENTION: NEW TRYPAPOSOMA CRUZI ANTIGEN, AND GENE
; TITLE OF INVENTION: ENCODING THE LATTER; THEIR APPLICATION TO THE DETECTION OF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oliff & Berridge
; STREET: 700 South Washington Street, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/480,917
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 36400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6400
; TELEFAX: 703-836-2787
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-480-917-5
```

```

Query Match      3.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 tcgggcactgacgcgcgcg 189
|||||
Db 1 TCGGGCAGCTGACGCGCGC 18
```

```

RESULT 7
US-08-480-917-8/c
; Sequence 8, Application US/08480917
; Patent No. 5820864
; GENERAL INFORMATION:
; APPLICANT: PARANHOS-BACCALA, Glaucia
; APPLICANT: LESSENECHAL, Mylene
; APPLICANT: JOLIVET, Michel
; TITLE OF INVENTION: NEW TRYPAPOSOMA CRUZI ANTIGEN, AND GENE
; TITLE OF INVENTION: ENCODING THE LATTER; THEIR APPLICATION TO THE DETECTION OF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oliff & Berridge
; STREET: 700 South Washington Street, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,917
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 36400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6400
; TELEFAX: 703-836-2787
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-480-917-8
```

Query Match 3.0%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 211 actctgcgcctcctcga 228  
|||||  
Db 18 ACTCTGCCGCTGCTGCA 1

RESULT 8  
US-08-454-557C-50  
Sequence 50, Application US/08454557C  
Patent No. 5830670

GENERAL INFORMATION:  
APPLICANT: de la Monte, Suzanne  
APPLICANT: Wands, Jack R.  
TITLE OF INVENTION: Neutral Thread Protein Gene Expression and Detection  
TITLE OF INVENTION: of Alzheimer's Disease  
NUMBER OF SEQUENCES: 121  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Avenue, Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-3934

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/454,557C  
FILING DATE: 30-MAY-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Ludwig, Steven R.  
REGISTRATION NUMBER: 36,203  
REFERENCE/DOCKET NUMBER: 0609,3840003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2520 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both

US-08-454-557C-50

Query Match 3.0%; Score 18; DB 2; Length 2520;  
Best Local Similarity 100.0%; Pred. No. 3.6;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 230 cccctgcatacccccctg 247  
|||||  
Db 298 CCCCTGCATCACCCCTG 315

RESULT 9  
US-08-340-426D-50  
Sequence 50, Application US/08340426D  
Patent No. 5948634

GENERAL INFORMATION:  
APPLICANT: de la Monte, Suzanne  
APPLICANT: Wands, Jack R.  
TITLE OF INVENTION: Neutral Thread Protein Gene Expression and Detection  
TITLE OF INVENTION: of Alzheimer's Disease  
NUMBER OF SEQUENCES: 121  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Sterne, Kessler, Goldstein & Fox P.L.L.C.

STREET: 1100 New York Avenue, Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-3934

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/340,426D  
FILING DATE: 14-NOV-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ludwig, Steven R.  
REGISTRATION NUMBER: 36,203  
REFERENCE/DOCKET NUMBER: 0609,3840002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2520 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both

US-08-340-426D-50

Query Match 3.0%; Score 18; DB 2; Length 2520;  
Best Local Similarity 100.0%; Pred. No. 3.6;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 230 cccctgcatacccccctg 247  
|||||  
Db 298 CCCCTGCATCACCCCTG 315

RESULT 10  
US-08-450-673C-50  
Sequence 50, Application US/08450673C  
Patent No. 5948888

GENERAL INFORMATION:  
APPLICANT: de la Monte, Suzanne  
APPLICANT: Wands, Jack R.  
TITLE OF INVENTION: Neutral Thread Protein Gene Expression and Detection  
TITLE OF INVENTION: of Alzheimer's Disease  
NUMBER OF SEQUENCES: 121  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Avenue, Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-3934

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,673C  
FILING DATE: 30-MAY-1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Ludwig, Steven R.  
REGISTRATION NUMBER: 36,203  
REFERENCE/DOCKET NUMBER: 0609,3840004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 50:

US-08-450-673C-50

SEQUENCE CHARACTERISTICS:  
LENGTH: 2520 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
US-08-450-673C-50

Query Match 3.0%; Score 18; DB 2; Length 2520;  
Best Local Similarity 100.0%; Pred. No. 3.6;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 230 cccctgcatcacccctg 247  
|||||  
DB 298 CCCCTGCATCACCCCTG 315

RESULT 11  
PCT-US95-17111A-50  
Sequence 50, Application PC/TUS9517111A

GENERAL INFORMATION:  
APPLICANT: de la Monte, Suzanne  
APPLICANT: Wands, Jack R.  
TITLE OF INVENTION: Neural Thread Protein Gene Expression and  
TITLE OF INVENTION: Detection of Alzheimer's Disease  
NUMBER OF SEQUENCES: 121  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Avenue, Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/17111A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/340,426  
FILING DATE: 14-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ludwig, Steven R.  
REGISTRATION NUMBER: 36,203  
REFERENCE/DOCKET NUMBER: 0609.3840002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2520 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
PCT-US95-17111A-50

Query Match 3.0%; Score 18; DB 5; Length 2520;  
Best Local Similarity 100.0%; Pred. No. 3.6;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 230 cccctgcatcacccctg 247  
|||||  
DB 298 CCCCTGCATCACCCCTG 315

RESULT 12  
US-09-335-409-1/C  
Sequence 1, Application US/09335409

Patent No. 6121029  
GENERAL INFORMATION:  
APPLICANT: Schnupp, Thomas  
APPLICANT: Ligon, James  
APPLICANT: Molnar, Istvan  
APPLICANT: Zirkle, Ross  
APPLICANT: Zirkle, Ross  
APPLICANT: Cyr, Devon  
APPLICANT: Goerlach, Joern  
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES  
FILE REFERENCE: 4-30582A  
CURRENT APPLICATION NUMBER: US/09/335,409  
CURRENT FILING DATE: 1999-06-17  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 1  
LENGTH: 68750  
TYPE: DNA  
ORGANISM: Sorangium cellulosum  
US-09-335-409-1

Query Match 3.0%; Score 18; DB 3; Length 68750;  
Best Local Similarity 100.0%; Pred. No. 3.5;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 517 tgcgtccacacgcgcg 534  
|||||  
DB 19020 TCGCTCCACACGCCGC 19003

RESULT 13  
US-08-692-787-4  
Sequence 4, Application US/08692787  
Patent No. 5882864  
GENERAL INFORMATION:  
APPLICANT: An, Gang  
APPLICANT: O'Hara, S. Mark  
APPLICANT: Ralph, David  
APPLICANT: Veltl, Robert  
TITLE OF INVENTION: BIOMARKERS AND TARGETS FOR DIAGNOSIS,  
TITLE OF INVENTION: PROGNOSIS AND MANAGEMENT OF PROSTATE  
DISEASE  
NUMBER OF SEQUENCES: 82  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: United States of America  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/692,787  
FILING DATE: Concurrently Herewith  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Corder, Timothy S.  
REGISTRATION NUMBER: 38,414  
REFERENCE/DOCKET NUMBER: UROC:012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 673 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-692-787-4

Query Match 2.9%; Score 17; DB 2; Length 673;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 537 gaaccacagagagaa 553  
|||||  
Db 542 GAACCAACAGAGAGAG 558

## RESULT 14

US-09-097-199-4  
; Sequence 4, Application US/09097199  
; Patent No. 6218529  
; GENERAL INFORMATION:  
; APPLICANT: An, Gang  
; APPLICANT: O'Hara, S. Mark  
; APPLICANT: Ralph, David  
; APPLICANT: Veltri, Robert  
; TITLE OF INVENTION: BIOMARKERS AND TARGETS FOR DIAGNOSIS,  
; TITLE OF INVENTION: PROGNOSIS AND MANAGEMENT OF PROSTATE DISEASE  
; NUMBER OF SEQUENCES: 87  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/097,199  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/692,787  
; FILING DATE: 31-JUL-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Nakashima, Richard A.  
; REGISTRATION NUMBER: P-42,023  
; REFERENCE/DOCKET NUMBER: UROC:018  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (512) 474-7577  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 673 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-09-097-199-4

Query Match 2.9%; Score 17; DB 4; Length 673;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 537 gaaccacagagagaa 553  
|||||  
Db 542 GAACCAACAGAGAGAG 558

## RESULT 15

US-08-072-610-1  
; Sequence 1, Application US/08072610  
; Patent No. 5532133  
; GENERAL INFORMATION:  
; APPLICANT: Barnwell, John

;; TITLE OF INVENTION: Plasmodium vivax Blood Stage Antigens,  
;; TITLE OF INVENTION: Monoclonal Antibodies, and Diagnostic Assays  
;; NUMBER OF SEQUENCES: 2  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Darby and Darby  
;; STREET: 805 Third Ave.  
;; CITY: New York  
;; STATE: New York  
;; COUNTRY: USA  
;; ZIP: 10022-7513

## COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/072,610  
;; FILING DATE: 19930602  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Gogoris, Adda  
;; REGISTRATION NUMBER: 29,714  
;; REFERENCE/DOCKET NUMBER: 5986/07686  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212)527-7700  
;; TELEFAX: (212)753-6237  
;; TELEX: 236687  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 3337 base pairs  
;; TYPE: NUCLEIC ACID  
;; STRANDEDNESS: double  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
;; ORIGINAL SOURCE:  
;; ORGANISM: Plasmodium vivax  
;; IMMEDIATE SOURCE:  
;; CLONE: PvMB3.3.1  
;; US-08-072-610-1

Query Match 2.9%; Score 17; DB 1; Length 3337;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 539 aaccacagagagagaa 555  
|||||  
Db 2029 AACCAACAGAGAGAGAA 2045

## RESULT 16

US-08-719-822B-1  
; Sequence 1, Application US/08719822B  
; Patent No. 5874527  
; GENERAL INFORMATION:  
; APPLICANT: Barnwell, John  
; TITLE OF INVENTION: Plasmodium vivax Blood Stage Antigens  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Darby and Darby  
; STREET: 805 Third Ave.  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10022-7513  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/719,822B  
FILING DATE: 09/30/96  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Gogoris, Adda  
REGISTRATION NUMBER: 29,714  
REFERENCE/DOCKET NUMBER: 5986/17686US2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)527-7700  
TELEFAX: (212)753-6237  
TELEX: 236687  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3337 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Plasmodium vivax  
IMMEDIATE SOURCE:  
CLONE: PVM3.3.1  
US-08-719-822B-1

Query Match 2.9%; Score 17; DB 2; Length 3337;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 539 aaccaacagagaaga 555  
|||||  
Db 2029 AACCAACAGAGAAGAA 2045

RESULT 17  
US-09-092-458-1  
Sequence 1, Application US/09092458  
Patent No. 6231861  
GENERAL INFORMATION:  
APPLICANT: Barnwell, John  
TITLE OF INVENTION: Plasmodium vivax Blood Stage Antigens,  
TITLE OF INVENTION: Monoclonal Antibodies, and Diagnostic Assays  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Darby and Darby  
STREET: 805 Third Ave.  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022-7513  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/092,458  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/719,821  
FILING DATE: 09/30/96  
ATTORNEY/AGENT INFORMATION:  
NAME: Gogoris, Adda  
REGISTRATION NUMBER: 29,714  
REFERENCE/DOCKET NUMBER: 5986/17686US3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)527-7700  
TELEFAX: (212)753-6237  
TELEX: 236687  
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
LENGTH: 3337 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Plasmodium vivax  
IMMEDIATE SOURCE:  
CLONE: PVM3.3.1  
US-09-092-458-1

Query Match 2.9%; Score 17; DB 4; Length 3337;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 539 aaccaacagagaaga 555  
|||||  
Db 2029 AACCAACAGAGAAGAA 2045

RESULT 18  
US-08-142-897-1/C  
Sequence 1, Application US/08142897  
Patent No. 5447852  
GENERAL INFORMATION:  
APPLICANT: Friedman, Jeffrey S.  
APPLICANT: Weissman, Irving L.  
TITLE OF INVENTION: No. 5447852el Cyclophilins, Associating Proteins  
TITLE OF INVENTION: and Uses  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Tracy J. Dunn  
STREET: One Market Plaza, Stewart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/142,897  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/005,917  
FILING DATE: 15-JAN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/740,375  
FILING DATE: 05-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Dunn, Tracy D.  
REGISTRATION NUMBER: 34,587  
REFERENCE/DOCKET NUMBER: 5490A-92-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 41 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Primer  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 1..41

OTHER INFORMATION: /note="Adaptor-Primer"  
US-08-142-897-1

Query Match 2.7%; Score 16; DB 1; Length 41;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 554 aaagcgctcgcgcc 569  
Db 27 AAAGCGCTCGCGCC 12

## RESULT 19

US-08-628-039-9/c  
Sequence 9, Application US/08628039  
Patent No. 5942660  
GENERAL INFORMATION:  
APPLICANT: Gruys, Kenneth J.  
APPLICANT: Misky, Timothy A.  
APPLICANT: Kishore, Ganesh M.  
APPLICANT: Slater, Steven C.  
APPLICANT: Padgett, Stephen R.  
APPLICANT: Stark, David M.  
APPLICANT: Hinchee, Maud A. W.  
APPLICANT: Clemente, Thomas E.  
APPLICANT: Connor-Ward, Dannelte V.  
APPLICANT: Fedele, Mary J.  
APPLICANT: Fry, Joyce E.  
APPLICANT: Howe, Arlene R.  
APPLICANT: Rozman, Renee J.  
TITLE OF INVENTION: Methods of Optimizing Substrate Pools and  
TITLE OF INVENTION: Biosynthesis of poly-B-hydroxybutyrate-co-poly-B-hydroxyvalerate  
TITLE OF INVENTION: In Bacteria and Plants  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Gary M. Bond, Monsanto Company, A3SB  
STREET: 800 No. 594260th Lindbergh Boulevard  
CITY: St. Louis  
STATE: Missouri  
COUNTRY: USA  
ZIP: 63167  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/628,039  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE: 13-MAR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Bond, Gary  
REGISTRATION NUMBER: 29,283  
REFERENCE/DOCKET NUMBER: 38-21(13585)A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314)694-3412  
TELEFAX: (314)695-5435  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1185 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-628-039-9

Query Match 2.7%; Score 16; DB 2; Length 1185;  
Best Local Similarity 100.0%; Pred. No. 39;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 506 ccagcgcgctcgctc 521  
Db 544 CCAGCGCGGCTCGCTC 529

## RESULT 20

US-08-912-205-9/c  
Sequence 9, Application US/08912205  
Patent No. 6091002  
GENERAL INFORMATION:  
APPLICANT: Asrar, Jawed  
APPLICANT: Misky, Timothy A.  
APPLICANT: Shah, Devang T.  
TITLE OF INVENTION: Polyhydroxyalkanoates of narrow molecular  
TITLE OF INVENTION: Weight distribution prepared in transgenic plants  
NUMBER OF SEQUENCES: 11  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/912,205  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/673,388  
FILING DATE: 28-JUN-1996  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1185 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-912-205-9

Query Match 2.7%; Score 16; DB 3; Length 1185;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 506 ccagcgcgctcgctc 521  
Db 544 CCAGCGCGGCTCGCTC 529

## RESULT 21

US-09-440-400-9/c  
Sequence 9, Application US/09440400  
Patent No. 6228623  
GENERAL INFORMATION:  
APPLICANT: Asrar, Jawed  
APPLICANT: Misky, Timothy A.  
APPLICANT: Shah, Devang T.  
TITLE OF INVENTION: Polyhydroxyalkanoates of narrow molecular  
TITLE OF INVENTION: Weight distribution prepared in transgenic plants  
NUMBER OF SEQUENCES: 11  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/440,400  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/912,205  
FILING DATE:  
INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:  
LENGTH: 1185 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-440-400-9

Query Match 2.7%; Score 16; DB 4; Length 1185;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 506 ccagcgcgccctgc 521  
|||||  
DB 544 CCAGCGCGCCCTGCTC 529

## RESULT 22

US-09-031-059-2  
Sequence 2, Application US/09031059  
Patent No. 5948659

## GENERAL INFORMATION:

APPLICANT: KATO, NOBUO  
APPLICANT: SAKAI, YASUYOSHI  
APPLICANT: TANI, YOSHIKI  
APPLICANT: FUKUYA, HIROSHI  
TITLE OF INVENTION: RECOMBINANT FRUCTOSYL AMINO ACID  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH  
STREET: PO BOX 747  
CITY: FALLS CHURCH  
STATE: VA  
COUNTRY: USA  
ZIP: 22040-0747

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/031,059  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/899,172  
FILING DATE:

## ATTORNEY/AGENT INFORMATION:

NAME: WEINER, MARC S  
REGISTRATION NUMBER: 32,181  
REFERENCE/DOCKET NUMBER: 0020-4253P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 205-8000  
TELEFAX: (703) 205-8050  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1314 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA to mRNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1311  
US-09-031-059-2

Query Match 2.7%; Score 16; DB 2; Length 1314;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 351 taatgtcaccacaag 366

|||||  
DB 1281 TAAATGTCACCAAGG 1296

## RESULT 23

US-07-952-817-10  
Sequence 10, Application US/07952817  
Patent No. 5356796

## GENERAL INFORMATION:

APPLICANT: Keller, John W.  
TITLE OF INVENTION: A Repressor Protein and Gene for Regulating  
EXPRESSION OF POLYPEPTIDES AND ITS USE IN THE PREPARATION OF  
TITLE OF INVENTION: 2,2-Dialkylglycine Decarboxylase of Pseudomonas Cepacia  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESS: Dunner  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
COUNTRY: US  
ZIP: 20005-3315

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/952,817  
FILING DATE: 19920928  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 01120.0002-01000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400

## INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:  
LENGTH: 1411 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-07-952-817-10

Query Match 2.7%; Score 16; DB 1; Length 1411;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 459 caatggccgacctgtg 474  
|||||  
DB 372 CAATGGCCGACCTGTG 387

## RESULT 24

US-07-5210025-3

APPLICANT: KELLER, JOHN W.  
TITLE OF INVENTION: REPRESSOR PROTEIN GENE FOR REGULATING  
EXPRESSION OF POLYPEPTIDES AND ITS USE IN THE PREPARATION OF  
2,2-DIALKYLGLYCINE DECARBOXYLASE OF PSEUDOMONAS CEPACIA  
NUMBER OF SEQUENCES: 18  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/501,814  
FILING DATE: 30-MAR-1990

SEQ ID NO:3:  
LENGTH: 1411  
US-07-5210025-3



Query Match 2.7%; Score 16; DB 6; Length 1411;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 459 caatgcccgcactgtg 474  
|||||  
Db 372 caatgcccgcactgtg 387

## RESULT 25

US-08-360-606B-29/c  
Sequence 29, Application US/08360606B  
Patent No. 5919617  
GENERAL INFORMATION:  
APPLICANT: Jnanendra K. Bhattacharjee  
APPLICANT: Richard C. Garrard  
APPLICANT: Paul L. Skatrud  
APPLICANT: Robert P. Peery  
TITLE OF INVENTION: Methods and Reagents for  
TITLE OF INVENTION: Detecting Fungal Pathogens in a  
TITLE OF INVENTION: Biological Sample  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
STREET: 300 S. Wacker Drive Suite 3200  
CITY: Chicago  
STATE: Illinois  
COUNTRY: U.S.A.  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MS Word 7.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/360,606B  
FILING DATE: December 21, 1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Berghoff, Paul H.  
REGISTRATION NUMBER: 30,243  
REFERENCE/DOCKET NUMBER: 94,319  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312)913-0001  
TELEFAX: (312)913-0002  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1856 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Saccharomyces cerevisiae  
US-08-360-606B-29

Query Match 2.7%; Score 16; DB 2; Length 1856;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 gtagtgcgcacgcga 154  
|||||  
Db 167 gtagtgcgcacgcga 152

## RESULT 26

US-08-673-388-9/c  
Sequence 9, Application US/08673388  
Patent No. 5958745  
GENERAL INFORMATION:  
APPLICANT: Gruys, Kenneth J.  
APPLICANT: Mitsky, Timothy A.

APPLICANT: Kishore, Ganesh M.  
APPLICANT: Slater, Steven C.  
APPLICANT: Padgett, Stephen R.  
APPLICANT: Stark, David M.  
APPLICANT: Hinchee, Maud A. W.  
APPLICANT: Clemente, Thomas E.  
APPLICANT: Connor-Ward, Dannelte V.  
APPLICANT: Fedele, Mary J.  
APPLICANT: Fry, Joyce E.  
APPLICANT: Howe, Arlene R.  
APPLICANT: Rozman, Renee J.

TITLE OF INVENTION: Methods of Optimizing Substrate Pools and  
TITLE OF INVENTION: Biosynthesis of Poly-B-hydroxybutyrate-co-poly-B-hydroxyval  
TITLE OF INVENTION: in Bacteria and Plants  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Charles E. Cohen, Monsanto Company, B&F  
STREET: 700 Chesterfield Parkway No. 5958745th  
CITY: St. Louis  
STATE: Missouri  
COUNTRY: USA  
ZIP: 63198

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/673,388  
FILING DATE: 13-MAR-1996  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Cohen, Charles E.  
REGISTRATION NUMBER: 34,565  
REFERENCE/DOCKET NUMBER: 38-21(13618)A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314)537-6224  
TELEFAX: (314)537-6047  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1864 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-673-388-9

Query Match 2.7%; Score 16; DB 2; Length 1864;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches <16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 506 ccagcgcgcgcctcgtc 521  
|||||  
Db 1073 CCAGCGCGCGCTCGTC 1058

## RESULT 27

US-08-614-877-9/c  
Sequence 9, Application US/08614877  
Patent No. 5959179  
GENERAL INFORMATION:  
APPLICANT: Gruys, Kenneth J.  
APPLICANT: Mitsky, Timothy A.  
APPLICANT: Kishore, Ganesh M.  
APPLICANT: Slater, Steven C.  
APPLICANT: Padgett, Stephen R.  
APPLICANT: Stark, David M.  
APPLICANT: Hinchee, Maud A. W.  
APPLICANT: Clemente, Thomas E.  
APPLICANT: Connor-Ward, Dannelte V.  
APPLICANT: Fedele, Mary J.  
APPLICANT: Fry, Joyce E.

APPLICANT: Howe, Arlene R.  
APPLICANT: Rozman, Renee J.  
TITLE OF INVENTION: Methods of Optimizing Substrate Pools and  
TITLE OF INVENTION: Biosynthesis of Poly-B-hydroxybutyrate-co-poly-B-hydroxyvalerate  
TITLE OF INVENTION: In Bacteria and Plants  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Charles E. Cohen, Monsanto Company, BBAF  
STREET: 700 Chesterfield Parkway No. 5959179th  
CITY: St. Louis  
STATE: Missouri  
COUNTRY: USA  
ZIP: 63198  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/614,877  
FILING DATE: 13-MAR-1996  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Cohen, Charles E.  
REGISTRATION NUMBER: 34,565  
REFERENCE/DOCKET NUMBER: 38-21(10695)A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314)537-6224  
TELEFAX: (314)537-6047  
INFORMATION FOR SEQ. ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1864 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-614-877-9

Query Match 2.7%; Score 16; DB 2; Length 1864;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 506 ccagcgcgctgc 521  
|||||

DB 1073 CCAGCGCGCTGC 1058

RESULT 28  
US-08-864-038A-1  
Sequence 1, Application US/08864038A  
Patent No. 6001592  
GENERAL INFORMATION:  
APPLICANT: Kunio NAKASHIMA et al.  
TITLE OF INVENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR  
CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID  
TITLE OF INVENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING  
TITLE OF INVENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: 812-5 Hirano  
STREET: Isshinuden  
CITY: Tsu-city  
STATE: Mie-prefecture  
COUNTRY: JAPAN  
ZIP: 514-01  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Microsoft Windows 95  
SOFTWARE: Word Perfect 6.1  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/864,038A  
FILING DATE: May 28, 1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-184459  
FILING DATE: 15-July-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: C. Bruce Hamburg  
REGISTRATION NUMBER: 22,389  
REFERENCE/DOCKET NUMBER: F-5610  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)986-2340  
TELEFAX: (212)953-7733  
INFORMATION FOR SEQ. ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2214  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
ORIGINAL SOURCE:  
ORGANISM: Pinctada fucata  
CELL TYPE: mantle epithelial cell  
US-08-864-038A-1

Query Match 2.7%; Score 16; DB 3; Length 2214;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 215 ctgcgcgtgc 230  
|||||

DB 1544 CTGCCTGCCTGCATC 1559

RESULT 29  
US-09-036-987A-25  
Sequence 25, Application US/09036987A  
Patent No. 6143526  
GENERAL INFORMATION:  
APPLICANT: Baltz, Richard H.  
APPLICANT: Broughton, Mary C.  
APPLICANT: Crawford, Kathryn P.  
APPLICANT: Madduri, Krishnamurthy  
APPLICANT: Merlo, Donald J.  
APPLICANT: Treadway, Patil J.  
APPLICANT: Turner, Jan R.  
APPLICANT: Waldron, Clive  
TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dow Agrosciences LLC Patent Department  
STREET: 9330 Zionsville Road  
CITY: Indianapolis  
STATE: Indiana  
COUNTRY: USA  
ZIP: 46268  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/036,987A  
FILING DATE: 09-MAR-1998  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Stuart, Donald R.  
REGISTRATION NUMBER: 28,479  
REFERENCE/DOCKET NUMBER: 50,608  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (317)337-4816  
TELEFAX: (317)337-4847  
INFORMATION FOR SEQ. ID NO: 25:

SEQUENCE CHARACTERISTICS:  
LENGTH: 2310 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 88..1077  
NAME/KEY: CDS  
LOCATION: 1165..1992  
US-09-036-987A-25

Query Match 2.7%; Score 16; DB 3; Length 2310;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 395 cgaacaggtctacgac 410  
|||||  
DB 468 CGACGAGGTCTACGAC 483

RESULT 30  
US-08-864-038A-2  
Sequence 2, Application US/08864038A  
Patent No. 6001592

GENERAL INFORMATION:  
APPLICANT: Kunio NAKASHIMA et al.  
TITLE OF INVENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR  
TITLE OF INVENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID  
TITLE OF INVENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING  
TITLE OF INVENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: 812-5 Hirano  
STREET: Isshinden  
CITY: Tsu-city  
STATE: Mie-prefecture  
COUNTRY: JAPAN  
ZIP: 514-01

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Microsoft Windows 95  
SOFTWARE: Word Perfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/864,038A  
FILING DATE: May 28, 1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-184459  
FILING DATE: 15-July-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: C. Bruce Hamburg  
REGISTRATION NUMBER: 22,389  
REFERENCE/DOCKET NUMBER: F-5610  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)986-2340  
TELEFAX: (212)953-7733  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3331  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
ORIGINAL SOURCE: Pinctada fucata  
ORGANISM: Pinctada fucata  
CELL TYPE: mantle epithelial cell  
FEATURE: mRNA  
LOCATION: from 1 to 3331

IDENTIFICATION METHOD: E (by experiment)  
US-08-864-038A-2

Query Match 2.7%; Score 16; DB 3; Length 3331;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 215 ctgccgtctgctcacc 230  
|||||  
DB 1593 CTGCCGCTCTGCTCACC 1608

RESULT 31  
US-08-864-038A-4  
Sequence 4, Application US/08864038A  
Patent No. 6001592

GENERAL INFORMATION:  
APPLICANT: Kunio NAKASHIMA et al.  
TITLE OF INVENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR  
TITLE OF INVENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID  
TITLE OF INVENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING  
TITLE OF INVENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBOD  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: 812-5 Hirano  
STREET: Isshinden  
CITY: Tsu-city  
STATE: Mie-prefecture  
COUNTRY: JAPAN  
ZIP: 514-01

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Microsoft Windows 95  
SOFTWARE: Word Perfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/864,038A  
FILING DATE: May 28, 1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-184459  
FILING DATE: 15-July-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: C. Bruce Hamburg  
REGISTRATION NUMBER: 22,389  
REFERENCE/DOCKET NUMBER: F-5610  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)986-2340  
TELEFAX: (212)953-7733  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3331  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
ORIGINAL SOURCE: Pinctada fucata  
ORGANISM: Pinctada fucata  
CELL TYPE: mantle epithelial cell  
FEATURE:  
NAME/KEY: CDS  
LOCATION: from 50 to 2263  
IDENTIFICATION METHOD: P (by similarity to some other pattern)  
US-08-864-038A-4

Query Match 2.7%; Score 16; DB 3; Length 3331;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 215 ctgccgtctgctcacc 230  
|||||

Db 1593 CTGCCGCTGCTGCATC 1608

## RESULT 32

US-08-854-585-1/C  
Sequence 1, Application US/08854585

Patent No. 6114140

GENERAL INFORMATION:

APPLICANT: Tonks, Nicholas K. and stman, Arne

TITLE OF INVENTION: Density Enhanced Protein Tyrosine Phosphatase

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &amp; Borun

STREET: 233 South Wacker Drive, Suite 6300

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/854,585

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/237,940

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Borun, Michael F.

REGISTRATION NUMBER: 25,447

REFERENCE/DOCKET NUMBER: 27866/31954

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-474-6300

TELEFAX: 312-474-0448

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 5117 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 350..4364

US-08-854-585-1

Query Match 2.7%; Score 16; DB 3; Length 5117;

Best Local Similarity 100.0%; Pred. No. 39;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 263 agcgagcgcgccctcc 278

Db 382 AGCGAGCGCGCCCTCC 367

## RESULT 33

PCT-US95-05512-1/C

Sequence 1, Application PC/TUS9505512

GENERAL INFORMATION:

APPLICANT: Tonks, Nicholas K. and stman, Arne

TITLE OF INVENTION: Density Enhanced Protein Tyrosine

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &amp;

STREET: 233 South Wacker Drive, Suite 6300

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/05512

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Borun, Michael F.

REGISTRATION NUMBER: 25,447

REFERENCE/DOCKET NUMBER: 27866/31954

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-474-6300

TELEFAX: 312-474-0448

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 5117 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 350..4364

PCT-US95-05512-1

Query Match 2.7%; Score 16; DB 5; Length 5117;

Best Local Similarity 100.0%; Pred. No. 39;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 263 agcgagcgcgccctcc 278

Db 382 AGCGAGCGCGCCCTCC 367

## RESULT 34

PCT-US95-13749-3

Sequence 3, Application PC/TUS9513749

GENERAL INFORMATION:

APPLICANT: Amgen Inc.

TITLE OF INVENTION: COMPOSITIONS FOR INCREASED

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Amgen Inc.

STREET: 1840 Denavilland Drive

CITY: Thousand Oaks

STATE: California

COUNTRY: USA

ZIP: 91320-1789

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/13749

FILING DATE:

CLASSIFICATION:

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 6545 base pairs

TYPE: nucleic acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 3630..4820

PCT-US95-13749-3

Query Match 2.7%: Score 16; DB 5; Length 6545;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 145 ggcagcgcgaacacg 160  
|||||  
Db 5380 GCGAGCGGGAACCGG 5395

## RESULT 35

US-08-056-200-93  
; Sequence 93, Application US/08056200  
; Patent No. 5616500  
; GENERAL INFORMATION:  
; APPLICANT: Steinert, Peter M.  
; APPLICANT: Lee, Seung-Chul  
; APPLICANT: Kim, In-Gyu  
; APPLICANT: Chung, Soo-Il  
; APPLICANT: Park, Sang-Chul  
; TITLE OF INVENTION: Trichohyalin and Transglutaminase-3 and  
; TITLE OF INVENTION: Methods of Using Same  
; NUMBER OF SEQUENCES: 117  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobbe, Martens, Olson & Bear  
; STREET: 620 Newport Center Drive, Sixteenth Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: U.S.A.  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/056,200  
; FILING DATE: 30-APR-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fedrick, Michael F.  
; REGISTRATION NUMBER: 36,799  
; REFERENCE/DOCKET NUMBER: NIH054.001A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (714) 760-0404  
; TELEFAX: (714) 760-9502  
; INFORMATION FOR SEQ ID NO: 93:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9551 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1507..1644  
; FEATURE:  
; NAME/KEY: Intron  
; LOCATION: 1645..2511  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 2512..8070  
; US-08-056-200-93

Query Match 2.7%: Score 16; DB 1; Length 9551;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 106 agggaagacagcagc 121

Db 6658 AGGGAAGACAGCAGC 6673  
|||||

## RESULT 36

US-08-800-644-93  
; Sequence 93, Application US/08800644  
; Patent No. 5958752  
; GENERAL INFORMATION:  
; APPLICANT: Steinert, Peter M.  
; APPLICANT: Lee, Seung-Chul  
; APPLICANT: Kim, In-Gyu  
; APPLICANT: Chung, Soo-Il  
; APPLICANT: Park, Sang-Chul  
; TITLE OF INVENTION: Trichohyalin and Transglutaminase-3 and  
; TITLE OF INVENTION: Methods of Using Same  
; NUMBER OF SEQUENCES: 117  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobbe, Martens, Olson & Bear  
; STREET: 620 Newport Center Drive, Sixteenth Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: U.S.A.  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/800,644  
; FILING DATE: 14-FEB-1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/056,200  
; FILING DATE: 30-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fedrick, Michael F.  
; REGISTRATION NUMBER: 36,799  
; REFERENCE/DOCKET NUMBER: NIH054.001A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (714) 760-0404  
; TELEFAX: (714) 760-9502  
; INFORMATION FOR SEQ ID NO: 93:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9551 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1507..1644  
; FEATURE:  
; NAME/KEY: Intron  
; LOCATION: 1645..2511  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 2512..8070  
; US-08-800-644-93

Query Match 2.7%: Score 16; DB 2; Length 9551;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 106 agggaagacagcagc 121  
|||||  
Db 6658 AGGGAAGACAGCAGC 6673

RESULT 37  
US-08-633-779-2/C  
Sequence 2, Application US/08633779  
Patent No. 5723332  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: TRANSLATIONAL ENHANCER DNA  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon & Vanderhye  
STREET: 1100 No. 5723332th Giebe Road, 8th Floor  
CITY: Arlington  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/633,779  
FILING DATE: 19-APR-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Leonard C. Mitchard  
REGISTRATION NUMBER: 29,009  
REFERENCE/DOCKET NUMBER: 604-381  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 60 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-633-779-2

Query Match 2.5%; Score 15; DB 1; Length 60;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 425 ctaccgccccgcagc 439  
|||||

Db 29 ctaccgccccgcagc 15

RESULT 38  
US-08-238-863-14  
Sequence 14, Application US/08238863  
Patent No. 5503978  
GENERAL INFORMATION:  
APPLICANT: SCHNEIDER, D. J., GOLD, L., AND FEIGON, J.  
TITLE OF INVENTION: HIGH-AFFINITY ssDNA LIGANDS OF HIV-1  
NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Beaton & Swanson, P.C.  
STREET: 4582 South Ulster Street Parkway, Suite  
STREET: #403  
CITY: Denver  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80237  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/238,863  
FILING DATE: 6-MAY-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Barry J. Swanson

APPLICATION NUMBER: 07/714,131  
FILING DATE: 10-JUNE-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/536,428  
FILING DATE: 11-JUNE-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/964,624  
FILING DATE: 21-OCTOBER-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Barry J. Swanson  
REGISTRATION NUMBER: 33,215  
REFERENCE/DOCKET NUMBER: NEX17  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 850-9900  
FAX: (303) 850-9401  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 81  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-238-863-14

Query Match 2.5%; Score 15; DB 1; Length 81;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 242 cccctgttcagcgc 256  
|||||

Db 30 cccctgttcagcgc 44

RESULT 39  
US-08-443-407-14  
Sequence 14, Application US/08443407  
Patent No. 5786462  
GENERAL INFORMATION:  
APPLICANT: SCHNEIDER, D. J., GOLD, L., AND FEIGON, J.  
TITLE OF INVENTION: HIGH-AFFINITY ssDNA LIGANDS OF HIV-1 REVERSE  
TITLE OF INVENTION: LIGANDS OF HIV-1 REVERSE  
NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Swanson & Bratschun, L.L.C.  
STREET: 8400 E. Prentice Avenue, Suite 200  
CITY: Englewood  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/443,407  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/238,863  
FILING DATE: 6-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/714,131  
FILING DATE: 10-JUNE-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/536,428  
FILING DATE: 11-JUNE-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/964,624  
FILING DATE: 21-OCTOBER-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Barry J. Swanson

REGISTRATION NUMBER: 33,215  
REFERENCE/DOCKET NUMBER: NEX17/C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 793-3333  
TELEFAX: (303) 793-3433  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 81  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-443-407-14

Query Match 2.5%; Score 15; DB 1; Length 81;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 242 cccctgttcagcgc 256  
|||||  
DB 30 CCCCTGTTCAAGCCG 44

RESULT 40  
PCT-US95-05600-158  
Sequence 158, Application PC/TUS9505600  
GENERAL INFORMATION:  
APPLICANT: GOLD, LARRY  
APPLICANT: NIEWLANDT, DAN  
APPLICANT: WICKER, MATTHEW  
APPLICANT: SCHNEIDER, DANIEL J.  
APPLICANT: FEIGON, JOEL  
APPLICANT: ALLEN, PATRICK  
APPLICANT: SULLINGER, BRUCE A.  
APPLICANT: DOUDNA, JENNIFER, A.  
TITLE OF INVENTION: HIGH-AFFINITY LIGANDS OF  
TITLE OF INVENTION: INSULIN RECEPTOR ANTIBODIES, TACHYKININ SUBSTANCE  
TITLE OF INVENTION: P, HIV INTEGRASE AND HIV-1 REVERSE TRANSCRIPTASE  
NUMBER OF SEQUENCES: 239  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Swanson & Bratschun, L.L.C.  
STREET: 8400 E. Prentice Avenue, Suite 200  
CITY: Englewood  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/05600  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/238,863  
FILING DATE: 06-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/248,632  
FILING DATE: 24-MAY-1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/303,362  
FILING DATE: 09-SEPTEMBER-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/361,795  
FILING DATE: 21-DECEMBER-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/117,991  
FILING DATE: 08-SEPTEMBER-1993  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/931,473  
FILING DATE: 17-AUGUST-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/964,624  
FILING DATE: 21-OCTOBER-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/536,428  
FILING DATE: 11-JUNE-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/714,131  
FILING DATE: 10-JUNE-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/536,428  
FILING DATE: 11-JUNE-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Barry J. Swanson  
REGISTRATION NUMBER: 33,215  
REFERENCE/DOCKET NUMBER: NEX17/PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 793-3333  
TELEFAX: (303) 793-3433  
INFORMATION FOR SEQ ID NO: 158:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 81 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
PCT-US95-05600-158

Query Match 2.5%; Score 15; DB 5; Length 81;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 242 cccctgttcagcgc 256  
|||||  
DB 30 CCCCTGTTCAAGCCG 44

RESULT 41  
US-08-994-946A-1  
Sequence 1, Application US/08994946A  
Patent No. 6046317  
GENERAL INFORMATION:  
APPLICANT: Koulou, Markku  
APPLICANT: Karvonen, Matti  
APPLICANT: Pesonen, Ullamari  
APPLICANT: Uusiluoma, Matti  
TITLE OF INVENTION: A DNA Molecule Encoding a Mutant  
TITLE OF INVENTION: Prepro-Neuropeptide Y, a Mutant Signal Peptide, and Uses  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.  
STREET: 555 13th Street NW, Suite 701-E  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/994,946A  
FILING DATE: 19-DEC-1997  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 2328-110  
TELECOMMUNICATION INFORMATION:





NAME/KEY: CDS  
LOCATION: 40..693  
US-09-154-874-1

Query Match 2.5%; Score 15; DB 3; Length 846;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 249 ttccagccagccca 263  
|||||  
DB 351 TTCAGCGCCAGCCAA 337

RESULT 45  
US-09-082-092-8/C  
Sequence 8, Application US/09082092

GENERAL INFORMATION:  
APPLICANT: Nakao, Atsuhito  
APPLICANT: Moren, Anita  
APPLICANT: Heuchel, Rainer  
APPLICANT: Itoh, Susumu  
APPLICANT: Afirakhte, Mozhgan  
APPLICANT: Souchehytskyi, Serhiy  
APPLICANT: Brodin, Greger  
APPLICANT: Landstrom, Marene  
APPLICANT: Heldin, Nils-Erik  
APPLICANT: Heldin, Carl-Henrik  
TITLE OF INVENTION: SMAD7 AND USES THEREOF  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: MA  
ZIP: 02210-2211

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/082.092  
FILING DATE: 20-MAY-1998  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/047,221  
FILING DATE: 20-MAY-1997  
APPLICATION NUMBER: 60/060,465  
FILING DATE: 30-SEP-1997  
APPLICATION NUMBER: 60/075,940  
FILING DATE: 25-FEB-1998  
APPLICATION NUMBER: 60/077,033  
FILING DATE: 06-MAR-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Van Amsterdam, John R.  
REGISTRATION NUMBER: 40,212  
REFERENCE/DOCKET NUMBER: L0461/7032  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-720-3500  
TELEFAX: 617-720-2441  
TELEX:

INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1281 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-09-082-092-8

Query Match 2.5%; Score 15; DB 4; Length 1281;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 241 cccctgttcagcg 255  
|||||  
DB 710 CCCCTGTTCAGCG 696

RESULT 46  
US-08-176-427B-7/C  
Sequence 7, Application US/08176427B  
Patent No. 5789543

GENERAL INFORMATION:  
APPLICANT: Ingham, Phillip W.  
APPLICANT: McMahon, Andrew P.  
APPLICANT: Tablin, Clifford J.  
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing  
TITLE OF INVENTION: Proteins and Uses Related Thereto  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street  
CITY: Boston  
STATE: MA

COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII(text)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/176.427B  
FILING DATE: 30-DEC-1993  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/DOCKET NUMBER: HMI-006  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:  
LENGTH: 1313 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1314  
US-08-176-427B-7

Query Match 2.5%; Score 15; DB 1; Length 1313;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 502 ggttcagcgcgcc 516  
|||||  
DB 1133 GGTTCAGCGCGCC 1119

RESULT 47  
US-08-356-060A-4/C  
Sequence 4, Application US/08356060A  
Patent No. 5844079  
GENERAL INFORMATION:  
APPLICANT: Ingham, Phillip W.

APPLICANT: McMahon, Andrew P.  
APPLICANT: Tablin, Clifford J.  
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing  
TITLE OF INVENTION: Proteins and Uses Related Thereto  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII(text)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/356,060A  
FILING DATE: 14-DEC-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/176,427  
FILING DATE: 30-DEC-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/DOCKET NUMBER: HMI-006CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1313 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1314  
US-08-356-060A-4

Query Match 2.5%; Score 15; DB 2; Length 1313;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 502 ggtgccagcgcgcc 516  
|||||  
DB 1133 ggtgccagcgcgcc 1119

RESULT 48  
US-08-460-900C-4/C  
Sequence 4, Application US/08460900C  
Patent No. 6165747  
GENERAL INFORMATION:  
APPLICANT: Ingham, Phillip W.  
APPLICANT: McMahon, Andrew P.  
APPLICANT: Tablin, Clifford J.  
APPLICANT: Bunecrot, David A.  
APPLICANT: Marti-Gorosita, Elisa  
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing  
TITLE OF INVENTION: Proteins and Uses Related Thereto  
NUMBER OF SEQUENCES: 62  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/460,900C  
FILING DATE: 5-JUNE-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/435,093  
FILING DATE: 4-MAY-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/356,060  
FILING DATE: 14-DEC-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/176,427  
FILING DATE: 30-DEC-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/DOCKET NUMBER: HMV-006.05  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 832-1000  
TELEFAX: (617) 832-7000  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1313 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1311  
US-08-460-900C-4

Query Match 2.5%; Score 15; DB 4; Length 1313;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 502 ggtgccagcgcgcc 516  
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DB 1133 ggtgccagcgcgcc 1119

RESULT 49  
US-08-855-910-5  
Sequence 5, Application US/08855910  
Patent No. 6221640  
GENERAL INFORMATION:  
APPLICANT: Tao, Jianshi  
APPLICANT: Sassanfar, Mandana  
APPLICANT: Gallant, Paul L.  
APPLICANT: Shen, Xiaoyu  
APPLICANT: Avruch, Anthony S.  
APPLICANT: Yu, Russell V.  
TITLE OF INVENTION: ENTEROCOCCAL AMINOACYL-tRNA SYNTHETASE  
TITLE OF INVENTION: PROTEINS, NUCLEIC ACIDS AND STRAINS COMPRISING SAME  
NUMBER OF SEQUENCES: 71  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Millitia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/855,910
; FILING DATE: 14-MAY-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
;   NAME: Brook, David E.
;   REGISTRATION NUMBER: 22,592
;   REFERENCE/DOCKET NUMBER: CP195-08
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (781) 861-6240
;   TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1338 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
; FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 187..1194
; US-08-855-910-5

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Query Match      2.5%; Score 15; DB 4; Length 1338;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 29 atcgtaacgacgagc 43
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Db 1259 ATCGTACGACGACG 1273

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RESULT 50
US-08-651-136C-9
; Sequence 9, Application US/08651136C
; Patent No. 6001639
; GENERAL INFORMATION:
;   APPLICANT: Schulein, Martin
;   APPLICANT: Andersen, Lene N.
;   APPLICANT: Lassen, Soren F.
;   APPLICANT: Kauppinen, Markus S.
;   APPLICANT: Lange, Lene
;   APPLICANT: Nielsen, Ruby I.
;   APPLICANT: Ihara, Michiko
;   APPLICANT: Takagi, Shinobu
; TITLE OF INVENTION: No. 6001639e1 Endoglucanases
; NUMBER OF SEQUENCES: 109
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: No. 6001639o No. 6001639disk of No. 6001639th America, Inc.
;   STREET: 405 Lexington Avenue, 64th Floor
;   CITY: New York
;   STATE: New York
;   COUNTRY: United States of America
;   ZIP: 10174-6401
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/651,136C
;   FILING DATE: 21-MAY-1996
;   CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
;   NAME: Lambiris, Elias J.
;   REGISTRATION NUMBER: 33,728
;   REFERENCE/DOCKET NUMBER: 4366,200-US
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 212-867-0123
;   TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1423 base pairs

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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 110..1156
; US-08-651-136C-9

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Query Match      2.5%; Score 15; DB 3; Length 1423;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 387 gccggccacgacgag 401
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Db 979 GCCGGCCACGACGAG 993

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Search completed: September 21, 2001, 16:24:12  
Job time: 8823 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 21, 2001, 13:40:55 : Search time 2753.51 Seconds  
(without alignments)  
3187.722 Million cell updates/sec

Title: US-09-138-735-1\_COPY\_1232\_1825

Perfect score: 594

Sequence: 1 caggtacagcgtacgctt.....aaacgagctccgtgctgata 594

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 14155048 seqs, 7388405095 residues

Word size: 0

Total number of hits satisfying chosen parameters: 28310096

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

Pending\_Patents\_MA\_Main.\*

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50: /cgnl\_7/ptodata/1/pna/US6018.COMB.seq:\*  
51: /cgnl\_7/ptodata/1/pna/US6019.COMB.seq:\*  
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54: /cgnl\_7/ptodata/1/pna/US6022.COMB.seq:\*  
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59: /cgnl\_7/ptodata/1/pna/US6027.COMB.seq:\*  
60: /cgnl\_7/ptodata/1/pna/US6028.COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID                   | Description        |
|------------|-------|-------------|--------|----------------------|--------------------|
| 1          | 594   | 100.0       | 3402   | US-08-988-242-1      | Sequence 1, Appl1  |
| 2          | 594   | 100.0       | 3402   | US-09-138-736-1      | Sequence 1, Appl1  |
| 3          | 22    | 3.7         | 22     | US-08-988-242-5      | Sequence 5, Appl1  |
| 4          | 22    | 3.7         | 22     | US-09-138-736-9      | Sequence 9, Appl1  |
| 5          | 20    | 3.4         | 718    | US-09-654-617-126156 | Sequence 126156,   |
| 6          | 20    | 3.4         | 718    | US-09-684-016-126156 | Sequence 126156,   |
| 7          | 20    | 3.4         | 5679   | US-09-620-392-64793  | Sequence 64793, A  |
| 8          | 20    | 3.4         | 5679   | US-09-702-134-21010  | Sequence 21010, A  |
| 9          | 20    | 3.4         | 11335  | US-60-173-464-11335  | Sequence 11335, A  |
| 10         | 20    | 3.4         | 11335  | US-60-191-637-13953  | Sequence 13953, A  |
| 11         | 20    | 3.4         | 11335  | US-60-191-681-13998  | Sequence 10998, A  |
| 12         | 20    | 3.4         | 11338  | US-60-167-217-13998  | Sequence 13998, A  |
| 13         | 20    | 3.4         | 91470  | US-09-534-859-19     | Sequence 19, Appl1 |
| 14         | 20    | 3.4         | 226706 | US-09-528-237A-1285  | Sequence 1285, Ap  |
| 15         | 19    | 3.2         | 718    | US-60-182-316-11355  | Sequence 2055, Ap  |
| 16         | 19    | 3.2         | 9855   | US-09-620-392-32691  | Sequence 32691, A  |
| 17         | 19    | 3.2         | 9855   | US-09-620-392-67713  | Sequence 67713, A  |
| 18         | 19    | 3.2         | 11873  | US-09-407-562-31     | Sequence 32, Appl1 |
| 19         | 19    | 3.2         | 11878  | US-09-407-562-28     | Sequence 31, Appl1 |
| 20         | 19    | 3.2         | 11883  | US-09-407-562-28     | Sequence 28, Appl1 |
| 21         | 19    | 3.2         | 15505  | US-09-620-392-10632  | Sequence 10632, A  |
| 22         | 19    | 3.2         | 25670  | US-09-620-392-4251   | Sequence 4251, Ap  |
| 23         | 19    | 3.2         | 31556  | US-09-702-134-5295   | Sequence 5295, Ap  |
| 24         | 19    | 3.2         | 159989 | US-09-702-134-5301   | Sequence 5301, Ap  |
| 25         | 18    | 3.0         | 18     | US-08-988-242-4      | Sequence 4, Appl1  |
| 26         | 18    | 3.0         | 18     | US-09-138-736-5      | Sequence 5, Appl1  |
| 27         | 18    | 3.0         | 18     | US-09-138-736-8      | Sequence 8, Appl1  |
| 28         | 18    | 3.0         | 70     | US-09-366-691A-1504  | Sequence 1504, Ap  |
| 29         | 18    | 3.0         | 85     | US-09-076-667-928    | Sequence 928, Ap   |
| 30         | 18    | 3.0         | 85     | US-09-540-292-15688  | Sequence 15688, A  |
| 31         | 18    | 3.0         | 85     | US-60-048-002-928    | Sequence 928, Ap   |
| 32         | 18    | 3.0         | 180    | US-09-513-991-2039   | Sequence 2039, Ap  |
| 33         | 18    | 3.0         | 234    | US-08-810-326-2151   | Sequence 2151, Ap  |
| 34         | 18    | 3.0         | 234    | US-09-540-212A-11685 | Sequence 11685, A  |
| 35         | 18    | 3.0         | 237    | US-08-878-507-222    | Sequence 222, App  |
| 36         | 18    | 3.0         | 237    | US-09-540-212A-16821 | Sequence 16821, A  |
| 37         | 18    | 3.0         | 237    | US-60-016-092-222    | Sequence 222, App  |
| 38         | 18    | 3.0         | 248    | US-09-100-454-2483   | Sequence 2483, App |
| 39         | 18    | 3.0         | 248    | US-09-540-212A-35497 | Sequence 35497, A  |
| 40         | 18    | 3.0         | 249    | US-60-051-749-2483   | Sequence 2483, Ap  |
| 41         | 18    | 3.0         | 249    | US-60-048-722-3053   | Sequence 3053, Ap  |
| 42         | 18    | 3.0         | 253    | US-08-992-625-3252   | Sequence 3252, Ap  |
| 43         | 18    | 3.0         | 253    | US-09-540-764-10498  | Sequence 10498, A  |
| 44         | 18    | 3.0         | 260    | US-60-197-872-21718  | Sequence 21718, A  |
| 45         | 18    | 3.0         | 261    | US-08-104-507A-4311  | Sequence 4311, Ap  |
| 46         | 18    | 3.0         | 261    | US-08-104-507C-4311  | Sequence 4311, Ap  |

















[illegible]

```

RESULT 2
US-09-138-736-1
Sequence 1, Application US/09138736
GENERAL INFORMATION:
APPLICANT: PARANHOS-BACCALA, Glaucaia
APPLICANT: LESENECHAL, Mylene
APPLICANT: JOLIVET, Michel
TITLE OF INVENTION: NEW TRYPA NOSOMA CRUZI ANTIGEN, AND GENE
TITLE OF INVENTION: ENCODING THE LATTER, THEIR APPLICATION TO THE DETECTION OF
TITLE OF INVENTION: CHAGAS DISEASE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oliff & Berridge
STREET: 700 South Washington Street, Suite 300
CITY: Alexandria
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/138,736
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,917
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 36400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
TELEFAX: 703-836-2787
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3402 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-138-736-1

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| Query Match  | 100.0%             | Score 594;    | DB 15;    | Length 3402; |
| Best Local   | Similarity 100.0%; | Pred. NO. 0;  |           |              |
| Matches 594; | Conservative 0;    | Mismatches 0; | Indels 0; | Gaps 0;      |

[illegible]

RESULT 3  
 US-08-988-242-5  
 Sequence 5, Application US/08988242  
 GENERAL INFORMATION:  
 APPLICANT: PARANHOS-BACCALA, GLAUCIA  
 APPLICANT: LESENECHAL, MYLENE  
 APPLICANT: JOLIVET, MICHEL  
 APPLICANT: MANDRAND, BERNARD  
 TITLE OF INVENTION: NEW TRYPTANOSOMA CRUZI ANTIGEN, GENE  
 TITLE OF INVENTION: ENCODING THEREFOR, AND METHODS OF DETECTING AND TREATING  
 NUMBER OF INVENTIONS: CHAGAS DISEASE  
 NUMBER OF SEQUENCES: '19  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: OLIEF & BERRIDGE, PLC  
 STREET: P.O. BOX 19928  
 CITY: Alexandria  
 STATE: Virginia  
 COUNTRY: U.S.A.  
 ZIP: 22320  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/988,242  
 FILING DATE: 10-DEC-1997

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Berridge, William P.  
REGISTRATION NUMBER: 30,024  
REFERENCE/DOCKET NUMBER: MPB 36400A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6400  
TELEFAX: 703-836-2787  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-988-242-5

Query Match 3.7%; Score 22; DB 13; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.93;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||  
DB 1 CAGCCGACGCTAGCTGCTCT 22

RESULT 4  
US-09-138-736-9  
Sequence 9, Application US/09138736  
GENERAL INFORMATION:  
APPLICANT: PARANHOS-BACCALA, Glaucia  
APPLICANT: LESENECHAL, Mylene  
TITLE OF INVENTION: NEW TRYPARANOSOMA CRUZI ANTIGEN, AND GENE  
TITLE OF INVENTION: ENCODING THE LATTER, THEIR APPLICATION TO THE DETECTION OF  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Oliff & Berridge  
STREET: 700 South Washington Street, Suite 300  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22314  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/138,736  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/480,917  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Berridge, William P.  
REGISTRATION NUMBER: 30,024  
REFERENCE/DOCKET NUMBER: MPB 36400  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6400  
TELEFAX: 703-836-2787  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-138-736-9

Query Match 3.7%; Score 22; DB 15; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.93;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 cagccgacgtagctgcgtctc 56  
|||||  
DB 1 CAGCCGACGCTAGCTGCTCT 22

RESULT 5  
US-09-654-617-126156  
Sequence 126156, Application US/09654617  
GENERAL INFORMATION:  
APPLICANT: Kovalic, David K.  
APPLICANT: Liu, Jingdong  
TITLE OF INVENTION: Annotated Plant Genes  
FILE REFERENCE: 38-21(15097)D  
CURRENT APPLICATION NUMBER: US/09/654,617  
CURRENT FILING DATE: 2000-09-05  
NUMBER OF SEQ ID NOS: 463173  
SEQ ID NO 126156  
LENGTH: 718  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
US-09-654-617-126156

Query Match 3.4%; Score 20; DB 25; Length 718;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 212 ctctgcgcgtctgcattcc 231  
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DB 586 ctctgcgcgtctgcattcc 605

RESULT 6  
US-09-684-016-126156  
Sequence 126156, Application US/09684016  
GENERAL INFORMATION:  
APPLICANT: Kovalic, David K.  
APPLICANT: Liu, Jingdong  
TITLE OF INVENTION: Annotated Plant Genes  
FILE REFERENCE: 38-21(15097)D  
CURRENT APPLICATION NUMBER: US/09/684,016  
CURRENT FILING DATE: 2000-10-10  
PRIOR APPLICATION NUMBER: US 09/654,617  
PRIOR FILING DATE: 2000-09-05  
NUMBER OF SEQ ID NOS: 463173  
SEQ ID NO 126156  
LENGTH: 718  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
US-09-684-016-126156

Query Match 3.4%; Score 20; DB 27; Length 718;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 212 ctctgcgcgtctgcattcc 231  
|||||  
DB 586 ctctgcgcgtctgcattcc 605

RESULT 7  
US-09-620-392-64793/C  
Sequence 64793, Application US/09620392  
GENERAL INFORMATION:  
APPLICANT: Boukharov, Andrey A.  
APPLICANT: Kovalic, David K.  
APPLICANT: Liu, Jingdong

```
; APPLICANT: McIninch, James
; TITLE OF INVENTION: Plant Genome Sequence And Uses Thereof
; FILE REFERENCE: 38-21(51237)E
; CURRENT APPLICATION NUMBER: US/09/620,392
; CURRENT FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 69652
; SEQ ID NO 64793
; LENGTH: 5679
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-620-392-64793
```

```
Query Match
Best Local Similarity 100.0%; Pred. No. 12; Length 5679;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 215 ctgcgcgtcgtcatccct 234
|||||
Db 3043 CTGCCGCTGCTGCATCCCT 3024
```

```
RESULT 8
US-09-702-134-21010/c
; Sequence 21010, Application US/09702134
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Cao, Yongwei
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: McIninch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Plant Genome Sequence and Uses Thereof
; FILE REFERENCE: 38-21(51237)F
; CURRENT APPLICATION NUMBER: US/09/702,134
; CURRENT FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 52202
; SEQ ID NO 21010
; LENGTH: 5679
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-702-134-21010
```

```
Query Match
Best Local Similarity 100.0%; Pred. No. 12; Length 5679;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 215 ctgcgcgtcgtcatccct 234
|||||
Db 3043 CTGCCGCTGCTGCATCCCT 3024
```

```
RESULT 9
US-60-173-464-11355
; Sequence 11355, Application US/60173464
; GENERAL INFORMATION:
; APPLICANT: Li, Peter W.D.
; TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS AND USES
; FILE REFERENCE: C1000173
; CURRENT APPLICATION NUMBER: US/60/173,464
; CURRENT FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 30269
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11355
; LENGTH: 11335
; TYPE: DNA
; ORGANISM: Drosophila
US-60-173-464-11355
```

```
Query Match
Best Local Similarity 100.0%; Pred. No. 12; Length 11335;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 50 gcgtctgctgacatgctcg 69
|||||
Db 6835 gcgtctgctgacatgctcg 6854
```

```
RESULT 10
US-60-191-637-13953/c
; Sequence 13953, Application US/60191637
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: NUCLEIC ACID DETECTION KITS COMPRISING
; TITLE OF INVENTION: GENE SEQUENCES EXPRESSED FROM THE DROSOPHILA GENOME, AND
; FILE REFERENCE: C1000392
; CURRENT APPLICATION NUMBER: US/60/191,637
; CURRENT FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 42660
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13953
; LENGTH: 11335
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-60-191-637-13953
```

```
Query Match
Best Local Similarity 100.0%; Pred. No. 12; Length 11335;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 50 gcgtctgctgacatgctcg 69
|||||
Db 4501 GCCTCTGCTGCATGTCG 4482
```

```
RESULT 11
US-60-191-681-10986/c
; Sequence 10986, Application US/60191681
; GENERAL INFORMATION:
; APPLICANT: Li, Peter, W.D.
; TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING ISOLATED DROSOPHILA PROTEINS AND
; FILE REFERENCE: C1000390
; CURRENT APPLICATION NUMBER: US/60/191,681
; CURRENT FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 30973
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 10986
; LENGTH: 11335
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-60-191-681-10986
```

```
Query Match
Best Local Similarity 100.0%; Pred. No. 12; Length 11335;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 50 gcgtctgctgacatgctcg 69
|||||
Db 4501 GCCTCTGCTGCATGTCG 4482
```

```
RESULT 12
US-60-167-217-13998
; Sequence 13998, Application US/60167217
; GENERAL INFORMATION:
; APPLICANT: Li, Peter W. D.
; TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
```

```

; TITLE OF INVENTION: ACID MOLECULES ENCODING DROSOPHILA PROTEINS, AND USES
; FILE REFERENCE: CL000152
; CURRENT APPLICATION NUMBER: US/60/167,217
; CURRENT FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 23195
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 13998
; LENGTH: 11338
; TYPE: DNA
; ORGANISM: Drosophila
; US-60-167-217-13998
```

```

Query Match          3.4%; Score 20; DB 48; Length 11338;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 gccgtcgtgctgacatgctg 69
|||||
Db 6836 gccgtcgtgctgacatgctg 6857
```

```

RESULT 13
; Sequence 19, Application US/09534859
; GENERAL INFORMATION:
; APPLICANT: Bush, David F.
; APPLICANT: Last, Robert L.
; APPLICANT: Levih, Irena M.
; APPLICANT: Norris, Susan R.
; APPLICANT: Parnell, Laurence D.
; APPLICANT: Rounsley, Steven D.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: PLANT POLYMORPHIC MARKERS AND USES THEREOF
; FILE REFERENCE: 38-10(15493)B
; CURRENT APPLICATION NUMBER: US/09/534,859
; CURRENT FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 1127
; SEQ ID NO 19
; LENGTH: 91470
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-09-534-859-19
```

```

Query Match          3.4%; Score 20; DB 20; Length 91470;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 212 ctctgcgcgtgctgcatcc 231
|||||
Db 42747 CTCTGCGCGTCTGCATCC 42728
```

```

RESULT 14
; Sequence 1285, Application US/09528237A
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: The Drosophila Genome, Primary Nucleic
; TITLE OF INVENTION: Acid Sequences, Systems Containing The Nucleic Acid
; FILE REFERENCE: CL000284
; CURRENT APPLICATION NUMBER: US/09/528,237A
; CURRENT FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 2926
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1285
; LENGTH: 226706
; TYPE: DNA
; ORGANISM: Drosophila
; US-09-528-237A-1285
```

```

Query Match          3.4%; Score 20; DB 19; Length 226706;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 gccgtcgtgctgacatgctg 69
|||||
Db 213597 gccgtcgtgctgacatgctg 213616
```

```

RESULT 15
; Sequence 2055, Application US/60182316
; GENERAL INFORMATION:
; APPLICANT: Curtis, Anne L.
; APPLICANT: Lagace, Robert E.
; APPLICANT: Klingler, Tod M.
; APPLICANT: Stuve, Laura L.
; TITLE OF INVENTION: CPG Island Polynucleotides
; FILE REFERENCE: PX-0003 P
; CURRENT APPLICATION NUMBER: US/60/182,316
; CURRENT FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 14,630
; SOFTWARE: PERL Program
; SEQ ID NO 2055
; LENGTH: 718
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: CPG_991027_B15_masked_fa.Contig49773
; US-60-182-316-2055
```

```

Query Match          3.2%; Score 19; DB 50; Length 718;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 280 gccgcgcgcgcgcgcgcgcgc 298
|||||
Db 213 GCCGCGCGCGCATCGCGCTG 195
```

```

RESULT 16
; Sequence 32691, Application US/09620392
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jindong
; APPLICANT: McIninch, James
; TITLE OF INVENTION: Plant Genome Sequence And Uses Thereof
; FILE REFERENCE: 38-21(51237)E
; CURRENT APPLICATION NUMBER: US/09/620,392
; CURRENT FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 69652
; SEQ ID NO 32691
; LENGTH: 9855
; TYPE: DNA
; ORGANISM: Oryza sativa
; US-09-620-392-32691
```

```

Query Match          3.2%; Score 19; DB 24; Length 9855;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 387 gccgcgcgcgcgcgcgcgcgc 405
|||||
Db 259 gccgcgcgcgcgcgcgcgcgc 277
```



```
RESULT 17
US-09-620-392-67713
; Sequence 67713, Application US/09620392
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Kovalev, David K.
; APPLICANT: Liu, Jindong
; APPLICANT: McIninch, James
; TITLE OF INVENTION: Plant Genome Sequence And Uses Thereof
; FILE REFERENCE: 38-21(51237)E
; CURRENT APPLICATION NUMBER: US/09/620,392
; CURRENT FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 69652
; SEQ ID NO 67713
; LENGTH: 9895
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-620-392-67713

Query Match          3.2%; Score 19; DB 24; Length 9895;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 387 gccggccacgacgagctct 405
    |||
Db 8100 gccggccacgacgagctct 8118

RESULT 18
US-09-407-562-32/c
; Sequence 32, Application US/09407562
; GENERAL INFORMATION:
; APPLICANT: Kathryn Meek
; TITLE OF INVENTION: Genetic Test For Equine Severe
; TITLE OF INVENTION: Combined Immunodeficiency Disease
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dr. Benjamin A. Adler
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/407,562
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/970,269
; FILING DATE: November 14, 1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler Ph.D., Benjamin A.
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D5860
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-777-2321
; TELEFAX: 713-777-6908
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11873 bp
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: other nucleic acid
; HYPOTHETICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; FEATURE:
US-09-407-562-31
```

```
ANTI-SENSE: no
ORIGINAL SOURCE:
FEATURE:
US-09-407-562-32

Query Match          3.2%; Score 19; DB 18; Length 11873;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 211 actctgcgcgtctgcac 229
    |||
Db 6446 ACTCTGCCGCTGCTGCAT 6428

RESULT 19
US-09-407-562-31/c
; Sequence 31, Application US/09407562
; GENERAL INFORMATION:
; APPLICANT: Kathryn Meek
; TITLE OF INVENTION: Genetic Test For Equine Severe
; TITLE OF INVENTION: Combined Immunodeficiency Disease
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dr. Benjamin A. Adler
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/407,562
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/970,269
; FILING DATE: November 14, 1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler Ph.D., Benjamin A.
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D5860
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-777-2321
; TELEFAX: 713-777-6908
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11878 bp
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: other nucleic acid
; HYPOTHETICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; FEATURE:
US-09-407-562-31

Query Match          3.2%; Score 19; DB 18; Length 11878;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 211 actctgcgcgtctgcac 229
    |||
Db 6446 ACTCTGCCGCTGCTGCAT 6428
```

RESULT 20  
US-09-407-562-28/C  
; Sequence 28, Application US/09407562  
; GENERAL INFORMATION:  
; APPLICANT: Katheryn Meek  
; TITLE OF INVENTION: Genetic Test For Equine Severe  
; TITLE OF INVENTION: Combined Immunodeficiency Disease  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dr. Benjamin A. Adler  
; STREET: 8011 Candle Lane  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple  
; OPERATING SYSTEM: Macintosh  
; SOFTWARE: Microsoft Word for Macintosh  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/407,562  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/970,269  
; FILING DATE: November 14, 1997  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Adler Ph.D., Benjamin A.  
; REGISTRATION NUMBER: 35,423  
; REFERENCE/DOCKET NUMBER: D5860  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 713-777-2321  
; TELEFAX: 713-777-6908  
; INFORMATION FOR SEQ. ID NO: 28:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11883 bp  
; TYPE: nucleic acid  
; STRANDEDNESS: double stranded  
; TOPOLOGY: linear  
; MOLECULE TYPE:  
; DESCRIPTION: other nucleic acid  
; HYPOTHETICAL: no  
; ANTI-SENSE: no  
; ORIGINAL SOURCE:  
US-09-407-562-28

Query Match 3.2%; Score 19; DB 18; Length 11883;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 211 actctgacgctgctgcat 229  
DB 6449 ACTTCTGCCCTGCTGCAT 6431

RESULT 21  
US-09-620-392-10632/C  
; Sequence 10632, Application US/09620392  
; GENERAL INFORMATION:  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Liu, Jingdong  
; APPLICANT: McIninch, James  
; TITLE OF INVENTION: Plant Genome Sequence And Uses Thereof  
; FILE REFERENCE: 38-21(51237)E  
; CURRENT APPLICATION NUMBER: US/09/620,392  
; CURRENT FILING DATE: 2000-07-19  
; NUMBER OF SEQ. ID NOS: 69652  
; SEQ. ID NO 10632

LENGTH: 19505  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
US-09-620-392-10632

Query Match 3.2%; Score 19; DB 24; Length 19505;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 387 gccgcgacgacgagctct 405  
DB 19008 GCCGCGCCAGCAGAGTCT 18990

RESULT 22  
US-09-620-392-4251/C  
; Sequence 4251, Application US/09620392  
; GENERAL INFORMATION:  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Liu, Jingdong  
; APPLICANT: McIninch, James  
; TITLE OF INVENTION: Plant Genome Sequence And Uses Thereof  
; FILE REFERENCE: 38-21(51237)E  
; CURRENT APPLICATION NUMBER: US/09/620,392  
; CURRENT FILING DATE: 2000-07-19  
; NUMBER OF SEQ. ID NOS: 69652  
; SEQ. ID NO 4251  
; LENGTH: 25670  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; OTHER INFORMATION: unsure at all n locations  
US-09-620-392-4251

Query Match 3.2%; Score 19; DB 24; Length 25670;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 387 gccgcgacgacgagctct 405  
DB 3582 GCCGCGCCAGCAGAGTCT 3564

RESULT 23  
US-09-702-134-5295/C  
; Sequence 5295, Application US/09702134  
; GENERAL INFORMATION:  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Liu, Jingdong  
; APPLICANT: McIninch, James  
; APPLICANT: Wu, Wei  
; TITLE OF INVENTION: Plant Genome Sequence and Uses Thereof  
; FILE REFERENCE: 38-21(51237)F  
; CURRENT APPLICATION NUMBER: US/09/702,134  
; CURRENT FILING DATE: 2000-10-31  
; NUMBER OF SEQ. ID NOS: 52202  
; SEQ. ID NO 5295  
; LENGTH: 31556  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(31556)  
; OTHER INFORMATION: unsure at all n locations  
US-09-702-134-5295

Query Match 3.2%; Score 19; DB 28; Length 31556;  
Best Local Similarity 100.0%; Pred. No. 42;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 387 gccggccacgacgaggtct 405  
|||||

Db 9468 gccggccacgacgaggtct 9450

## RESULT 24

US-09-702-134-5301

; Sequence 5301, Application US/09702134

; GENERAL INFORMATION:

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Cao, Yongwei

; APPLICANT: Kovalic, David K.

; APPLICANT: Liu, Jingdong

; APPLICANT: McIninch, James

; TITLE OF INVENTION: Plant Genome Sequence and Uses Thereof

; FILE REFERENCE: 38-21(51237)F

; CURRENT APPLICATION NUMBER: US/09/702,134

; CURRENT FILING DATE: 2000-10-31

; NUMBER OF SEQ ID NOS: 52202

; SEQ ID NO 5301

; LENGTH: 159989

; TYPE: DNA

; ORGANISM: Oryza sativa

US-09-702-134-5301

Query Match 3.2%; Score 19; DB 28; Length 159989;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 387 gccggccacgacgaggtct 405  
|||||

Db 32451 gccggccacgacgaggtct 32469

## RESULT 25

US-08-988-242-4/c

; Sequence 4, Application US/08988242

; GENERAL INFORMATION:

; APPLICANT: PARANHOS-BACCALA, GLAUCIA

; APPLICANT: LESENECHAL, MYLENE

; APPLICANT: JOLIVET, MICHEL

; TITLE OF INVENTION: NEW TRYPAOSOMA CRUZI ANTIGEN, GENE

; TITLE OF INVENTION: ENCODING THEREFOR, AND METHODS OF DETECTING AND TREATING

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OLIFF & BERRIDGE, PLC

; STREET: P.O. BOX 19928

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: U.S.A.

; ZIP: 22320

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/988,242

; FILING DATE: 10-DEC-1997

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Berridge, William P.

; REGISTRATION NUMBER: 30,024

; REFERENCE/DOCKET NUMBER: WPB 36400A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-836-6400

; TELEFAX: 703-836-2787

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

US-08-988-242-4

Query Match 3.0%; Score 18; DB 13; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1,4e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 211 actctgcgcgtcgtcga 228  
|||||

Db 18 actctgcgcgtcgtcga 1

## RESULT 26

US-09-138-736-5

; Sequence 5, Application US/09138736

; GENERAL INFORMATION:

; APPLICANT: PARANHOS-BACCALA, Glaucia

; APPLICANT: LESENECHAL, Mylene

; APPLICANT: JOLIVET, Michel

; TITLE OF INVENTION: NEW TRYPAOSOMA CRUZI ANTIGEN, AND GENE

; TITLE OF INVENTION: ENCODING THE LATTER, THEIR APPLICATION TO THE DETECTION OF

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Oliff & Berridge

; STREET: 700 South Washington Street, Suite 300

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: U.S.A.

; ZIP: 22314

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/138,736

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/480,917

; FILING DATE: 07-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Berridge, William P.

; REGISTRATION NUMBER: 30,024

; REFERENCE/DOCKET NUMBER: WPB 36400

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-836-6400

; TELEFAX: 703-836-2787

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

US-09-138-736-5

Query Match 3.0%; Score 18; DB 15; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1,4e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 172 tcgggactgacgcgcgcg 189  
|||||

Db 1 tcgggactgacgcgcgcg 18

```

RESULT 27
US-09-138-736-8/c
; Sequence 8, Application US/09138736
; GENERAL INFORMATION:
; APPLICANT: PARANHOS-BACCALA, Glaucia
; APPLICANT: LESENECHAL, Mylene
; APPLICANT: JOLIVET, Michel
; TITLE OF INVENTION: NEW TRYPAOSOMA CRUZI ANTIGEN, AND GENE
; TITLE OF INVENTION: ENCODING THE LATTER; THEIR APPLICATION TO THE DETECTION OF
; TITLE OF INVENTION: CHAGAS DISEASE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oliff & Berridge
; STREET: 700 South Washington Street, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/138,736
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480, 917
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: MPB 36400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6400
; TELEFAX: 703-836-2787
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-138-736-8

Query Match          3.08; Score 18; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 211 actctgcgcgtctgta 228
      |||||||
Db 18 ACTTCTGCCGCTGCTGCA 1

RESULT 28
US-09-366-691A-1504/c
; Sequence 1504, Application US/09366691A
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A., et al.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 38
; FILE REFERENCE: PO-38
; CURRENT APPLICATION NUMBER: US/09/366, 691A
; PRIOR APPLICATION NUMBER: 1999-08-04
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 8319
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1504
; LENGTH: 70

```

```

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (10)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (60)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (65)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (70)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-366-691A-1504

Query Match          3.08; Score 18; DB 17; Length 70;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 216 tgcgcgtcgtcgtcctccc 233
      |||||||
Db 31 TGCCGCTGCTGCATCCCC 14

RESULT 29
US-09-076-667-928/c
; Sequence 928, Application US/09076667
; GENERAL INFORMATION:
; APPLICANT: Gooding, Douglas H.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Akerbloom, Ingrid E.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Naughton, Rebecca E.
; APPLICANT: Klingler, Tod M.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
; NUMBER OF SEQUENCES: 4483
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/076, 667
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 855-0555
; TELEFAX: (415) 845-4166
; INFORMATION FOR SEQ ID NO: 928:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 85 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:

```

CLONE: 3244053H1  
US-09-076-667-928

Query Match  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 111 agaacagcagccagcca 128  
Db 29 AGAACAGCAGCCAGCCCA 12

RESULT 30  
US-09-540-229-15688/C  
Sequence 15688, Application US/09540229  
GENERAL INFORMATION:  
APPLICANT: Sellhamer, Jeffrey J.  
APPLICANT: Delegeane, Angelo M.  
APPLICANT: Stuart, Susan G.  
APPLICANT: Stuve, Laura L.  
APPLICANT: Mullahy, Sara J.  
APPLICANT: Naughton, Rebecca E.  
TITLE OF INVENTION: POLYNUCLEOTIDES OF NERVOUS SYSTEM AND SENSORY ORGANS  
FILE REFERENCE: PD-1033 CIP  
CURRENT APPLICATION NUMBER: US/09/540,229  
CURRENT FILING DATE: 2000-03-31  
Prior application data removed - refer to PALM or file wrapper  
NUMBER OF SEQ ID NOS: 193582  
SOFTWARE: PERL Program  
SEQ ID NO 15688  
LENGTH: 85  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
OTHER INFORMATION: Incyte ID No: hu00290743  
NAME/KEY: unsure  
LOCATION: 3, 81  
OTHER INFORMATION: a, t, c, g, or other  
US-09-540-229-15688

Query Match  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 111 agaacagcagccagcca 128  
Db 29 AGAACAGCAGCCAGCCCA 12

RESULT 31  
US-60-048-002-928/C  
Sequence 928, Application US/60048002  
GENERAL INFORMATION:  
APPLICANT: Gooding, Douglas H.  
APPLICANT: Stuve, Laura L.  
APPLICANT: Stuart, Susan G.  
APPLICANT: Ito, Laura Y.  
APPLICANT: Akerblom, Ingrid E.  
APPLICANT: Delegeane, Angelo M.  
APPLICANT: Naughton, Rebecca E.  
APPLICANT: Klingler, Tod M.  
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM  
TITLE OF INVENTION: HUMAN BRAIN  
NUMBER OF SEQUENCES: 4483  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA

ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/60/048,002  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: CERRONE, MICHAEL C.  
REGISTRATION NUMBER: 39,132  
REFERENCE/DOCKET NUMBER: PD-0370P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 855-0555  
TELEFAX: (415) 845-4166  
INFORMATION FOR SEQ ID NO: 928:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 85 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
IMMEDIATE SOURCE:  
CLONE: 3244053H1  
US-60-048-002-928

Query Match  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 111 agaacagcagccagcca 128  
Db 29 AGAACAGCAGCCAGCCCA 12

RESULT 32  
US-09-513-991-2039  
Sequence 2039, Application US/09513991  
GENERAL INFORMATION:  
APPLICANT: Gearing, David P.  
APPLICANT: Fraser, Christopher C.  
APPLICANT: Holtzman, Douglas A.  
APPLICANT: Jakubowski, Joseph A.  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM  
FILE REFERENCE: 1600.1083-001  
CURRENT APPLICATION NUMBER: US/09/513,991  
EARLIER APPLICATION NUMBER: 60/123,397  
EARLIER FILING DATE: 1999-03-08  
NUMBER OF SEQ ID NOS: 3378  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2039  
LENGTH: 180  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)-(180)  
OTHER INFORMATION: n = A,T,C or G  
US-09-513-991-2039

Query Match  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 92 tcggtctctccgcagcg 109  
Db 1 tcggtctctccgcagcg 18

RESULT 33  
US-08-810-326-2151/C  
; Sequence 2151, Application US/08810326  
; GENERAL INFORMATION:  
; APPLICANT: Gooding, Douglas H.  
; APPLICANT: Stuve, Laura L.  
; APPLICANT: Stuart, Susan G.  
; APPLICANT: Ito, Laura Y.  
; APPLICANT: Akerblom, Ingrid E.  
; APPLICANT: Delegeane, Angela E.  
; APPLICANT: Naughton, Rebecca E.  
; APPLICANT: Klingler, Tod M.  
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM  
; TITLE OF INVENTION: HUMAN LUNG  
; NUMBER OF SEQUENCES: 3314  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/810,326  
; FILING DATE: HEREWITH  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/012,699  
; FILING DATE: FEBRUARY 29, 1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/015,173  
; FILING DATE: APRIL 10, 1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CERRONE, MICHAEL C.  
; REGISTRATION NUMBER: 39,132  
; REFERENCE/DOCKET NUMBER: PD-0121 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 855-0555  
; TELEFAX: (415) 845-4166  
; INFORMATION FOR SEQ ID NO: 2151:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 234 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; IMMEDIATE SOURCE:  
; CLONE: 765907  
; US-08-810-326-2151

Query Match 3.0%; Score 18; DB 12; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 gtagctgcgtcgtcgctg 61  
|||||  
Db 136 GTAGCTGCGTCTGCGCTG 119

RESULT 34  
US-09-540-212A-11685/C  
; Sequence 11685, Application US/09540212A  
; GENERAL INFORMATION:

; APPLICANT: Seilhamer, Jeffrey J.  
; APPLICANT: Delegeane, Angelo M.  
; APPLICANT: Stuart, Susan G.  
; APPLICANT: Stuve, Laura L.  
; APPLICANT: Mullahy, Sara J.  
; APPLICANT: Naughton, Rebecca E.  
; TITLE OF INVENTION: POLYNUCLEOTIDES OF AIRWAY AND LUNG SYSTEM TISSUE  
; FILE REFERENCE: PD-1034 CIP  
; CURRENT APPLICATION NUMBER: US/09/540,212A  
; CURRENT FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 67551  
; SOFTWARE: PERL Program  
; SEQ ID NO 11685  
; LENGTH: 234  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Incyte ID No: hu00594097  
; LOCATION: 84, 99  
; OTHER INFORMATION: a, t, c, g, or other  
; US-09-540-212A-11685

Query Match 3.0%; Score 18; DB 21; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 gtagctgcgtcgtcgctg 61  
|||||  
Db 136 GTAGCTGCGTCTGCGCTG 119

RESULT 35  
US-08-878-507-222/C  
; Sequence 222, Application US/08878507  
; GENERAL INFORMATION:  
; APPLICANT: Gooding, Douglas H.  
; APPLICANT: Stuve, Laura L.  
; APPLICANT: Stuart, Susan G.  
; APPLICANT: Ito, Laura Y.  
; APPLICANT: Akerblom, Ingrid E.  
; APPLICANT: Delegeane, Angela M.  
; APPLICANT: Naughton, Rebecca E.  
; APPLICANT: Klingler, Tod M.  
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM  
; TITLE OF INVENTION: HUMAN LUNG  
; NUMBER OF SEQUENCES: 1429  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/878,507  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/016,092  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: GLAISTER, DEBRA J., PATENT AGENT  
; REGISTRATION NUMBER: 33888  
; REFERENCE/DOCKET NUMBER: PD-0188P  
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 855-0555  
TELEFAX: (415) 845-4166  
INFORMATION FOR SEQ ID NO: 222:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 237 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: 1360155  
US-08-878-507-222

Query Match 3.0%; Score 18; DB 12; Length 237;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 gtagctgcgtcctgctg 61  
|||||  
DB 165 GTAGCTGCCTCCTGCGCTG 148

RESULT 36  
US-09-540-212A-16821/C  
Sequence 16821, Application US/09540212A  
GENERAL INFORMATION:  
APPLICANT: Seilhamer, Jeffrey J.  
APPLICANT: Delegeane, Angelo M.  
APPLICANT: Stuart, Susan G.  
APPLICANT: Stuve, Laura L.  
APPLICANT: Mullahy, Sara J.  
APPLICANT: Naughton, Rebecca E.  
TITLE OF INVENTION: POLYNUCLEOTIDES OF AIRWAY AND LUNG SYSTEM TISSUE  
FILE REFERENCE: PD-1034 CIP  
CURRENT APPLICATION NUMBER: US/09/540.212A  
CURRENT FILING DATE: 2000-03-31  
NUMBER OF SEQ ID NOS: 67551  
SOFTWARE: PERL Program  
SEQ ID NO 16821  
LENGTH: 237  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
OTHER INFORMATION: Incyte ID No: hu00152336  
US-09-540-212A-16821

Query Match 3.0%; Score 18; DB 21; Length 237;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 gtagctgcgtcctgctg 61  
|||||  
DB 165 GTAGCTGCCTCCTGCGCTG 148

RESULT 37  
US-60-016-092-222/C  
Sequence 222, Application US/60016092  
GENERAL INFORMATION:  
APPLICANT: Gooding, Douglas H.  
APPLICANT: Stuve, Laura L.  
APPLICANT: Stuart, Susan G.  
APPLICANT: Ito, Laura Y.  
APPLICANT: Akherblom, Ingrid E.  
APPLICANT: Delegeane, Angelo M.  
APPLICANT: Naughton, Rebecca E.  
APPLICANT: Klingler, Tod M.  
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM  
TITLE OF INVENTION: HUMAN LUNG  
NUMBER OF SEQUENCES: 1429

CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/60/016.092  
FILING DATE:

CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: GLAISTER, DEBRA J., PATENT AGENT  
REGISTRATION NUMBER: 33888  
REFERENCE/DOCKET NUMBER: PD-0188P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 855-0555  
TELEFAX: (415) 845-4166  
INFORMATION FOR SEQ ID NO: 222:

SEQUENCE CHARACTERISTICS:  
LENGTH: 237 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: 1360155  
US-60-016-092-222

Query Match 3.0%; Score 18; DB 33; Length 237;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 gtagctgcgtcctgctg 61  
|||||  
DB 165 GTAGCTGCCTCCTGCGCTG 148

RESULT 38  
US-09-100-454-2483/C  
Sequence 2483, Application US/09100454  
GENERAL INFORMATION:  
APPLICANT: Gooding, Douglas H.  
APPLICANT: Stuart, Susan G.  
APPLICANT: Ito, Laura Y.  
APPLICANT: Naughton, Rebecca E.  
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM  
TITLE OF INVENTION: HUMAN LUNG  
NUMBER OF SEQUENCES: 3617  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/100.454  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/051.749

FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: CERRONE, MICHAEL C.  
REGISTRATION NUMBER: 39,132  
REFERENCE/DOCKET NUMBER: PD-0388P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 855-0555  
TELEFAX: (415) 845-4166  
INFORMATION FOR SEQ ID NO: 2483:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 248 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: 2691009H1  
US-09-100-454-2483

Query Match 3.0%; Score 18; DB 15; Length 248;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 44 gtatcgctgcctgcctgctg 61  
|||||  
DB 209 GTAGCTGCGTCTGGCTG 192

RESULT 39  
US-09-540-212A-35497/C  
Sequence 35497, Application US/09540212A  
GENERAL INFORMATION:  
APPLICANT: Sellhauer, Jeffrey J.  
APPLICANT: Delegeane, Angelo M.  
APPLICANT: Stuart, Susan G.  
APPLICANT: Stuve, Laura L.  
APPLICANT: Mullahy, Sara J.  
APPLICANT: Naughton, Rebecca E.  
TITLE OF INVENTION: POLYNUCLEOTIDES OF AIRWAY AND LUNG SYSTEM TISSUE  
FILE REFERENCE: PD-1034 CIP  
CURRENT APPLICATION NUMBER: US/09/540,212A  
CURRENT FILING DATE: 2000-03-31  
NUMBER OF SEQ ID NOS: 67551  
SOFTWARE: PERL Program  
SEQ ID NO 35497  
LENGTH: 248  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
OTHER INFORMATION: Incyte ID No: hu00026037  
US-09-540-212A-35497

Query Match 3.0%; Score 18; DB 21; Length 248;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 44 gtatcgctgcctgcctgctg 61  
|||||  
DB 209 GTAGCTGCGTCTGGCTG 192

RESULT 40  
US-60-051-749-2483/C  
Sequence 2483, Application US/60051749  
GENERAL INFORMATION:  
APPLICANT: Gooding, Douglas H.  
APPLICANT: Stuart, Susan G.  
APPLICANT: Ito, Laura Y.  
APPLICANT: Naughton, Rebecca E.  
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM

TITLE OF INVENTION: HUMAN LUNG  
NUMBER OF SEQUENCES: 3617  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/60/051,749  
FILING DATE: HERewith  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: CERRONE, MICHAEL C.  
REGISTRATION NUMBER: 39,132  
REFERENCE/DOCKET NUMBER: PD-0388P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 855-0555  
TELEFAX: (415) 845-4166  
INFORMATION FOR SEQ ID NO: 2483:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 248 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: 2691009H1  
US-60-051-749-2483

Query Match 3.0%; Score 18; DB 37; Length 248;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 44 gtatcgctgcctgcctgctg 61  
|||||  
DB 209 GTAGCTGCGTCTGGCTG 192

RESULT 41  
US-60-048-722-3053/C  
Sequence 3053, Application US/60048722  
GENERAL INFORMATION:  
APPLICANT: Gooding, Douglas H.  
APPLICANT: Stuve, Laura L.  
APPLICANT: Stuart, Susan G.  
APPLICANT: Ito, Laura Y.  
APPLICANT: Akerblom, Ingrid E.  
APPLICANT: Delegeane, Angelo M.  
APPLICANT: Naughton, Rebecca E.  
APPLICANT: Klingler, Tod M.  
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM  
NUMBER OF SEQUENCES: 3106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2



;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/60/048,722  
;; FILING DATE: HEREMITH  
;; CLASSIFICATION:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: CERRONE, MICHAEL C.  
;; REGISTRATION NUMBER: 39,132  
;; REFERENCE/DOCKET NUMBER: PD-0381P  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 855-0555  
;; TELEFAX: (415) 845-4166  
;; INFORMATION FOR SEQ ID NO: 3053:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 249 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: cDNA  
;; IMMEDIATE SOURCE:  
;; CLONE: 2933007H1  
;; US-60-048-722-3053

Query Match 3.0%; Score 18; DB 36; Length 249;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 gcagggaagacagcagc 121  
|||||  
Db 190 GCAGGAGAGACAGCAGC 173

## RESULT 42

US-08-992-625-3252/C

Sequence 3252, Application US/08992625

GENERAL INFORMATION:

APPLICANT: Gooding, Douglas H.

APPLICANT: Stuve, Laura L.

APPLICANT: Stuart, Susan G.

APPLICANT: Ito, Laura Y.

APPLICANT: Aketblom, Ingrid E.

APPLICANT: Delegeane, Angelo M.

APPLICANT: Naughton, Rebecca E.

APPLICANT: Klingler, Tod M.

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM

NUMBER OF INVENTIONS: HUMAN UTERUS

NUMBER OF SEQUENCES: 3446

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/992,625

FILING DATE: HEREMITH

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/036,187

FILING DATE: DECEMBER 18, 1996

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: CERRONE, MICHAEL C.

REGISTRATION NUMBER: 39,132

REFERENCE/DOCKET NUMBER: PD-0288 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 855-0555

;; TELEFAX: (650) 845-4166  
;; INFORMATION FOR SEQ ID NO: 3252:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 253 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: cDNA  
;; IMMEDIATE SOURCE:  
;; CLONE: 2264459H1  
;; US-08-992-625-3252

Query Match 3.0%; Score 18; DB 13; Length 253;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 44 gtagctgcgtcctgcgtg 61  
|||||  
Db 59 GTAGCTGCCTCCTGCCTG 42

## RESULT 43

US-09-540-764-10498/C

Sequence 10498, Application US/09540764

GENERAL INFORMATION:

APPLICANT: Sellhammer, Jeffrey J.

APPLICANT: Delegeane, Angelo M.

APPLICANT: Stuart, Susan G.

APPLICANT: Stuve, Laura L.

APPLICANT: Mullahy, Sara J.

APPLICANT: Naughton, Rebecca E.

TITLE OF INVENTION: POLYNUCLEOTIDES OF CELLS AND TISSUES OF THE FEMALE REPRODUCTI

FILE REFERENCE: PD-1028 CIP

CURRENT APPLICATION NUMBER: US/09/540,764

CURRENT FILING DATE: 2000-03-30

Prior application data removed - refer to PALM or file wrapper

NUMBER OF SEQ ID NOS: 61458

SOFTWARE: PERL Program

SEQ ID NO 10498

LENGTH: 253

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc.feature

OTHER INFORMATION: Incyte ID No: hu0822021

US-09-540-764-10498

Query Match 3.0%; Score 18; DB 21; Length 253;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 44 gtagctgcgtcctgcgtg 61  
|||||  
Db 59 GTAGCTGCCTCCTGCCTG 42

## RESULT 44

US-60-197-872-21718

Sequence 21718, Application US/60197872

GENERAL INFORMATION:

APPLICANT: Bougri, Olegs

APPLICANT: Byrum, Joseph R.

APPLICANT: De La Pena, Robert C.

APPLICANT: La Rosa, Thomas J.

APPLICANT: Shukla, Hridayabhiranjan

TITLE OF INVENTION: Nucleic acid Molecules and other molecules associated w/1

TITLE REFERENCE: 38-21(51892)A

CURRENT APPLICATION NUMBER: US/60/197,872

CURRENT FILING DATE: 2000-04-19

NUMBER OF SEQ ID NOS: 76255



FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-270-849B-53924

Query Match 3.0%; Score 18; DB 16; Length 269;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 240 accccctgttcagcgcc 257  
|||||  
Db 25 ACCCCCTGTTTCAGCGCC 8

RESULT 48  
US-09-298-329A-4053/C  
Sequence 4053, Application US/09298329A  
GENERAL INFORMATION:  
APPLICANT: Laljudi, Raghunath V.  
APPLICANT: Ito, Laura Y.  
APPLICANT: Sherman, Bradley K.  
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING  
FILE REFERENCE: PL-0012 US  
CURRENT APPLICATION NUMBER: US/09/298,329A  
CURRENT FILING DATE: 1999-04-21  
PRIOR APPLICATION NUMBER: 60/085,331  
PRIOR FILING DATE: 1998-05-12  
NUMBER OF SEQ ID NOS: 6332  
SOFTWARE: PERL Program  
SEQ ID NO 4053  
LENGTH: 271  
TYPE: DNA  
ORGANISM: Zea mays  
FEATURE:  
NAME/KEY: misc\_feature  
OTHER INFORMATION: Incyte ID No: 700454335H1  
NAME/KEY: unsure  
LOCATION: 56, 83, 164, 235  
OTHER INFORMATION: a, t, c, g, or other  
US-09-298-329A-4053

Query Match 3.0%; Score 18; DB 16; Length 271;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 524 ccacagccgagcggaac 541  
|||||  
Db 102 CCACAGCCGCGGCGAAC 85

RESULT 49  
US-60-087-762-211/C  
Sequence 211, Application US/60087762  
GENERAL INFORMATION:  
APPLICANT: Christine Shewmaker  
APPLICANT: Dang Yang Ke  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules  
TITLE OF INVENTION: Associated with the Isoflavone pathway  
NUMBER OF SEQUENCES: 336  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lawrence M. Lavin, Jr.  
STREET: BB4F  
STREET: Monsanto Company  
STREET: 700 Chesterfield Parkway North  
CITY: St. Louis  
STATE: MO  
COUNTRY: United States  
ZIP: 63198  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette (3.5in, 1.44 Mb)  
COMPUTER: IBM PC/XT/AT, IBM PS/2 or compatibles

OPERATING SYSTEM: Windows 95/NT  
SOFTWARE: Stuffit Deluxe 4.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/60/087,762  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Lavin Jr., Lawrence M.  
REGISTRATION NUMBER: 30,768  
REFERENCE/DOCKET NUMBER: 04983,0037/38-21(15405)A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 737-6670  
TELEFAX: (314) 737-6047  
INFORMATION FOR SEQ ID NO: 211:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 271 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Zea mays  
DEVELOPMENTAL STAGE: etiolated 4 days  
TISSUE TYPE: seedling  
IMMEDIATE SOURCE:  
LIBRARY: SATMON029  
CLONE: 700454335  
US-60-087-762-211

Query Match 3.0%; Score 18; DB 40; Length 271;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 524 ccacagccgagcggaac 541  
|||||  
Db 102 CCACAGCCGCGGCGAAC 85

RESULT 50  
US-60-092-036-941/C  
Sequence 941, Application US/60092036  
GENERAL INFORMATION:  
APPLICANT: Mitsky, Timothy A.  
APPLICANT: Liu, Jingdong  
TITLE OF INVENTION: Nucleic acid molecules and other molecules  
TITLE OF INVENTION: associated with the Phenylpropanoid Biosynthetic pathway  
NUMBER OF SEQUENCES: 2020  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lawrence M. Lavin, Jr.  
STREET: BB4F  
STREET: Monsanto Company  
STREET: 700 Chesterfield Parkway North  
CITY: St. Louis  
STATE: MO  
COUNTRY: United States  
ZIP: 63198  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette (3.5in, 1.44 Mb)  
COMPUTER: IBM PC/XT/AT, IBM PS/2 or compatibles  
OPERATING SYSTEM: Windows 95/NT  
SOFTWARE: Winzip 6.3  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/60/092,036  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Lavin Jr., Lawrence M.  
REGISTRATION NUMBER: 30,768  
REFERENCE/DOCKET NUMBER: 04983,0045/38-21(15427)A  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (314) 737-6670  
 TELEFAX: (314) 737-6047  
 INFORMATION FOR SEQ ID NO: 941:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 271 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Zea mays  
 DEVELOPMENTAL STAGE: etiolated 4 days  
 TISSUE TYPE: seedling  
 IMMEDIATE SOURCE:  
 LIBRARY: SATMON029  
 CLONE: 700454335  
 US-60-092-036-941

Query Match 3.0%; Score 18; DB 41; Length 271;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 524 ccacagccgcgcgcgaac 541  
 ||||||||||||||||  
 DB 102 CCACAGCCGCGCGCAAC 85

Search completed: September 21, 2001, 16:15:12  
 Job time: 9257 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 21, 2001, 21:10:19 : Search time 15806.4 Seconds  
(without alignments)  
955.089 Million cell updates/sec

Title: US-09-138-735-1\_COPY\_1232\_2207  
Perfect score: 976  
Sequence: 1 caggtacagcgtacagcgtc.....tctgaacagcgcattatgt 976

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 1344157 seqs, 7733874588 residues

Word size: 0

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database:

GenEmbl:

- 1: gb\_ba1:\*
- 2: gb\_ba2:\*
- 3: gb\_ba3:\*
- 4: gb\_in1:\*
- 5: gb\_in2:\*
- 6: gb\_in3:\*
- 7: gb\_on:\*
- 8: gb\_ov:\*
- 9: gb\_pat1:\*
- 10: gb\_pat2:\*
- 11: gb\_ph:\*
- 12: gb\_pl1:\*
- 13: gb\_pl2:\*
- 14: gb\_pl3:\*
- 15: gb\_pl4:\*
- 16: em\_ba1:\*
- 17: em\_ba2:\*
- 18: em\_fun:\*
- 19: em\_htgo\_hum:\*
- 20: em\_htgo\_inv:\*
- 21: em\_htgo\_rod:\*
- 22: em\_htg\_hum1:\*
- 23: em\_htg\_hum2:\*
- 24: em\_htg\_hum3:\*
- 25: em\_htg\_hum4:\*
- 26: em\_htg\_hum5:\*
- 27: em\_htg\_hum6:\*
- 28: em\_htg\_hum7:\*
- 29: em\_htg\_hum8:\*
- 30: em\_htg\_inv1:\*
- 31: em\_htg\_inv2:\*
- 32: em\_htg\_other:\*
- 33: em\_htg\_rod:\*
- 34: em\_hum1:\*
- 35: em\_hum2:\*
- 36: em\_hum3:\*
- 37: em\_hum4:\*
- 38: em\_hum5:\*
- 39: em\_hum6:\*
- 40: em\_hum7:\*
- 41: em\_in:\*
- 42: em\_on:\*
- 43: em\_or:\*

Oligo search  
ST

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | ID       | Description |
|------------|-------|--------------------|----------|-------------|
| 1          | 976   | 100.0              | 3402 9   | AR047920    |
| 2          | 874   | 89.5               | 3402 9   | A48910      |
| 3          | 874   | 89.5               | 3402 96  | TCU24190    |
| 4          | 22    | 2.3                | 22 9     | A48918      |
| 5          | 22    | 2.3                | 22 9     | AR047927    |
| 6          | 22    | 2.3                | 331801 3 | NMA422491   |
| 7          | 21    | 2.2                | 21 9     | A48919      |
| 8          | 21    | 2.2                | 21 9     | A48921      |

- 44: em\_ov:\*
- 45: em\_pat:\*
- 46: em\_ph:\*
- 47: em\_pl:\*
- 48: em\_ro:\*
- 49: em\_sts:\*
- 50: em\_sy:\*
- 51: em\_un:\*
- 52: em\_vl:\*
- 53: gb\_sts1:\*
- 54: gb\_sts2:\*
- 55: gb\_sts3:\*
- 56: gb\_sy:\*
- 57: gb\_un:\*
- 58: gb\_vl1:\*
- 59: gb\_vl2:\*
- 60: gb\_hcg1:\*
- 61: gb\_hcg2:\*
- 62: gb\_hcg3:\*
- 63: gb\_hcg4:\*
- 64: gb\_hcg5:\*
- 65: gb\_hcg6:\*
- 66: gb\_hcg7:\*
- 67: gb\_hcg8:\*
- 68: gb\_hcg9:\*
- 69: gb\_hcg10:\*
- 70: gb\_hcg11:\*
- 71: gb\_hcg12:\*
- 72: gb\_hcg13:\*
- 73: gb\_hcg14:\*
- 74: gb\_hcg15:\*
- 75: gb\_hcg16:\*
- 76: gb\_hcg17:\*
- 77: gb\_hcg18:\*
- 78: gb\_hcg19:\*
- 79: gb\_hcg20:\*
- 80: gb\_hcg21:\*
- 81: gb\_hcg22:\*
- 82: gb\_hcg23:\*
- 83: gb\_hcg24:\*
- 84: gb\_hcg25:\*
- 85: gb\_pr1:\*
- 86: gb\_pr2:\*
- 87: gb\_pr3:\*
- 88: gb\_pr4:\*
- 89: gb\_pr5:\*
- 90: gb\_pr6:\*
- 91: gb\_pr7:\*
- 92: gb\_pr8:\*
- 93: gb\_pr9:\*
- 94: gb\_fo1:\*
- 95: gb\_fo2:\*
- 96: gb\_in4:\*
- 97: gb\_pr10:\*
- 98: em\_ba3:\*

|   |    |    |     |        |    |            |                    |   |     |    |     |        |    |              |                                 |
|---|----|----|-----|--------|----|------------|--------------------|---|-----|----|-----|--------|----|--------------|---------------------------------|
| C | 9  | 21 | 2.2 | 21     | 9  | AR047928   | AR047928 Sequence  | C | 82  | 18 | 1.8 | 58733  | 2  | AF217189     | AF217189 Scorangium             |
| C | 10 | 21 | 2.0 | 21     | 9  | AR047930   | AR047930 Sequence  | C | 83  | 18 | 1.8 | 62271  | 13 | ATAC013454   | ATAC013454 Arabidops            |
| C | 11 | 20 | 2.0 | 72056  | 62 | AC011183   | AC011183 Homo sapi | C | 84  | 18 | 1.8 | 68750  | 2  | AF210843     | AF210843 Sorangium              |
| C | 12 | 20 | 2.0 | 91470  | 12 | AC011438   | AC011438 Genomic s | C | 85  | 18 | 1.8 | 78596  | 12 | AB010695     | AB010695 Arabidops              |
| C | 13 | 20 | 2.0 | 115243 | 90 | AL157771   | AL157771 Human DNA | C | 86  | 18 | 1.8 | 80515  | 87 | AC011992     | AC011992 Homo sapi              |
| C | 14 | 20 | 2.0 | 153259 | 88 | AC087859   | AC087859 Homo sapi | C | 87  | 18 | 1.8 | 87045  | 13 | ATAC012393   | ATAC012393 Arabidops            |
| C | 15 | 20 | 2.0 | 155075 | 65 | AC018355   | AC018355 Homo sapi | C | 88  | 18 | 1.8 | 91470  | 12 | AC011438     | AC011438 Genomic s              |
| C | 16 | 20 | 2.0 | 171714 | 88 | AC034187   | AC034187 Homo sapi | C | 89  | 18 | 1.8 | 96424  | 14 | ATP22911     | ATP22911 Arabidops              |
| C | 17 | 20 | 2.0 | 177816 | 65 | AC017643   | AC017643 Drosophil | C | 90  | 18 | 1.8 | 97749  | 85 | AC004906     | AC004906 Homo sapi              |
| C | 18 | 20 | 2.0 | 182365 | 81 | AL512648   | AL512648 Homo sapi | C | 91  | 18 | 1.8 | 110000 | 61 | AC009579     | AC009579 Continuation (2 of     |
| C | 19 | 20 | 2.0 | 194897 | 4  | AC007697   | AC007697 Drosophil | C | 92  | 18 | 1.8 | 110000 | 75 | AC073763     | AC073763 Mus muscu              |
| C | 20 | 20 | 2.0 | 203195 | 67 | AC022397   | AC022397 Mus muscu | C | 93  | 18 | 1.8 | 110000 | 84 | LMFLCHR32_03 | LMFLCHR32_03 Continuation (4 of |
| C | 21 | 20 | 2.0 | 223589 | 69 | AC025210   | AC025210 Homo sapi | C | 94  | 18 | 1.8 | 110684 | 12 | AC006601     | AC006601 Arabidops              |
| C | 22 | 20 | 2.0 | 262395 | 5  | AE003802   | AE003802 Drosophil | C | 95  | 18 | 1.8 | 113345 | 88 | AF109076     | AF109076 Homo sapi              |
| C | 23 | 19 | 1.9 | 1152   | 14 | D89210     | D89210 Schizosacch | C | 96  | 18 | 1.8 | 115429 | 81 | AL500525     | AL500525 Homo sapi              |
| C | 24 | 19 | 1.9 | 1279   | 94 | AF273691   | AF273691 Mus muscu | C | 97  | 18 | 1.8 | 115925 | 75 | AC074128     | AC074128 Homo sapi              |
| C | 25 | 19 | 1.9 | 10128  | 94 | AE005021   | AE005021 Halobacte | C | 98  | 18 | 1.8 | 124510 | 88 | AC027306     | AC027306 Homo sapi              |
| C | 26 | 19 | 1.9 | 11873  | 9  | AR083116   | AR083116 Sequence  | C | 99  | 18 | 1.8 | 127593 | 86 | AC006236     | AC006236 Homo sapi              |
| C | 27 | 19 | 1.9 | 11878  | 9  | AR083115   | AR083115 Sequence  | C | 100 | 18 | 1.8 | 129606 | 83 | AP003379     | AP003379 Oryza sat              |
| C | 28 | 19 | 1.9 | 11883  | 9  | AR083114   | AR083114 Sequence  | C | 101 | 18 | 1.8 | 132910 | 64 | AC016342     | AC016342 Homo sapi              |
| C | 29 | 19 | 1.9 | 36493  | 15 | SPBC262    | AL022103 S.pombe   | C | 102 | 18 | 1.8 | 135303 | 73 | AC068257     | AC068257 Homo sapi              |
| C | 30 | 19 | 1.9 | 67442  | 63 | AC015691   | AC015691 Homo sapi | C | 103 | 18 | 1.8 | 137506 | 85 | AC004824     | AC004824 Homo sapi              |
| C | 31 | 19 | 1.9 | 79970  | 62 | AC011428   | AC011428 Homo sapi | C | 104 | 18 | 1.8 | 139043 | 78 | AC090974     | AC090974 Oryza sat              |
| C | 32 | 19 | 1.9 | 82033  | 94 | AC068903   | AC068903 Mus muscu | C | 105 | 18 | 1.8 | 144057 | 78 | AL138798     | AL138798 Homo sapi              |
| C | 33 | 19 | 1.9 | 95232  | 94 | AC068952   | AC068952 Mus muscu | C | 106 | 18 | 1.8 | 147042 | 62 | AC011647     | AC011647 Homo sapi              |
| C | 34 | 19 | 1.9 | 11000  | 79 | AL534832_1 | Continuation (2 of | C | 107 | 18 | 1.8 | 154461 | 69 | AC025711     | AC025711 Homo sapi              |
| C | 35 | 19 | 1.9 | 111071 | 68 | AC020962   | AC020962 Mus muscu | C | 108 | 18 | 1.8 | 154788 | 66 | AC021498     | AC021498 Homo sapi              |
| C | 36 | 19 | 1.9 | 128562 | 66 | AC020962   | AC020962 Mus muscu | C | 109 | 18 | 1.8 | 157349 | 78 | AF145206     | AF145206 Homo sapi              |
| C | 37 | 19 | 1.9 | 130734 | 94 | AC073882   | AC073882 Mus muscu | C | 110 | 18 | 1.8 | 157981 | 85 | AC005184     | AC005184 Homo sapi              |
| C | 38 | 19 | 1.9 | 131888 | 93 | HS1057D4   | AL121777 Human DNA | C | 111 | 18 | 1.8 | 158427 | 79 | AL355516     | AL355516 Homo sapi              |
| C | 39 | 19 | 1.9 | 134506 | 86 | AC005738   | AC005738 Homo sapi | C | 112 | 18 | 1.8 | 162474 | 79 | AL158169     | AL158169 Homo sapi              |
| C | 40 | 19 | 1.9 | 141158 | 68 | AC023898   | AC023898 Mus muscu | C | 113 | 18 | 1.8 | 164679 | 86 | AC005921     | AC005921 Homo sapi              |
| C | 41 | 19 | 1.9 | 147009 | 76 | AC083479   | AC083479 Homo sapi | C | 114 | 18 | 1.8 | 169195 | 67 | AC023165     | AC023165 Homo sapi              |
| C | 42 | 19 | 1.9 | 156599 | 76 | AC083840   | AC083840 Homo sapi | C | 115 | 18 | 1.8 | 169804 | 71 | AC027741     | AC027741 Homo sapi              |
| C | 43 | 19 | 1.9 | 160404 | 71 | AC034236   | AC034236 Homo sapi | C | 116 | 18 | 1.8 | 173081 | 78 | AL137001     | AL137001 Homo sapi              |
| C | 44 | 19 | 1.9 | 161549 | 64 | AC015815   | AC015815 Homo sapi | C | 117 | 18 | 1.8 | 173843 | 77 | AC084405     | AC084405 Oryza sat              |
| C | 45 | 19 | 1.9 | 170431 | 61 | AC009108   | AC009108 Homo sapi | C | 118 | 18 | 1.8 | 176816 | 62 | AC011372     | AC011372 Homo sapi              |
| C | 46 | 19 | 1.9 | 175249 | 63 | AC013543   | AC013543 Homo sapi | C | 119 | 18 | 1.8 | 177424 | 61 | AC009832     | AC009832 Homo sapi              |
| C | 47 | 19 | 1.9 | 178751 | 80 | AL356772   | AL356772 Homo sapi | C | 120 | 18 | 1.8 | 177720 | 69 | AC025680     | AC025680 Homo sapi              |
| C | 48 | 19 | 1.9 | 179844 | 83 | AP002501   | AP002501 Homo sapi | C | 121 | 18 | 1.8 | 180788 | 76 | AC083757     | AC083757 Homo sapi              |
| C | 49 | 19 | 1.9 | 180717 | 73 | AC068169   | AC068169 Homo sapi | C | 122 | 18 | 1.8 | 180863 | 76 | AC079809     | AC079809 Homo sapi              |
| C | 50 | 19 | 1.9 | 181853 | 68 | AC024507   | AC024507 Homo sapi | C | 123 | 18 | 1.8 | 183235 | 66 | AC020714     | AC020714 Homo sapi              |
| C | 51 | 19 | 1.9 | 184012 | 87 | AC017080   | AC017080 Homo sapi | C | 124 | 18 | 1.8 | 185417 | 77 | AC084356     | AC084356 Homo sapi              |
| C | 52 | 19 | 1.9 | 185380 | 78 | AL136119   | AL136119 Homo sapi | C | 125 | 18 | 1.8 | 185317 | 62 | AC012059     | AC012059 Homo sapi              |
| C | 53 | 19 | 1.9 | 185892 | 78 | AC090652   | AC090652 Mus muscu | C | 126 | 18 | 1.8 | 193444 | 13 | AF229199     | AF229199 Oryza sat              |
| C | 54 | 19 | 1.9 | 191257 | 74 | AC069560   | AC069560 Mus muscu | C | 127 | 18 | 1.8 | 197772 | 60 | AC008129     | AC008129 Homo sapi              |
| C | 55 | 19 | 1.9 | 194575 | 81 | AL512653   | AL512653 Homo sapi | C | 128 | 18 | 1.8 | 199588 | 69 | AC026083     | AC026083 Homo sapi              |
| C | 56 | 19 | 1.9 | 198453 | 62 | AC011359   | AC011359 Homo sapi | C | 129 | 18 | 1.8 | 203200 | 87 | AC008744     | AC008744 Homo sapi              |
| C | 57 | 19 | 1.9 | 200860 | 81 | AL445211   | AL445211 Homo sapi | C | 130 | 18 | 1.8 | 207221 | 62 | AC012564     | AC012564 Homo sapi              |
| C | 58 | 19 | 1.9 | 235141 | 85 | AC004615   | AC004615 Homo sapi | C | 131 | 18 | 1.8 | 217730 | 77 | AC084823     | AC084823 Mus muscu              |
| C | 59 | 19 | 1.9 | 296050 | 79 | AL354813   | AL354813 Homo sapi | C | 132 | 18 | 1.8 | 218553 | 76 | AC079940     | AC079940 Mus muscu              |
| C | 60 | 18 | 1.8 | 18     | 9  | A48914     | A48914 Sequence 5  | C | 133 | 18 | 1.8 | 220459 | 75 | AC074307     | AC074307 Mus muscu              |
| C | 61 | 18 | 1.8 | 18     | 9  | A48917     | A48917 Sequence 8  | C | 134 | 18 | 1.8 | 224376 | 61 | AC010538     | AC010538 Homo sapi              |
| C | 62 | 18 | 1.8 | 18     | 9  | AR047923   | AR047923 Sequence  | C | 135 | 18 | 1.8 | 230760 | 74 | AC073714     | AC073714 Mus muscu              |
| C | 63 | 18 | 1.8 | 18     | 9  | AR047926   | AR047926 Sequence  | C | 136 | 18 | 1.8 | 326419 | 76 | AC079635     | AC079635 Mus muscu              |
| C | 64 | 18 | 1.8 | 339    | 53 | AU049339   | AU049339 Rattus no | C | 137 | 17 | 1.7 | 138    | 58 | AF065721     | AF065721 Stealch v              |
| C | 65 | 18 | 1.8 | 939    | 12 | AF134126   | AF134126 Arabidops | C | 138 | 17 | 1.7 | 339    | 93 | HSNOS2E17    | HSNOS2E17 X85773 H.sapiens N    |
| C | 66 | 18 | 1.8 | 942    | 13 | AF143691   | AF143691 Arabidops | C | 139 | 17 | 1.7 | 368    | 54 | G02521       | G02521 human STS W              |
| C | 67 | 18 | 1.8 | 952    | 13 | AF361858   | AF361858 Arabidops | C | 140 | 17 | 1.7 | 376    | 53 | AU026316     | AU026316 Rattus no              |
| C | 68 | 18 | 1.8 | 1589   | 10 | AX086831   | AX086831 Sequence  | C | 141 | 17 | 1.7 | 383    | 76 | AC080428     | AC080428 Giardia i              |
| C | 69 | 18 | 1.8 | 1589   | 93 | HSW801826  | AL136858 Homo sapi | C | 142 | 17 | 1.7 | 388    | 54 | G47871       | G47871 Z26401.1 ze              |
| C | 70 | 18 | 1.8 | 2520   | 9  | AR051460   | AR051460 Sequence  | C | 143 | 17 | 1.7 | 400    | 58 | AF174900     | AF174900 HIV-1 iso              |
| C | 71 | 18 | 1.8 | 2520   | 9  | AR072620   | AR072620 Sequence  | C | 144 | 17 | 1.7 | 424    | 54 | AF174963     | AF174963 HIV-1 iso              |
| C | 72 | 18 | 1.8 | 2520   | 9  | AR073165   | AR073165 Sequence  | C | 145 | 17 | 1.7 | 424    | 54 | G24099       | G24099 human STS W              |
| C | 73 | 18 | 1.8 | 2723   | 89 | AK026431   | AK026431 Homo sapi | C | 146 | 17 | 1.7 | 661    | 8  | AF243428     | AF243428 Oncorhync              |
| C | 74 | 18 | 1.8 | 4126   | 4  | AC006817   | AC006817 Ceenorhab | C | 147 | 17 | 1.7 | 663    | 88 | AF001597     | AF001597 Homo sapi              |
| C | 75 | 18 | 1.8 | 9450   | 59 | HPC06817   | D63821 Hepatitis C | C | 148 | 17 | 1.7 | 687    | 9  | AX017873     | AX017873 Sequence               |
| C | 76 | 18 | 1.8 | 10863  | 1  | AE005678   | AE005678 Caulodact | C | 149 | 17 | 1.7 | 804    | 88 | AF110775     | AF110775 Homo sapi              |
| C | 77 | 18 | 1.8 | 11031  | 1  | AE004648   | AE004648 Pseudomon | C | 150 | 17 | 1.7 | 839    | 93 | HS250393     | HS250393 Homo sapi              |
| C | 78 | 18 | 1.8 | 14704  | 1  | AE001970   | AE001970 Deinococc | C | 151 | 17 | 1.7 | 915    | 77 | AC085350     | AC085350 Giardia i              |
| C | 79 | 18 | 1.8 | 33803  | 6  | CELC3443   | AC006614 Ceenorhab | C | 152 | 17 | 1.7 | 920    | 71 | AC034857     | AC034857 Giardia i              |
| C | 80 | 18 | 1.8 | 38000  | 61 | AC010079   | AC010079 Leishmani | C | 153 | 17 | 1.7 | 925    | 53 | CNS07446     | CNS07446 Clone BA0              |
| C | 81 | 18 | 1.8 | 42000  | 77 | AC087836   | AC087836 Leishmani | C | 154 | 17 | 1.7 | 945    | 7  | BOVCCOSD     | BOVCCOSD Bos taurus             |

|       |    |     |       |    |            |                     |       |    |     |        |    |              |                        |
|-------|----|-----|-------|----|------------|---------------------|-------|----|-----|--------|----|--------------|------------------------|
| 155   | 17 | 1.7 | 969   | 93 | MSM800753  | AL080224 Homo sapi  | c 228 | 17 | 1.7 | 35525  | 77 | AC087068     | AC087068 Leishmani     |
| 156   | 17 | 1.7 | 977   | 94 | MMU250394  | AJ250394 Mus muscu  | 229   | 17 | 1.7 | 35896  | 12 | AB024027     | AB024027 Arabidops     |
| 157   | 17 | 1.7 | 990   | 53 | CNS0272C   | AT426862 clone BA0  | 230   | 17 | 1.7 | 36849  | 3  | SC1C3        | AL023702 Streptomy     |
| 158   | 17 | 1.7 | 993   | 5  | AF190457   | AF190457 Trypanoso  | c 231 | 17 | 1.7 | 37056  | 85 | AC004700     | AC004700 Homo sapi     |
| c 159 | 17 | 1.7 | 1009  | 71 | AC029282   | AC029282 Giardia 1  | c 232 | 17 | 1.7 | 38024  | 6  | CLEP52B10    | U41990 Caenorhabdi     |
| c 160 | 17 | 1.7 | 1046  | 89 | AF161497   | AF161497 Homo sapi  | c 233 | 17 | 1.7 | 38919  | 86 | AC005947     | AC005947 Homo sapi     |
| c 161 | 17 | 1.7 | 1067  | 54 | CNS07B1H   | AL437919 T7 end of  | c 234 | 17 | 1.7 | 39207  | 3  | SC4G1        | AL391039 Streptomy     |
| c 162 | 17 | 1.7 | 1062  | 94 | BC004726   | BC004726 Mus muscu  | c 235 | 17 | 1.7 | 39266  | 86 | AC005791     | AC005791 Homo sapi     |
| c 163 | 17 | 1.7 | 1063  | 5  | AF316150   | AF316150 Trypanoso  | c 236 | 17 | 1.7 | 39436  | 85 | AB000879     | AB000879 Homo sapi     |
| c 164 | 17 | 1.7 | 1151  | 53 | CNS06TMT   | AL414747 T3 end of  | c 237 | 17 | 1.7 | 40121  | 3  | MSGY414A     | AD000007 Mycobacte     |
| c 165 | 17 | 1.7 | 1181  | 97 | H0UMH1     | L93976 Homo sapien  | c 238 | 17 | 1.7 | 40673  | 6  | LMFL377      | AL136326 Leishmani     |
| c 166 | 17 | 1.7 | 1454  | 1  | AF075168   | AF075168 Brucella   | c 239 | 17 | 1.7 | 40881  | 85 | AC004679     | AC004679 Homo sapi     |
| c 167 | 17 | 1.7 | 1499  | 2  | BSP29998   | Z99998 Uncultured   | c 240 | 17 | 1.7 | 40910  | 85 | AC005260     | AC005260 Homo sapi     |
| c 168 | 17 | 1.7 | 1516  | 8  | AF247363   | AF247363 Palaeosuch | c 241 | 17 | 1.7 | 42139  | 85 | AC004654     | AC004654 Homo sapi     |
| c 169 | 17 | 1.7 | 1517  | 15 | ZMA5702    | Y13733 Zea mays mr  | c 242 | 17 | 1.7 | 42467  | 6  | CEPFL26R12   | U55373 Caenorhabdi     |
| c 170 | 17 | 1.7 | 1517  | 15 | ZMA5702    | AA005702 Zea mays   | c 243 | 17 | 1.7 | 42584  | 89 | AF215839     | AF215839 Homo sapi     |
| c 171 | 17 | 1.7 | 1671  | 53 | AF309358   | AF309358 Hordeum v  | c 244 | 17 | 1.7 | 42649  | 88 | AC024077     | AC024077 Homo sapi     |
| c 172 | 17 | 1.7 | 1675  | 3  | RS06694    | U03632 Chlamydomon  | c 245 | 17 | 1.7 | 43147  | 3  | SC4A10       | AL109663 Streptomy     |
| c 173 | 17 | 1.7 | 2002  | 14 | CRU03632   | Z70290 S. macrospor | c 246 | 17 | 1.7 | 43401  | 3  | MTY13E12     | Z95390 Mycobacteri     |
| c 174 | 17 | 1.7 | 2242  | 15 | SMTUBA     | U63336 Human MHC C  | c 247 | 17 | 1.7 | 43430  | 3  | MTY13E12     | Z81331 Mycobacteri     |
| c 175 | 17 | 1.7 | 2261  | 97 | HSU63336   | AL117521 Homo sapi  | c 248 | 17 | 1.7 | 43600  | 85 | AC004209     | AC004209 Homo sapi     |
| c 176 | 17 | 1.7 | 2271  | 93 | HSU63336   | AF177346 Mus muscu  | c 249 | 17 | 1.7 | 43690  | 85 | AC005238     | AC005238 Homo sapi     |
| c 177 | 17 | 1.7 | 2298  | 94 | AF177346   | AF177346 Homo sapi  | c 250 | 17 | 1.7 | 43784  | 64 | AC017442     | AC017442 Drosophi      |
| c 178 | 17 | 1.7 | 2341  | 89 | AF119857   | AF119857 Homo sapi  | c 251 | 17 | 1.7 | 44710  | 85 | AC004184     | AC004184 Homo sapi     |
| c 179 | 17 | 1.7 | 2402  | 89 | AK022628   | AK022628 Homo sapi  | c 252 | 17 | 1.7 | 44760  | 85 | AC004784     | AC004784 Homo sapi     |
| c 180 | 17 | 1.7 | 2459  | 10 | AX077260   | AK077260 Sequence   | c 253 | 17 | 1.7 | 45087  | 82 | AL590645     | AL590645 Homo sapi     |
| c 181 | 17 | 1.7 | 2474  | 94 | MMU278891  | AJ278891 Mus muscu  | c 254 | 17 | 1.7 | 45344  | 90 | AL356967     | AL356967 Human DNA     |
| c 182 | 17 | 1.7 | 2545  | 9  | AR035063   | AR035063 Sequence   | c 255 | 17 | 1.7 | 51082  | 78 | AC090454     | AC090454 Homo sapi     |
| c 183 | 17 | 1.7 | 2545  | 93 | HSUHMIG    | XJ2735 H. sapiens H | c 256 | 17 | 1.7 | 51082  | 78 | AC090454     | AC090454 Homo sapi     |
| c 184 | 17 | 1.7 | 2585  | 58 | AF247522   | AF247522 HIV-1 Iso  | c 257 | 17 | 1.7 | 57399  | 91 | AP000433     | AP000433 Homo sapi     |
| c 185 | 17 | 1.7 | 2833  | 6  | DR0DIF     | L23015 Drosophilla  | c 258 | 17 | 1.7 | 65174  | 69 | AC025214     | AC025214 Homo sapi     |
| c 186 | 17 | 1.7 | 2920  | 91 | BC002350   | BC002350 Homo sapi  | c 259 | 17 | 1.7 | 66066  | 70 | AC026566     | AC026566 Homo sapi     |
| c 187 | 17 | 1.7 | 2928  | 89 | AK025328   | AK025328 Homo sapi  | c 260 | 17 | 1.7 | 66688  | 77 | AC087757     | AC087757 Homo sapi     |
| c 188 | 17 | 1.7 | 2984  | 91 | BC002482   | BC002482 Homo sapi  | c 261 | 17 | 1.7 | 67392  | 65 | AC018284     | AC018284 Drosophi      |
| c 189 | 17 | 1.7 | 3240  | 3  | LHPEP1GN   | Z56283 L. helveticu | c 262 | 17 | 1.7 | 67392  | 75 | AC079066     | AC079066 Homo sapi     |
| c 190 | 17 | 1.7 | 3337  | 10 | I23337     | I23337 Sequence 1   | c 263 | 17 | 1.7 | 74371  | 85 | AC005369     | AC005369 Homo sapi     |
| c 191 | 17 | 1.7 | 3348  | 2  | D83672     | D83672 Streptomyce  | c 264 | 17 | 1.7 | 80099  | 13 | AP002040     | AP002040 Arabidops     |
| c 192 | 17 | 1.7 | 3453  | 3  | MTU43540   | U43540 Mycobacteri  | c 265 | 17 | 1.7 | 82604  | 91 | AL500522     | AL500522 Homo sapi     |
| c 193 | 17 | 1.7 | 4308  | 3  | SSU38802   | U38802 Synecocyst   | c 266 | 17 | 1.7 | 84957  | 12 | AC006420     | AC006420 Arabidops     |
| c 194 | 17 | 1.7 | 4501  | 85 | AB056760   | AB056760 Macaca fa  | c 267 | 17 | 1.7 | 85657  | 12 | AC069473     | AC069473 Arabidops     |
| c 195 | 17 | 1.7 | 4501  | 94 | AB030448S1 | AB030448 Mus muscu  | c 268 | 17 | 1.7 | 86155  | 90 | AL159169     | AL159169 Human DNA     |
| c 196 | 17 | 1.7 | 4601  | 3  | PAU67315   | U67315 Pseudomonas  | c 269 | 17 | 1.7 | 88296  | 88 | AC027328     | AC027328 Homo sapi     |
| c 197 | 17 | 1.7 | 4624  | 88 | AF064104   | AF064104 Homo sapi  | c 270 | 17 | 1.7 | 88401  | 14 | F23M19       | AC007454 Arabidops     |
| c 198 | 17 | 1.7 | 4823  | 89 | AK001661   | AK001661 Homo sapi  | c 271 | 17 | 1.7 | 88614  | 70 | AC026865     | AC026865 Homo sapi     |
| c 199 | 17 | 1.7 | 4960  | 88 | AF064105   | AF064105 Homo sapi  | c 272 | 17 | 1.7 | 88784  | 63 | AC012997     | AC012997 Drosophi      |
| c 200 | 17 | 1.7 | 5186  | 3  | SADNAIE2   | X87940 S. aurantiac | c 273 | 17 | 1.7 | 90767  | 84 | H0510A06     | AF257499 Homo sapi     |
| c 201 | 17 | 1.7 | 5851  | 94 | AF15253S1  | AF152533 Mus muscu  | c 274 | 17 | 1.7 | 94641  | 78 | AF257499     | AF257499 Homo sapi     |
| c 202 | 17 | 1.7 | 6074  | 94 | MUSP3VPR1  | AF098866 Mus sp. 1  | c 275 | 17 | 1.7 | 98758  | 92 | HS223H9      | AL136081 Human DNA     |
| c 203 | 17 | 1.7 | 6167  | 85 | AB023148   | AB023148 Homo sapi  | c 276 | 17 | 1.7 | 99850  | 89 | AL136081     | AL136081 Human DNA     |
| c 204 | 17 | 1.7 | 6867  | 7  | BOYCOX7AL  | L09603 Bovine cyto  | c 277 | 17 | 1.7 | 100000 | 91 | AP000506     | AP000506 Homo sapi     |
| c 205 | 17 | 1.7 | 8677  | 8  | GGU35037   | U35037 Gallus gall  | c 278 | 17 | 1.7 | 100000 | 91 | AP000513     | AP000513 Homo sapi     |
| c 206 | 17 | 1.7 | 9083  | 58 | AF193253   | AF193253 HIV-1 sub  | c 279 | 17 | 1.7 | 103419 | 78 | AL139221     | AL139221 Homo sapi     |
| c 207 | 17 | 1.7 | 10599 | 1  | AE001037   | AE001037 Methanoba  | c 280 | 17 | 1.7 | 104597 | 92 | HS393P12     | HS393P12 Homo sapi     |
| c 208 | 17 | 1.7 | 11008 | 1  | AE001037   | AE001037 Archaeogl  | c 281 | 17 | 1.7 | 107150 | 60 | AC008839     | AC008839 Homo sapi     |
| c 209 | 17 | 1.7 | 11421 | 1  | AE004505   | AE004505 Pseudomon  | c 282 | 17 | 1.7 | 107152 | 88 | AC020930     | AC020930 Homo sapi     |
| c 210 | 17 | 1.7 | 11672 | 2  | ECOPHN     | D90227 Escherichia  | c 283 | 17 | 1.7 | 109279 | 92 | HS394F12     | HS394F12 Homo sapi     |
| c 211 | 17 | 1.7 | 11908 | 1  | AE005822   | AE005822 Caulobact  | c 284 | 17 | 1.7 | 109626 | 87 | AC008727     | AC008727 Homo sapi     |
| c 212 | 17 | 1.7 | 12213 | 1  | AE004441   | AE004441 Pseudomon  | c 285 | 17 | 1.7 | 109626 | 87 | AC010346     | AC010346 Homo sapi     |
| c 213 | 17 | 1.7 | 12857 | 1  | AE005375   | AE005375 Escherich  | c 286 | 17 | 1.7 | 110000 | 83 | CEY81G3_0    | CEY81G3_0 Homo sapi    |
| c 214 | 17 | 1.7 | 15552 | 1  | AE004049   | AE004049 Xylella f  | c 287 | 17 | 1.7 | 110000 | 84 | LMFLCHR16_03 | LMFLCHR16_03 Homo sapi |
| c 215 | 17 | 1.7 | 15611 | 2  | ECOPHNAQ   | J05260 E. coli psid | c 288 | 17 | 1.7 | 110000 | 84 | LMFLCHR25_03 | LMFLCHR25_03 Homo sapi |
| c 216 | 17 | 1.7 | 20102 | 3  | SC9B2      | AL035212 Streptomy  | c 289 | 17 | 1.7 | 110000 | 84 | LMFLCHR36_09 | LMFLCHR36_09 Homo sapi |
| c 217 | 17 | 1.7 | 20303 | 6  | CEY81G3A   | AL034543 Caenorhab  | c 290 | 17 | 1.7 | 110000 | 84 | LMFLCHR36_11 | LMFLCHR36_11 Homo sapi |
| c 218 | 17 | 1.7 | 20906 | 1  | AE000482   | AE000482 Escherich  | c 291 | 17 | 1.7 | 110000 | 84 | LMFLCHR36_12 | LMFLCHR36_12 Homo sapi |
| c 219 | 17 | 1.7 | 27887 | 4  | SCES0      | AL163672 Streptomy  | c 292 | 17 | 1.7 | 110603 | 93 | AC010662     | AC010662 Homo sapi     |
| c 220 | 17 | 1.7 | 27887 | 4  | AE002700   | AE002700 Drosophi   | c 293 | 17 | 1.7 | 113620 | 61 | AC015138     | AC015138 Homo sapi     |
| c 221 | 17 | 1.7 | 28719 | 85 | AB023052   | AB023052 Homo sapi  | c 294 | 17 | 1.7 | 117273 | 63 | AC015138     | AC015138 Homo sapi     |
| c 222 | 17 | 1.7 | 29139 | 65 | AC020057   | AC020057 Drosophi   | c 295 | 17 | 1.7 | 119919 | 89 | AF241734     | AF241734 Homo sapi     |
| c 223 | 17 | 1.7 | 30200 | 15 | SPAC2068   | Z95334 S. pombe chr | c 296 | 17 | 1.7 | 122258 | 80 | AL356427     | AL356427 Homo sapi     |
| c 224 | 17 | 1.7 | 31015 | 3  | MTY15      | Z92770 Mycobacteri  | c 297 | 17 | 1.7 | 123085 | 90 | AL157406     | AL157406 Homo sapi     |
| c 225 | 17 | 1.7 | 33451 | 12 | AC007293   | Z69970 Arabidops    | c 298 | 17 | 1.7 | 123585 | 85 | AC004707     | AC004707 Homo sapi     |
| c 226 | 17 | 1.7 | 33490 | 6  | CEMK20     | Z69904 Caenorhabdi  | c 299 | 17 | 1.7 | 126152 | 92 | HS433M19     | Z95703 Human DNA s     |
| c 227 | 17 | 1.7 | 33758 | 6  | CEW79      | Z50806 Caenorhabdi  | c 300 | 17 | 1.7 | 132275 | 72 | AC048388     | AC048388 Homo sapi     |

|       |    |            |    |           |           |             |     |            |            |          |           |           |           |
|-------|----|------------|----|-----------|-----------|-------------|-----|------------|------------|----------|-----------|-----------|-----------|
| c 301 | 17 | 1.7 133751 | 92 | HS1131C10 | AL121931  | Human DNA   | 374 | 17         | 1.7 167237 | 66       | AC021609  | AC021609  | Homo sapi |
| c 302 | 17 | 1.7 137570 | 77 | AC084844  | AC084844  | Homo sapi   | 375 | 17         | 1.7 167310 | 73       | AC068972  | AC068972  | Homo sapi |
| c 303 | 17 | 1.7 137928 | 78 | AC090419  | AC090419  | Homo sapi   | 376 | 17         | 1.7 167555 | 64       | AC016044  | AC016044  | Homo sapi |
| c 304 | 17 | 1.7 137943 | 76 | AC084022  | Oryza sat | 377         | 17  | 1.7 167590 | 80         | AL356221 | AL356221  | Homo sapi |           |
| c 305 | 17 | 1.7 138141 | 65 | AC018433  | AC018433  | Homo sapi   | 378 | 17         | 1.7 168524 | 72       | AC046148  | AC046148  | Homo sapi |
| c 306 | 17 | 1.7 138675 | 92 | HS1057B20 | AL109822  | Human DNA   | 379 | 17         | 1.7 169241 | 81       | AL445987  | AL445987  | Homo sapi |
| c 307 | 17 | 1.7 139505 | 93 | HS1591C20 | AL118506  | Human DNA   | 380 | 17         | 1.7 169256 | 72       | AC048358  | AC048358  | Homo sapi |
| c 308 | 17 | 1.7 140154 | 72 | AC055843  | AC055843  | Homo sapi   | 381 | 17         | 1.7 170030 | 86       | AC005829  | AC005829  | Homo sapi |
| c 309 | 17 | 1.7 141017 | 12 | AC037197  | AC037197  | Oryza sat   | 382 | 17         | 1.7 170324 | 4        | AC007805  | AC007805  | Homo sapi |
| c 310 | 17 | 1.7 141924 | 89 | AL138830  | AL138830  | Human DNA   | 383 | 17         | 1.7 170324 | 4        | AC007805  | AC007805  | Homo sapi |
| c 311 | 17 | 1.7 142203 | 76 | AC079521  | AC079521  | Mus muscu   | 384 | 17         | 1.7 170431 | 61       | AC009108  | AC009108  | Homo sapi |
| c 312 | 17 | 1.7 143759 | 88 | AC073532  | AC073532  | Homo sapi   | 385 | 17         | 1.7 170457 | 76       | AC083944  | AC083944  | Oryza sat |
| c 313 | 17 | 1.7 144316 | 79 | AL162582  | AL162582  | Homo sapi   | 386 | 17         | 1.7 170711 | 71       | AC032020  | AC032020  | Homo sapi |
| c 314 | 17 | 1.7 144704 | 64 | AC016595  | AC016595  | Homo sapi   | 387 | 17         | 1.7 170854 | 83       | AP002383  | AP002383  | Homo sapi |
| c 315 | 17 | 1.7 145642 | 71 | AC027805  | AC027805  | Homo sapi   | 388 | 17         | 1.7 170856 | 73       | AC068160  | AC068160  | Homo sapi |
| c 316 | 17 | 1.7 146018 | 65 | AC018404  | AC018404  | Homo sapi   | 389 | 17         | 1.7 170872 | 69       | AC004951  | AC004951  | Homo sapi |
| c 317 | 17 | 1.7 146271 | 3  | SYCS1RB   | DE4000    | Synechocyst | 390 | 17         | 1.7 170891 | 66       | AC002118  | AC002118  | Homo sapi |
| c 318 | 17 | 1.7 146393 | 70 | AC026791  | AC026791  | Homo sapi   | 391 | 17         | 1.7 171539 | 81       | AL512788  | AL512788  | Homo sapi |
| c 319 | 17 | 1.7 148960 | 85 | AB000882  | AB000882  | Homo sapi   | 392 | 17         | 1.7 171775 | 70       | AC027015  | AC027015  | Homo sapi |
| c 320 | 17 | 1.7 149143 | 62 | AC011591  | AC011591  | Homo sapi   | 393 | 17         | 1.7 171790 | 62       | AC011106  | AC011106  | Homo sapi |
| c 321 | 17 | 1.7 149773 | 71 | AC041029  | AC041029  | Homo sapi   | 394 | 17         | 1.7 171917 | 82       | AL590638  | AL590638  | Homo sapi |
| c 322 | 17 | 1.7 150250 | 70 | AC027573  | AC027573  | Homo sapi   | 395 | 17         | 1.7 172004 | 86       | AC008482  | AC008482  | Homo sapi |
| c 323 | 17 | 1.7 150399 | 63 | AC015784  | AC015784  | Homo sapi   | 396 | 17         | 1.7 172024 | 75       | AC078971  | AC078971  | Homo sapi |
| c 324 | 17 | 1.7 151289 | 83 | AP003228  | Oryza sat | 397         | 17  | 1.7 172312 | 80         | AL359822 | AL359822  | Homo sapi |           |
| c 325 | 17 | 1.7 151496 | 83 | AP003312  | Oryza sat | 398         | 17  | 1.7 172650 | 62         | AC011042 | AC011042  | Homo sapi |           |
| c 326 | 17 | 1.7 151497 | 71 | AC027809  | AC027809  | Homo sapi   | 399 | 17         | 1.7 173235 | 68       | AC023756  | AC023756  | Homo sapi |
| c 327 | 17 | 1.7 151654 | 62 | AC012265  | AC012265  | Homo sapi   | 400 | 17         | 1.7 173254 | 62       | AC012057  | AC012057  | Homo sapi |
| c 328 | 17 | 1.7 151983 | 70 | AC027178  | AC027178  | Homo sapi   | 401 | 17         | 1.7 173425 | 65       | AC021482  | AC021482  | Homo sapi |
| c 329 | 17 | 1.7 152159 | 70 | AC027334  | AC027334  | Homo sapi   | 402 | 17         | 1.7 173973 | 75       | AC073871  | AC073871  | Homo sapi |
| c 330 | 17 | 1.7 152513 | 83 | AP003207  | Oryza sat | 403         | 17  | 1.7 174006 | 72         | AC027062 | AC027062  | Homo sapi |           |
| c 331 | 17 | 1.7 152517 | 87 | AC009468  | AC009468  | Homo sapi   | 404 | 17         | 1.7 174250 | 70       | AC063950  | AC063950  | Homo sapi |
| c 332 | 17 | 1.7 152714 | 80 | AL357042  | AL357042  | Homo sapi   | 405 | 17         | 1.7 174476 | 75       | AC079171  | AC079171  | Homo sapi |
| c 333 | 17 | 1.7 154254 | 66 | AC021360  | AC021360  | Homo sapi   | 406 | 17         | 1.7 174517 | 77       | AC087831  | AC087831  | Homo sapi |
| c 334 | 17 | 1.7 154685 | 66 | AC007214  | AC007214  | Par trogl   | 407 | 17         | 1.7 174831 | 72       | AC068089  | AC068089  | Homo sapi |
| c 335 | 17 | 1.7 154745 | 61 | AC010860  | AC010860  | Homo sapi   | 408 | 17         | 1.7 174852 | 61       | AC010195  | AC010195  | Homo sapi |
| c 336 | 17 | 1.7 155068 | 70 | AC027307  | AC027307  | Homo sapi   | 409 | 17         | 1.7 175191 | 87       | AC010251  | AC010251  | Homo sapi |
| c 337 | 17 | 1.7 155258 | 84 | HS66C13   | AL354047  | Homo sapi   | 410 | 17         | 1.7 175202 | 70       | AC027254  | AC027254  | Homo sapi |
| c 338 | 17 | 1.7 155399 | 69 | AC025663  | AC025663  | Homo sapi   | 411 | 17         | 1.7 175706 | 63       | AC013708  | AC013708  | Homo sapi |
| c 339 | 17 | 1.7 155645 | 66 | AC021153  | AC021153  | Homo sapi   | 412 | 17         | 1.7 176300 | 71       | AC027709  | AC027709  | Homo sapi |
| c 340 | 17 | 1.7 155813 | 65 | AC019350  | AC019350  | Homo sapi   | 413 | 17         | 1.7 176552 | 76       | AC079452  | AC079452  | Homo sapi |
| c 341 | 17 | 1.7 156241 | 80 | AL358034  | AL358034  | Homo sapi   | 414 | 17         | 1.7 176683 | 72       | AC055801  | AC055801  | Homo sapi |
| c 342 | 17 | 1.7 156557 | 63 | AC015545  | AC015545  | Homo sapi   | 415 | 17         | 1.7 177364 | 86       | AC005409  | AC005409  | Homo sapi |
| c 343 | 17 | 1.7 157189 | 4  | AC008307  | AC008307  | Drosophill  | 416 | 17         | 1.7 177654 | 59       | AC025988  | AC025988  | Homo sapi |
| c 344 | 17 | 1.7 158219 | 86 | AC005534  | AC005534  | Homo sapi   | 417 | 17         | 1.7 177656 | 76       | AC079911  | AC079911  | Mus muscu |
| c 345 | 17 | 1.7 158447 | 75 | AC079071  | AC079071  | Homo sapi   | 418 | 17         | 1.7 177754 | 66       | AC021034  | AC021034  | Homo sapi |
| c 346 | 17 | 1.7 158458 | 86 | AC007395  | AC007395  | Homo sapi   | 419 | 17         | 1.7 177826 | 64       | AC016852  | AC016852  | Homo sapi |
| c 347 | 17 | 1.7 158646 | 79 | AL354708  | AL354708  | Homo sapi   | 420 | 17         | 1.7 177942 | 81       | AL391803  | AL391803  | Homo sapi |
| c 348 | 17 | 1.7 158989 | 81 | AL391826  | AL391826  | Homo sapi   | 421 | 17         | 1.7 178395 | 81       | AL512664  | AL512664  | Homo sapi |
| c 349 | 17 | 1.7 159007 | 74 | AC073059  | AC073059  | Homo sapi   | 422 | 17         | 1.7 178518 | 69       | AC025332  | AC025332  | Homo sapi |
| c 350 | 17 | 1.7 159452 | 63 | AC015746  | AC015746  | Homo sapi   | 423 | 17         | 1.7 178630 | 64       | AC016219  | AC016219  | Homo sapi |
| c 351 | 17 | 1.7 160972 | 4  | AC007723  | AC007723  | Drosophill  | 424 | 17         | 1.7 179471 | 75       | AC078868  | AC078868  | Homo sapi |
| c 352 | 17 | 1.7 161087 | 65 | AC018850  | AC018850  | Homo sapi   | 425 | 17         | 1.7 180340 | 65       | AC016233  | AC016233  | Homo sapi |
| c 353 | 17 | 1.7 162014 | 75 | AC074323  | AC074323  | Homo sapi   | 426 | 17         | 1.7 180530 | 64       | AC018613  | AC018613  | Homo sapi |
| c 354 | 17 | 1.7 162066 | 73 | AC068317  | AC068317  | Homo sapi   | 427 | 17         | 1.7 182244 | 74       | AC069150  | AC069150  | Homo sapi |
| c 355 | 17 | 1.7 162427 | 87 | AC010205  | AC010205  | Homo sapi   | 428 | 17         | 1.7 182718 | 64       | AC017095  | AC017095  | Homo sapi |
| c 356 | 17 | 1.7 162681 | 94 | AC003061  | AC003061  | Mouse Chr   | 429 | 17         | 1.7 183019 | 70       | AC027564  | AC027564  | Homo sapi |
| c 357 | 17 | 1.7 162853 | 13 | AP003285  | AP003285  | Oryza sat   | 430 | 17         | 1.7 183251 | 82       | AC013555  | AC013555  | Homo sapi |
| c 358 | 17 | 1.7 163134 | 65 | AC019286  | AC019286  | Homo sapi   | 431 | 17         | 1.7 183615 | 82       | AP001494  | AP001494  | Homo sapi |
| c 359 | 17 | 1.7 163570 | 87 | AC016910  | AC016910  | Homo sapi   | 432 | 17         | 1.7 184165 | 60       | AC008763  | AC008763  | Homo sapi |
| c 360 | 17 | 1.7 163578 | 74 | AC073657  | AC073657  | Homo sapi   | 433 | 17         | 1.7 184651 | 81       | AL450317  | AL450317  | Mus muscu |
| c 361 | 17 | 1.7 163836 | 88 | AC073917  | AC073917  | Homo sapi   | 434 | 17         | 1.7 185260 | 64       | AC016065  | AC016065  | Homo sapi |
| c 362 | 17 | 1.7 163861 | 80 | AL356099  | AL356099  | Homo sapi   | 435 | 17         | 1.7 185551 | 93       | HS1171K16 | HS1171K16 | Human DNA |
| c 363 | 17 | 1.7 163894 | 62 | AC011985  | AC011985  | Homo sapi   | 436 | 17         | 1.7 185948 | 67       | AC022370  | AC022370  | Homo sapi |
| c 364 | 17 | 1.7 164034 | 87 | AC011489  | AC011489  | Homo sapi   | 437 | 17         | 1.7 186102 | 83       | AP001963  | AP001963  | Homo sapi |
| c 365 | 17 | 1.7 164408 | 83 | CNS01DRF  | AL117190  | Homo sapi   | 438 | 17         | 1.7 186208 | 65       | AC019204  | AC019204  | Homo sapi |
| c 366 | 17 | 1.7 165405 | 61 | AC009420  | AC009420  | Homo sapi   | 439 | 17         | 1.7 187965 | 64       | AC017010  | AC017010  | Homo sapi |
| c 367 | 17 | 1.7 165443 | 76 | AC079939  | AC079939  | Mus muscu   | 440 | 17         | 1.7 188465 | 74       | AC073413  | AC073413  | Homo sapi |
| c 368 | 17 | 1.7 165725 | 68 | AC024380  | AC024380  | Homo sapi   | 441 | 17         | 1.7 188526 | 62       | AC012342  | AC012342  | Homo sapi |
| c 369 | 17 | 1.7 165764 | 67 | AC022527  | AC022527  | Homo sapi   | 442 | 17         | 1.7 188713 | 88       | AC024167  | AC024167  | Homo sapi |
| c 370 | 17 | 1.7 165817 | 60 | AC007935  | AC007935  | Homo sapi   | 443 | 17         | 1.7 188755 | 87       | AC013562  | AC013562  | Homo sapi |
| c 371 | 17 | 1.7 166107 | 68 | AC024427  | AC024427  | Homo sapi   | 444 | 17         | 1.7 188812 | 63       | AC013419  | AC013419  | Homo sapi |
| c 372 | 17 | 1.7 167020 | 87 | AC010238  | AC010238  | Homo sapi   | 445 | 17         | 1.7 189333 | 76       | AC079445  | AC079445  | Mus muscu |
| c 373 | 17 | 1.7 167083 | 70 | AC027459  | AC027459  | Homo sapi   | 446 | 17         | 1.7 189496 | 77       | AC084353  | AC084353  | Homo sapi |



|       |    |     |        |      |           |           |       |    |     |        |          |            |             |
|-------|----|-----|--------|------|-----------|-----------|-------|----|-----|--------|----------|------------|-------------|
| 447   | 17 | 1.7 | 189786 | 73   | AC068015  | Homo sapi | 520   | 17 | 1.7 | 310360 | 75       | AC074172   | Mus muscu   |
| 448   | 17 | 1.7 | 190388 | 75   | AC074216  | Homo sapi | 521   | 17 | 1.7 | 310565 | 79       | CEY62FE5   | Caenorhab   |
| 449   | 17 | 1.7 | 190844 | 75   | AC073990  | Homo sapi | 522   | 17 | 1.7 | 311771 | 83       | AL554714   | Homo sapi   |
| C 450 | 17 | 1.7 | 191111 | 86   | AC007458  | Homo sapi | 523   | 17 | 1.7 | 334686 | 80       | AL359078   | Homo sapi   |
| C 451 | 17 | 1.7 | 191352 | 74   | AC073565  | Mus muscu | C 524 | 17 | 1.7 | 337101 | 97       | H5KX9P8R   | Homo sapi   |
| C 452 | 17 | 1.7 | 192431 | 67   | AC022059  | Homo sapi | 525   | 17 | 1.7 | 338534 | 2        | EC0W993    | Homo sapi   |
| C 453 | 17 | 1.7 | 192868 | 88   | AC023484  | Homo sapi | C 526 | 17 | 1.7 | 339485 | 13       | AF172282   | Oryza sat   |
| C 454 | 17 | 1.7 | 193098 | 89   | AL137140  | Human DNA | C 527 | 17 | 1.7 | 340000 | 91       | AF001675   | Homo sapi   |
| C 455 | 17 | 1.7 | 193426 | 73   | AC067942  | Homo sapi | C 528 | 16 | 1.6 | 41     | 114300   | Sequence 1 |             |
| C 456 | 17 | 1.7 | 193503 | 79   | AL139818  | Homo sapi | C 529 | 16 | 1.6 | 71     | AF016206 | Homo sapi  |             |
| C 457 | 17 | 1.7 | 193816 | 69   | AC025874  | Mus muscu | 530   | 16 | 1.6 | 222    | 10       | EB08211    |             |
| C 458 | 17 | 1.7 | 194151 | 66   | AC021185  | Homo sapi | 531   | 16 | 1.6 | 222    | 14       | OST0S11A   |             |
| C 459 | 17 | 1.7 | 194159 | 75   | AC074117  | Mus muscu | 532   | 16 | 1.6 | 224    | 14       | ROALP1TS2  | Roscoe a    |
| C 460 | 17 | 1.7 | 194812 | 76   | AC079858  | Homo sapi | 533   | 16 | 1.6 | 224    | 14       | ROAUR1TS2  | Roscoe a    |
| C 461 | 17 | 1.7 | 195310 | 68   | AC024189  | Homo sapi | 534   | 16 | 1.6 | 224    | 14       | ROBRA1TS2  | Roscoe b    |
| C 462 | 17 | 1.7 | 195418 | 68   | AC032524  | Homo sapi | 535   | 16 | 1.6 | 224    | 14       | ROGAN1TS2  | Roscoe a    |
| C 463 | 17 | 1.7 | 195466 | 71   | AC032024  | Homo sapi | 536   | 16 | 1.6 | 224    | 14       | ROPUR1TS2  | Roscoe a    |
| C 464 | 17 | 1.7 | 195472 | 65   | AC018338  | Homo sapi | 537   | 16 | 1.6 | 224    | 14       | ROPMU1TS2  | Roscoe a    |
| C 465 | 17 | 1.7 | 196556 | 66   | AC018332  | Homo sapi | 538   | 16 | 1.6 | 225    | 14       | CGRAC1TS2  | Caulieya    |
| C 466 | 17 | 1.7 | 196900 | 65   | AC020851  | Mus muscu | 539   | 16 | 1.6 | 225    | 14       | CSPIC1TS2  | Caulieya    |
| C 467 | 17 | 1.7 | 197871 | 73   | AC068053  | Homo sapi | 540   | 16 | 1.6 | 225    | 14       | ROAUS1TS2  | Roscoe a    |
| C 468 | 17 | 1.7 | 198388 | 74   | AC073426  | Homo sapi | 541   | 16 | 1.6 | 225    | 14       | ROCAT1TS2  | Roscoe a    |
| C 469 | 17 | 1.7 | 198677 | 1    | AE001863  | Deinococc | 542   | 16 | 1.6 | 225    | 14       | ROHUM1TS2  | Roscoe h    |
| C 470 | 17 | 1.7 | 199243 | 71   | AC040925  | Homo sapi | 543   | 16 | 1.6 | 225    | 14       | ROPRAT1TS2 | Roscoe p    |
| C 471 | 17 | 1.7 | 199314 | 61   | AC009097  | Homo sapi | 544   | 16 | 1.6 | 225    | 14       | ROSCHT1TS2 | Roscoe s    |
| C 472 | 17 | 1.7 | 199853 | 93   | AC073785  | Mus muscu | 545   | 16 | 1.6 | 225    | 14       | ROSCIT1TS2 | Roscoe s    |
| C 473 | 17 | 1.7 | 200033 | 93   | HSA251973 | HS251973  | 546   | 16 | 1.6 | 225    | 14       | ROTHIT1TS2 | Roscoe t    |
| C 474 | 17 | 1.7 | 200349 | 97   | HS085195  | HS085195  | 547   | 16 | 1.6 | 225    | 14       | ROMAR1TS2  | Roscoe a    |
| C 475 | 17 | 1.7 | 200360 | 69   | AC025105  | Homo sapi | 548   | 16 | 1.6 | 225    | 14       | ROU28639   | Roscoe a    |
| C 476 | 17 | 1.7 | 201846 | 60   | AC009036  | Homo sapi | C 549 | 16 | 1.6 | 227    | 13       | AY028639   | Kaluts no   |
| C 477 | 17 | 1.7 | 205251 | 85   | AC005332  | Homo sapi | 550   | 16 | 1.6 | 293    | 54       | AY021772   | Oryza sat   |
| C 478 | 17 | 1.7 | 206518 | 72   | AC069091  | Homo sapi | 551   | 16 | 1.6 | 299    | 92       | HS98C10R   | human SFS W |
| C 479 | 17 | 1.7 | 207083 | 73   | AC055797  | Homo sapi | 552   | 16 | 1.6 | 334    | 89       | AX000736   | Sequence    |
| C 480 | 17 | 1.7 | 207103 | 73</ |           |           |       |    |     |        |          |            |             |

|     |    |     |     |    |          |        |       |     |    |     |     |    |            |            |              |       |
|-----|----|-----|-----|----|----------|--------|-------|-----|----|-----|-----|----|------------|------------|--------------|-------|
| 593 | 16 | 1.6 | 386 | 58 | AF028584 | HIV-1  | iso   | 666 | 16 | 1.6 | 400 | 58 | AF174967   | AF174967   | HIV-1        | iso   |
| 594 | 16 | 1.6 | 386 | 58 | AF028587 | HIV-1  | iso   | 667 | 16 | 1.6 | 400 | 58 | AF174968   | AF174968   | HIV-1        | iso   |
| 595 | 16 | 1.6 | 388 | 58 | AF014238 | HIV-1  | Pat   | 668 | 16 | 1.6 | 400 | 58 | AF174969   | AF174969   | HIV-1        | iso   |
| 596 | 16 | 1.6 | 388 | 58 | AF014239 | HIV-1  | Pat   | 669 | 16 | 1.6 | 400 | 58 | AF174970   | AF174970   | HIV-1        | iso   |
| 597 | 16 | 1.6 | 388 | 58 | AF014240 | HIV-1  | Pat   | 670 | 16 | 1.6 | 400 | 58 | AF174971   | AF174971   | HIV-1        | iso   |
| 598 | 16 | 1.6 | 388 | 58 | AF014344 | HIV-1  | Pat   | 671 | 16 | 1.6 | 401 | 58 | AF028583   | AF028583   | HIV-1        | iso   |
| 599 | 16 | 1.6 | 388 | 58 | AF014345 | HIV-1  | Pat   | 672 | 16 | 1.6 | 401 | 58 | AF073401   | AF073401   | HIV-1        | iso   |
| 600 | 16 | 1.6 | 388 | 58 | AF014358 | HIV-1  | Pat   | 673 | 16 | 1.6 | 406 | 58 | AF073400   | AF073400   | HIV-1        | iso   |
| 601 | 16 | 1.6 | 390 | 58 | AF015406 | HIV-1  | str   | 674 | 16 | 1.6 | 409 | 58 | AF014214   | AF014214   | HIV-1        | Pat   |
| 602 | 16 | 1.6 | 390 | 58 | AF062050 | HIV-1  | iso   | 675 | 16 | 1.6 | 411 | 94 | AF020210   | AF020210   | Rattus       | no    |
| 603 | 16 | 1.6 | 391 | 58 | AF014194 | HIV-1  | Pat   | 676 | 16 | 1.6 | 412 | 58 | AF014335   | AF014335   | HIV-1        | Pat   |
| 604 | 16 | 1.6 | 391 | 58 | AF014199 | HIV-1  | Pat   | 677 | 16 | 1.6 | 414 | 4  | AB040074   | AB040074   | Hydra        | mag   |
| 605 | 16 | 1.6 | 391 | 58 | AF014202 | HIV-1  | Pat   | 678 | 16 | 1.6 | 414 | 58 | AF028577   | AF028577   | HIV-1        | iso   |
| 606 | 16 | 1.6 | 391 | 58 | AF014216 | HIV-1  | Pat   | 679 | 16 | 1.6 | 416 | 97 | HUM0293F03 | HUM0293F03 | Homo         | sapi  |
| 607 | 16 | 1.6 | 391 | 58 | AF014225 | HIV-1  | Pat   | 680 | 16 | 1.6 | 420 | 58 | AF028580   | AF028580   | HIV-1        | iso   |
| 608 | 16 | 1.6 | 391 | 58 | AF014228 | HIV-1  | Pat   | 681 | 16 | 1.6 | 422 | 54 | G65449     | G65449     | SMCY-M81     | Ra    |
| 609 | 16 | 1.6 | 391 | 58 | AF014233 | HIV-1  | Pat   | 682 | 16 | 1.6 | 448 | 58 | AF073403   | AF073403   | HIV-1        | iso   |
| 610 | 16 | 1.6 | 391 | 58 | AF050899 | HIV-1  | mat   | 683 | 16 | 1.6 | 452 | 8  | AF076295   | AF076295   | Lampbrush    |       |
| 611 | 16 | 1.6 | 391 | 58 | AF050900 | HIV-1  | mat   | 684 | 16 | 1.6 | 454 | 58 | AF028586   | AF028586   | HIV-1        | iso   |
| 612 | 16 | 1.6 | 391 | 58 | AF050927 | HIV-1  | iso   | 685 | 16 | 1.6 | 480 | 14 | CNS01BXR   | CNS01BXR   | Boltylis     |       |
| 613 | 16 | 1.6 | 391 | 58 | AF050928 | HIV-1  | iso   | 686 | 16 | 1.6 | 492 | 3  | SCSCYEGEN  | SCSCYEGEN  | S. cyanogen  |       |
| 614 | 16 | 1.6 | 391 | 58 | AF050929 | HIV-1  | iso   | 687 | 16 | 1.6 | 492 | 3  | SGSGHE     | SGSGHE     | S. glaucense |       |
| 615 | 16 | 1.6 | 391 | 58 | AF050931 | HIV-1  | iso   | 688 | 16 | 1.6 | 492 | 3  | SGSGLEGEN  | SGSGLEGEN  | S. glaucense |       |
| 616 | 16 | 1.6 | 391 | 58 | AF050936 | HIV-1  | iso   | 689 | 16 | 1.6 | 504 | 97 | S63672     | S63672     | trichophylli |       |
| 617 | 16 | 1.6 | 391 | 58 | AF050942 | HIV-1  | iso   | 690 | 16 | 1.6 | 523 | 97 | HUM0285H04 | HUM0285H04 | Homo         | sapi  |
| 618 | 16 | 1.6 | 391 | 58 | AF050944 | HIV-1  | iso   | 691 | 16 | 1.6 | 541 | 9  | RP038304   | RP038304   | Roscoe       | p     |
| 619 | 16 | 1.6 | 391 | 58 | AF050946 | HIV-1  | iso   | 692 | 16 | 1.6 | 559 | 14 | CSP388301  | CSP388301  | Caulleya     |       |
| 620 | 16 | 1.6 | 391 | 58 | AF050951 | HIV-1  | iso   | 693 | 16 | 1.6 | 561 | 14 | HM0388297  | HM0388297  | Hedychium    |       |
| 621 | 16 | 1.6 | 391 | 58 | AF050952 | HIV-1  | iso   | 694 | 16 | 1.6 | 562 | 14 | CGR388299  | CGR388299  | Caulleya     |       |
| 622 | 16 | 1.6 | 391 | 58 | AF050953 | HIV-1  | iso   | 695 | 16 | 1.6 | 563 | 14 | HEU388296  | HEU388296  | Hedychium    |       |
| 623 | 16 | 1.6 | 391 | 58 | AF050959 | HIV-1  | iso   | 696 | 16 | 1.6 | 565 | 14 | HS421120S  | HS421120S  | H. sapientis |       |
| 624 | 16 | 1.6 | 391 | 58 | AF050960 | HIV-1  | iso   | 697 | 16 | 1.6 | 567 | 54 | G37344     | G37344     | SHGC-57583   |       |
| 625 | 16 | 1.6 | 391 | 58 | AF051008 | HIV-1  | iso   | 698 | 16 | 1.6 | 574 | 54 | AX034339   | AX034339   | Sequence     |       |
| 626 | 16 | 1.6 | 391 | 58 | AF051009 | HIV-1  | iso   | 699 | 16 | 1.6 | 598 | 9  | AF320100   | AF320100   | Dendronep    |       |
| 627 | 16 | 1.6 | 391 | 58 | AF051010 | HIV-1  | iso   | 700 | 16 | 1.6 | 602 | 5  | AF320102   | AF320102   | Dendronep    |       |
| 628 | 16 | 1.6 | 391 | 58 | AF051012 | HIV-1  | iso   | 701 | 16 | 1.6 | 603 | 5  | AF320103   | AF320103   | Dendronep    |       |
| 629 | 16 | 1.6 | 391 | 58 | AF051013 | HIV-1  | iso   | 702 | 16 | 1.6 | 603 | 5  | AF320098   | AF320098   | Dendronep    |       |
| 630 | 16 | 1.6 | 391 | 58 | AF051014 | HIV-1  | iso   | 703 | 16 | 1.6 | 604 | 5  | G39591     | G39591     | Zebra        |       |
| 631 | 16 | 1.6 | 391 | 58 | AF051016 | HIV-1  | iso   | 704 | 16 | 1.6 | 608 | 54 | AF320099   | AF320099   | Dendronep    |       |
| 632 | 16 | 1.6 | 391 | 58 | AF051019 | HIV-1  | iso   | 705 | 16 | 1.6 | 610 | 5  | AF202374   | AF202374   | Hedychium    |       |
| 633 | 16 | 1.6 | 391 | 58 | AF051022 | HIV-1  | iso   | 706 | 16 | 1.6 | 612 | 13 | AF202374   | AF202374   | Hedychium    |       |
| 634 | 16 | 1.6 | 391 | 58 | AF051024 | HIV-1  | iso   | 707 | 16 | 1.6 | 621 | 13 | AF202403   | AF202403   | Hedychium    |       |
| 635 | 16 | 1.6 | 391 | 58 | AF051027 | HIV-1  | iso   | 708 | 16 | 1.6 | 621 | 13 | AF202405   | AF202405   | Pommereuc    |       |
| 636 | 16 | 1.6 | 391 | 58 | AF051030 | HIV-1  | iso   | 709 | 16 | 1.6 | 621 | 13 | AF202419   | AF202419   | Caulleya     |       |
| 637 | 16 | 1.6 | 393 | 94 | AF020209 | Rattus | no    | 710 | 16 | 1.6 | 623 | 13 | AF202385   | AF202385   | Hedychium    |       |
| 638 | 16 | 1.6 | 396 | 58 | AF084766 | HIV-1  | Pat   | 711 | 16 | 1.6 | 626 | 13 | AF202395   | AF202395   | Hedychium    |       |
| 639 | 16 | 1.6 | 396 | 58 | AF084767 | HIV-1  | Pat   | 712 | 16 | 1.6 | 626 | 13 | AF202388   | AF202388   | Hedychium    |       |
| 640 | 16 | 1.6 | 396 | 58 | AF084768 | HIV-1  | Pat   | 713 | 16 | 1.6 | 626 | 13 | AF202406   | AF202406   | Roscoe       | h     |
| 641 | 16 | 1.6 | 396 | 58 | AF084769 | HIV-1  | Pat   | 714 | 16 | 1.6 | 626 | 13 | AF202376   | AF202376   | Hedychium    |       |
| 642 | 16 | 1.6 | 396 | 58 | AF084770 | HIV-1  | Pat   | 715 | 16 | 1.6 | 627 | 13 | AF202380   | AF202380   | Hedychium    |       |
| 643 | 16 | 1.6 | 396 | 58 | AF084771 | HIV-1  | Pat   | 716 | 16 | 1.6 | 627 | 13 | AF202381   | AF202381   | Hedychium    |       |
| 644 | 16 | 1.6 | 396 | 58 | AF084772 | HIV-1  | Pat   | 717 | 16 | 1.6 | 627 | 13 | AF202382   | AF202382   | Hedychium    |       |
| 645 | 16 | 1.6 | 396 | 58 | AF084773 | HIV-1  | Pat   | 718 | 16 | 1.6 | 627 | 13 | AF202393   | AF202393   | Hedychium    |       |
| 646 | 16 | 1.6 | 396 | 58 | AF084774 | HIV-1  | Pat   | 719 | 16 | 1.6 | 627 | 13 | AF202394   | AF202394   | Hedychium    |       |
| 647 | 16 | 1.6 | 396 | 58 | AF084775 | HIV-1  | Pat   | 720 | 16 | 1.6 | 627 | 13 | AF202397   | AF202397   | Hedychium    |       |
| 648 | 16 | 1.6 | 396 | 58 | AF084776 | HIV-1  | Pat   | 721 | 16 | 1.6 | 628 | 13 | AF202378   | AF202378   | Hedychium    |       |
| 649 | 16 | 1.6 | 396 | 58 | AF084777 | HIV-1  | Pat   | 722 | 16 | 1.6 | 628 | 13 | AF202392   | AF202392   | Hedychium    |       |
| 650 | 16 | 1.6 | 396 | 58 | AF084778 | HIV-1  | Pat   | 723 | 16 | 1.6 | 628 | 13 | AF202396   | AF202396   | Hedychium    |       |
| 651 | 16 | 1.6 | 396 | 59 | HIV1DUMC | Human  | immun | 724 | 16 | 1.6 | 628 | 13 | AF202384   | AF202384   | Hedychium    |       |
| 652 | 16 | 1.6 | 396 | 59 | HIV1DUMC | Human  | immun | 725 | 16 | 1.6 | 628 | 13 | AF202389   | AF202389   | Hedychium    |       |
| 653 | 16 | 1.6 | 397 | 58 | AF014195 | HIV-1  | Pat   | 726 | 16 | 1.6 | 628 | 13 | AF202390   | AF202390   | Hedychium    |       |
| 654 | 16 | 1.6 | 399 | 58 | AF174897 | HIV-1  | iso   | 727 | 16 | 1.6 | 628 | 13 | AF202391   | AF202391   | Hedychium    |       |
| 655 | 16 | 1.6 | 399 | 58 | AF174898 | HIV-1  | iso   | 728 | 16 | 1.6 | 628 | 13 | AF202392   | AF202392   | Hedychium    |       |
| 656 | 16 | 1.6 | 399 | 58 | AF174899 | HIV-1  | iso   | 729 | 16 | 1.6 | 628 | 13 | AF202393   | AF202393   | Hedychium    |       |
| 657 | 16 | 1.6 | 400 | 58 | AF014222 | HIV-1  | Pat   | 730 | 16 | 1.6 | 629 | 13 | AF202401   | AF202401   | Hedychium    |       |
| 658 | 16 | 1.6 | 400 | 58 | AF174851 | HIV-1  | iso   | 731 | 16 | 1.6 | 629 | 13 | AF202402   | AF202402   | Hedychium    |       |
| 659 | 16 | 1.6 | 400 | 58 | AF174895 | HIV-1  | iso   | 732 | 16 | 1.6 | 629 | 13 | AF202401   | AF202401   | Hedychium    |       |
| 660 | 16 | 1.6 | 400 | 58 | AF174896 | HIV-1  | iso   | 733 | 16 | 1.6 | 631 | 13 | AF221933   | AF221933   | Mustelus     |       |
| 661 | 16 | 1.6 | 400 | 58 | AF174902 | HIV-1  | iso   | 734 | 16 | 1.6 | 651 | 97 | HUM02858F  | HUM02858F  | Human        | Cpg 1 |
| 662 | 16 | 1.6 | 400 | 58 | AF174962 | HIV-1  | iso   | 735 | 16 | 1.6 | 679 | 8  | AB056582   | AB056582   | Xenopus      | 1     |
| 663 | 16 | 1.6 | 400 | 58 | AF174964 | HIV-1  | iso   | 736 | 16 | 1.6 | 704 | 54 | G61829     | G61829     | SHGC-89440   |       |
| 664 | 16 | 1.6 | 400 | 58 | AF174965 | HIV-1  | iso   | 737 | 16 | 1.6 | 720 | 9  | AX065817   | AX065817   | Sequence     |       |
| 665 | 16 | 1.6 | 400 | 58 | AF174966 | HIV-1  | iso   | 738 | 16 | 1.6 | 720 | 9  | AX065817   | AX065817   | Sequence     |       |

|     |    |     |      |    |           |                      |     |    |     |      |    |           |                     |
|-----|----|-----|------|----|-----------|----------------------|-----|----|-----|------|----|-----------|---------------------|
| 739 | 16 | 1.6 | 729  | 58 | AF071291  | HIV-1 iso            | 812 | 16 | 1.6 | 1669 | 94 | AF273686  | AF273686 Mus muscu  |
| 740 | 16 | 1.6 | 729  | 58 | AF071300  | HIV-1 iso            | 813 | 16 | 1.6 | 1669 | 94 | AF273687  | AF273687 Mus muscu  |
| 741 | 16 | 1.6 | 729  | 58 | AF196682  | HIV-1 iso            | 814 | 16 | 1.6 | 1671 | 2  | AX024351  | AX024351 Sequence   |
| 742 | 16 | 1.6 | 737  | 9  | AB6380    | Sequence 10          | 815 | 16 | 1.6 | 1671 | 9  | AX024244  | AX024244 Sequence   |
| 743 | 16 | 1.6 | 737  | 10 | EB6398    | Genome DNA           | 816 | 16 | 1.6 | 1699 | 3  | SABLA     | E09684              |
| 744 | 16 | 1.6 | 738  | 58 | AF071302  | HIV-1 iso            | 817 | 16 | 1.6 | 1722 | 45 | EB0684    | X13597 Streptomyces |
| 745 | 16 | 1.6 | 738  | 58 | AF071308  | HIV-1 iso            | 818 | 16 | 1.6 | 1723 | 94 | AF273688  | E09684 cDNA encodi  |
| 746 | 16 | 1.6 | 759  | 96 | TV4250739 | Tyranos              | 819 | 16 | 1.6 | 1734 | 45 | E11874    | AF273688 Mus muscu  |
| 747 | 16 | 1.6 | 774  | 14 | MA293103  | Sequence 25          | 820 | 16 | 1.6 | 1780 | 89 | AK023355  | E11874 Genomic DNA  |
| 748 | 16 | 1.6 | 774  | 14 | MA293103  | Sequence 25          | 821 | 16 | 1.6 | 1788 | 93 | HSHP512   | AK023355 Homo sapi  |
| 749 | 16 | 1.6 | 785  | 6  | DM0BX1    | X03723 D. melanog    | 822 | 16 | 1.6 | 1790 | 12 | AF18126   | X12433 Human PMS1-  |
| 750 | 16 | 1.6 | 785  | 6  | DM0BX1    | X03723 D. melanog    | 823 | 16 | 1.6 | 1803 | 10 | AX090436  | AF18126 Magnapor    |
| 751 | 16 | 1.6 | 790  | 53 | CNS07270  | AL425866 clone BAO   | 824 | 16 | 1.6 | 1810 | 9  | AX047400  | AX090436 Sequence   |
| 752 | 16 | 1.6 | 849  | 53 | CNS07270  | AL425866 clone BAO   | 825 | 16 | 1.6 | 1834 | 93 | HSMB00543 | AX047400 Sequence   |
| 753 | 16 | 1.6 | 863  | 91 | BC005052  | BC005052 Homo sapi   | 826 | 16 | 1.6 | 1839 | 12 | AB045892  | AL050369 Homo sapi  |
| 754 | 16 | 1.6 | 863  | 91 | BC005052  | BC005052 Homo sapi   | 827 | 16 | 1.6 | 1845 | 89 | AF308303  | AB045892 Sequence   |
| 755 | 16 | 1.6 | 886  | 53 | CNS07502  | AL430428 clone BAO   | 828 | 16 | 1.6 | 1864 | 9  | AR076171  | AF308303 Homo sapi  |
| 756 | 16 | 1.6 | 892  | 72 | AC052426  | AC052426 clone BAO   | 829 | 16 | 1.6 | 1864 | 9  | AR076171  | AR076171 Sequence   |
| 757 | 16 | 1.6 | 900  | 88 | AF077206  | AF077206 Homo sapi   | 830 | 16 | 1.6 | 1870 | 14 | CIN242538 | AF076862 Sequence   |
| 758 | 16 | 1.6 | 901  | 91 | BC005156  | BC005156 Homo sapi   | 831 | 16 | 1.6 | 1900 | 94 | AF287300  | AF036549 Zea mays   |
| 759 | 16 | 1.6 | 902  | 93 | HSMB00572 | AL080071 Homo sapi   | 832 | 16 | 1.6 | 1907 | 10 | AX086887  | AF287300 Cichorid   |
| 760 | 16 | 1.6 | 904  | 91 | BC005393  | BC005393 Homo sapi   | 833 | 16 | 1.6 | 1907 | 10 | AX086887  | AF287300 Rattus no  |
| 761 | 16 | 1.6 | 910  | 75 | AC075071  | AC075071 Giardia i   | 834 | 16 | 1.6 | 1984 | 4  | AB012617  | AX086887 Sequence   |
| 762 | 16 | 1.6 | 912  | 53 | CNS06KRW  | AL403445 T7 end of   | 835 | 16 | 1.6 | 2025 | 3  | RE041754  | AB012617 Caenorhab  |
| 763 | 16 | 1.6 | 926  | 53 | CNS06KRW  | AL403445 T7 end of   | 836 | 16 | 1.6 | 2027 | 94 | AB041037  | U41754 Rhizobium e  |
| 764 | 16 | 1.6 | 926  | 53 | CNS06KRW  | AL403445 T7 end of   | 837 | 16 | 1.6 | 2037 | 2  | CGGDH     | AB041037 Mus muscu  |
| 765 | 16 | 1.6 | 948  | 53 | CNS06G78  | AL397338 T7 end of   | 838 | 16 | 1.6 | 2037 | 2  | CGGDH     | X59404 Corynebacte  |
| 766 | 16 | 1.6 | 948  | 53 | CNS06G78  | AL397338 T7 end of   | 839 | 16 | 1.6 | 2040 | 9  | AX009994  | X72855 C. glutamicu |
| 767 | 16 | 1.6 | 952  | 76 | AC083683  | AC083683 Giardia i   | 840 | 16 | 1.6 | 2045 | 94 | AB016230  | AX009994 Sequence   |
| 768 | 16 | 1.6 | 966  | 53 | CNS07630  | AF137286 Gallus ga   | 841 | 16 | 1.6 | 2047 | 94 | AB016230  | AB016229 Mus muscu  |
| 769 | 16 | 1.6 | 981  | 10 | AX089467  | AX089467 Sequence    | 842 | 16 | 1.6 | 2063 | 9  | AX048734  | AB016230 Mus muscu  |
| 770 | 16 | 1.6 | 990  | 10 | AX089467  | AX089467 Sequence    | 843 | 16 | 1.6 | 2065 | 88 | AF049459  | AX048734 Sequence   |
| 771 | 16 | 1.6 | 993  | 93 | HSMB01069 | AL117544 Homo sapi   | 844 | 16 | 1.6 | 2076 | 58 | AF075682  | AF049459 Homo sapi  |
| 772 | 16 | 1.6 | 999  | 74 | AC070320  | AC070320 Giardia i   | 845 | 16 | 1.6 | 2089 | 89 | AF075682  | AF075682 Hemorrhag  |
| 773 | 16 | 1.6 | 1016 | 53 | CNS06KBA  | AL402668 T3 end of   | 846 | 16 | 1.6 | 2140 | 97 | H0MTNEBA  | AK026182 Homo sapi  |
| 774 | 16 | 1.6 | 1024 | 76 | AC080628  | AC080628 Giardia i   | 847 | 16 | 1.6 | 2159 | 89 | AK000953  | M55913 Human tumor  |
| 775 | 16 | 1.6 | 1024 | 76 | AC080628  | AC080628 Giardia i   | 848 | 16 | 1.6 | 2163 | 94 | BC004039  | AK000953 Homo sapi  |
| 776 | 16 | 1.6 | 1047 | 72 | AC060129  | AC060129 Giardia i   | 849 | 16 | 1.6 | 2184 | 94 | AF132727  | BC004039 Mus muscu  |
| 777 | 16 | 1.6 | 1047 | 53 | CNS06LVS  | AL404810 T3 end of   | 850 | 16 | 1.6 | 2192 | 15 | SCYNL253W | AF132727 Rattus no  |
| 778 | 16 | 1.6 | 1061 | 53 | CNS0738M  | AL427196 clone BAO   | 851 | 16 | 1.6 | 2199 | 95 | RATSE     | 271529 S. cerevisia |
| 779 | 16 | 1.6 | 1081 | 94 | AB018562  | AB018562 Mus muscu   | 852 | 16 | 1.6 | 2214 | 10 | AR093957  | D37920 Rat mRNA fo  |
| 780 | 16 | 1.6 | 1150 | 94 | OC077896  | U77896 Oryctolagus   | 853 | 16 | 1.6 | 2214 | 10 | AR093957  | AR093957 Sequence   |
| 781 | 16 | 1.6 | 1159 | 94 | AF148849  | AF148849 Mus muscu   | 854 | 16 | 1.6 | 2226 | 2  | AX024347  | E15639 Pinctada fu  |
| 782 | 16 | 1.6 | 1208 | 91 | BC001852  | BC001852 Homo sapi   | 855 | 16 | 1.6 | 2226 | 9  | AX024347  | AX024347 Sequence   |
| 783 | 16 | 1.6 | 1216 | 93 | HSMB01637 | AL136659 Homo sapi   | 856 | 16 | 1.6 | 2232 | 2  | AF270038  | AX024347 Sequence   |
| 784 | 16 | 1.6 | 1233 | 89 | AK000553  | AK000553 Homo sapi   | 857 | 16 | 1.6 | 2239 | 94 | AF270371  | AF270371 Staphyloc  |
| 785 | 16 | 1.6 | 1247 | 85 | AB051152  | AB051152 Macaca fa   | 858 | 16 | 1.6 | 2247 | 94 | MHT000001 | AF270371 Staphyloc  |
| 786 | 16 | 1.6 | 1250 | 94 | MMCD40    | X55453 M. musculus   | 859 | 16 | 1.6 | 2255 | 6  | DMREFPNN  | AL133300 Mus muscu  |
| 787 | 16 | 1.6 | 1260 | 94 | AF202778  | AF202778 Mus muscu   | 860 | 16 | 1.6 | 2263 | 89 | AK021663  | X69630 D. melanog   |
| 788 | 16 | 1.6 | 1292 | 3  | UBU85123  | UBU85123 Unidentifie | 861 | 16 | 1.6 | 2271 | 96 | TRBPEPCK  | AF270038 Staphyloc  |
| 789 | 16 | 1.6 | 1299 | 5  | AF017268  | AF017268 Toxoplasma  | 862 | 16 | 1.6 | 2274 | 2  | AX024349  | AK021663 Homo sapi  |
| 790 | 16 | 1.6 | 1314 | 9  | AR072866  | AR072866 Sequence    | 863 | 16 | 1.6 | 2274 | 9  | AX024349  | M91163 Trypanosoma  |
| 791 | 16 | 1.6 | 1314 | 10 | E14942    | E14942 Aspergillus   | 864 | 16 | 1.6 | 2292 | 94 | AF006071  | AX024349 Sequence   |
| 792 | 16 | 1.6 | 1314 | 10 | E14955    | E14955 Aspergillus   | 865 | 16 | 1.6 | 2324 | 89 | AF148713  | AF006071 Mus muscu  |
| 793 | 16 | 1.6 | 1314 | 13 | ATFAOA    | E27570 Thermostabi   | 866 | 16 | 1.6 | 2329 | 88 | AF049460  | AF148713 Homo sapi  |
| 794 | 16 | 1.6 | 1381 | 94 | MMU77630  | Y09020 A. terreus m  | 867 | 16 | 1.6 | 2332 | 94 | STMHRDB   | AF049460 Homo sapi  |
| 795 | 16 | 1.6 | 1381 | 94 | MMU77630  | Y09020 A. terreus m  | 868 | 16 | 1.6 | 2335 | 94 | DA33961   | M90411 Streptomyces |
| 796 | 16 | 1.6 | 1417 | 96 | TEU64517  | U77630 Mus muscu     | 869 | 16 | 1.6 | 2336 | 14 | CRAU765   | DA33961 Mus muscu   |
| 797 | 16 | 1.6 | 1417 | 96 | TEU64517  | U77630 Mus muscu     | 870 | 16 | 1.6 | 2344 | 7  | RABPKC    | AJ000765 Chlamydom  |
| 798 | 16 | 1.6 | 1449 | 89 | AF287302  | AF287302 Homo sapi   | 871 | 16 | 1.6 | 2361 | 10 | AX089466  | M19338 Rabbit prot  |
| 799 | 16 | 1.6 | 1455 | 97 | IR1845189 | AL359057 Homo sapi   | 872 | 16 | 1.6 | 2363 | 10 | DMREFPCK  | X64301 G.gallus mr  |
| 800 | 16 | 1.6 | 1464 | 9  | AX063811  | AX063811 Sequence    | 873 | 16 | 1.6 | 2394 | 88 | AF061795  | AX089466 Sequence   |
| 801 | 16 | 1.6 | 1468 | 3  | TTASNS    | X91009 T. thermophi  | 874 | 16 | 1.6 | 2394 | 88 | AF061795  | X69829 D. melanog   |
| 802 | 16 | 1.6 | 1468 | 89 | AF119879  | AF119879 Homo sapi   | 875 | 16 | 1.6 | 2416 | 91 | BC000770  | AF061795 Homo sapi  |
| 803 | 16 | 1.6 | 1477 | 59 | H1V1205   | L11785 Human Immun   | 876 | 16 | 1.6 | 2449 | 85 | AB006965  | BC000770 Homo sapi  |
| 804 | 16 | 1.6 | 1513 | 10 | AX082314  | AX082314 Sequence    | 877 | 16 | 1.6 | 2452 | 94 | AF273685  | AB006965 Homo sapi  |
| 805 | 16 | 1.6 | 1519 | 94 | AF273689  | AF273689 Mus muscu   | 878 | 16 | 1.6 | 2472 | 89 | AF151685  | AF273685 Mus muscu  |
| 806 | 16 | 1.6 | 1525 | 94 | AB005049  | AB005049 Cavia por   | 879 | 16 | 1.6 | 2480 | 94 | MUSEMTX   | AF151685 Homo sapi  |
| 807 | 16 | 1.6 | 1543 | 94 | AF134488  | AF134488 Cavia por   | 880 | 16 | 1.6 | 2487 | 94 | AF075533  | L10628 Mus muscu    |
| 808 | 16 | 1.6 | 1581 | 94 | AF134488  | AF134488 Cavia por   | 881 | 16 | 1.6 | 2493 | 88 | AF000430  | AF075533 Mus muscu  |
| 809 | 16 | 1.6 | 1600 | 3  | RCANIFD   | M26323 Rhododactyl   | 882 | 16 | 1.6 | 2512 | 8  | X1U68724  | AF000430 Homo sapi  |
| 810 | 16 | 1.6 | 1662 | 94 | AB016423  | AB016423 Mus muscu   | 883 | 16 | 1.6 | 2529 | 1  | AF028831  | U68724 Xenopus lae  |
| 811 | 16 | 1.6 | 1668 | 8  | AF258786  | AF258786 Danio rer   | 884 | 16 | 1.6 | 2544 | 58 | AF037263  | AF028831 Ctenarctae |

|       |    |     |      |    |           |                     |
|-------|----|-----|------|----|-----------|---------------------|
| C 885 | 16 | 1.6 | 2545 | 59 | SLI011858 | At011858 Spodopter  |
| C 886 | 16 | 1.6 | 2610 | 95 | AX023369  | At023369 Sequence   |
| C 887 | 16 | 1.6 | 2610 | 95 | RNAJ3148  | AJ003148 Rattus no  |
| C 888 | 16 | 1.6 | 2632 | 94 | AF273684  | AF273684 Mus muscu  |
| C 889 | 16 | 1.6 | 2661 | 15 | TRAGLUCS  | 268706 T. reeset mr |
| C 890 | 16 | 1.6 | 2673 | 14 | PAM133148 | AJ133148 Persea am  |
| C 891 | 16 | 1.6 | 2684 | 6  | DMU23926  | At023926 Drosophila |
| C 892 | 16 | 1.6 | 2689 | 1  | AF128272  | AF128272 Streptomy  |
| C 893 | 16 | 1.6 | 2691 | 6  | DMU23923  | U23923 Drosophila   |
| C 894 | 16 | 1.6 | 2691 | 6  | DMU23927  | U23927 Drosophila   |
| C 895 | 16 | 1.6 | 2691 | 6  | DMU23932  | U23932 Drosophila   |
| C 896 | 16 | 1.6 | 2707 | 6  | DSU23930  | U23930 Drosophila   |
| C 897 | 16 | 1.6 | 2708 | 6  | DMU23928  | U23928 Drosophila   |
| C 898 | 16 | 1.6 | 2708 | 6  | DMU23932  | U23932 Drosophila   |
| C 899 | 16 | 1.6 | 2708 | 6  | DMU23932  | U23932 Drosophila   |
| C 900 | 16 | 1.6 | 2709 | 6  | DMU23929  | U23929 Drosophila   |
| C 901 | 16 | 1.6 | 2719 | 6  | DMU23924  | U23924 Drosophila   |
| C 902 | 16 | 1.6 | 2720 | 6  | DMU23925  | U23925 Drosophila   |
| C 903 | 16 | 1.6 | 2772 | 89 | AK002127  | AK002127 Homo sapi  |
| C 904 | 16 | 1.6 | 2776 | 91 | BC004237  | BC004237 Homo sapi  |
| C 905 | 16 | 1.6 | 2795 | 95 | RNU78889  | U78889 Rattus norv  |
| C 906 | 16 | 1.6 | 2823 | 2  | ECOHSD    | L18758 Escherichia  |
| C 907 | 16 | 1.6 | 2891 | 9  | AX065435  | AX065435 Sequence   |
| C 908 | 16 | 1.6 | 2916 | 8  | CHKCMPOLE | D28598 Chicken mRN  |
| C 909 | 16 | 1.6 | 2932 | 93 | HSMB01716 | AL136748 Homo sapi  |
| C 910 | 16 | 1.6 | 2955 | 58 | AF020660  | AF020660 Tomato sp  |
| C 911 | 16 | 1.6 | 3045 | 9  | A96458    | A96458 Sequence 49  |
| C 912 | 16 | 1.6 | 3045 | 9  | A96462    | A96462 Sequence 49  |
| C 913 | 16 | 1.6 | 3055 | 94 | AF273683  | AF273683 Mus muscu  |
| C 914 | 16 | 1.6 | 3153 | 30 | E15417    | E15417 Arthrobacte  |
| C 915 | 16 | 1.6 | 3216 | 3  | SCU51332  | U51332 Streptomyce  |
| C 916 | 16 | 1.6 | 3226 | 91 | BC000136  | BC000136 Homo sapi  |
| C 917 | 16 | 1.6 | 3233 | 95 | RNND4P    | X66022 R. norvegicu |
| C 918 | 16 | 1.6 | 3258 | 92 | HS361H4B  | Z69085 Human DNA s  |
| C 919 | 16 | 1.6 | 3290 | 1  | AF006675  | AF006675 Rhodother  |
| C 920 | 16 | 1.6 | 3331 | 6  | D86074    | D86074 Pinctada fu  |
| C 921 | 16 | 1.6 | 3331 | 9  | AR093958  | AR093958 Sequence   |
| C 922 | 16 | 1.6 | 3331 | 9  | AK093959  | AK093959 Sequence   |
| C 923 | 16 | 1.6 | 3331 | 10 | E15640    | E15640 Pinctada fu  |
| C 924 | 16 | 1.6 | 3351 | 91 | BC001211  | BC001211 Homo sapi  |
| C 925 | 16 | 1.6 | 3381 | 8  | S63276    | S63276 SC1-100 kda  |
| C 926 | 16 | 1.6 | 3444 | 8  | CHKMYLCC  | J03397 Chicken myo  |
| C 927 | 16 | 1.6 | 3453 | 3  | DMU76378  | U76378 Drosophila   |
| C 928 | 16 | 1.6 | 3492 | 3  | RCSOR     | X57478 Rhodobacter  |
| C 929 | 16 | 1.6 | 3500 | 3  | SEORF1    | L37354 Saccharopol  |
| C 930 | 16 | 1.6 | 3539 | 94 | D78349    | D78349 Mouse DNA f  |
| C 931 | 16 | 1.6 | 3577 | 3  | RNDNAB    | Y13813 Rhodothermu  |
| C 932 | 16 | 1.6 | 3600 | 14 | NEURDHA   | L13964 Neurospora   |
| C 933 | 16 | 1.6 | 3621 | 85 | AB033116  | AB033116 Homo sapi  |
| C 934 | 16 | 1.6 | 3682 | 89 | AK001713  | AK001713 Homo sapi  |
| C 935 | 16 | 1.6 | 3747 | 14 | BEPA71    | AJ001045 Blastocla  |
| C 936 | 16 | 1.6 | 3750 | 14 | CRU279021 | AJ279021 Candida r  |
| C 937 | 16 | 1.6 | 3755 | 14 | AC008239  | AC008239 Leishmani  |
| C 938 | 16 | 1.6 | 3845 | 94 | AF019043  | AF019043 Rattus no  |
| C 939 | 16 | 1.6 | 3892 | 94 | DERER2PE  | X69831 D. erecta re |
| C 940 | 16 | 1.6 | 3919 | 3  | KPU00985  | U00985 Klebsiella   |
| C 941 | 16 | 1.6 | 3952 | 3  | PSEDCD    | J05282 P. cepacia 2 |
| C 942 | 16 | 1.6 | 3957 | 91 | AY009106  | AY009106 Homo sapi  |
| C 943 | 16 | 1.6 | 3960 | 6  | CHKMLF    | D28596 Chicken gen  |
| C 944 | 16 | 1.6 | 3984 | 6  | DMREF2P01 | X16993 Drosophila   |
| C 945 | 16 | 1.6 | 4088 | 94 | MUSB3RP   | M75870 Xenopus lae  |
| C 946 | 16 | 1.6 | 4107 | 59 | MOCREPSQB | J04036 Mus musculu  |
| C 947 | 16 | 1.6 | 4231 | 94 | MUSYRKIN  | M98815 Molluscu c   |
| C 948 | 16 | 1.6 | 4231 | 94 | MUSYRKIN  | D14042 Mus musculu  |
| C 949 | 16 | 1.6 | 4261 | 1  | AB016241  | L05631 Mouse tyros  |
| C 950 | 16 | 1.6 | 4265 | 1  | AB028210  | AB028210 Streptomy  |
| C 951 | 16 | 1.6 | 4294 | 94 | MUSITKA   | L00619 Mouse T-cell |
| C 952 | 16 | 1.6 | 4394 | 2  | D84102    | D84102 Corynebacte  |
| C 953 | 16 | 1.6 | 4394 | 2  | AR083912  | AR083912 Sequence   |
| C 954 | 16 | 1.6 | 4394 | 2  | E14601    | E14601 Brevibacter  |
| C 955 | 16 | 1.6 | 4412 | 10 | CGU13922  | U13922 Corynebacte  |
| C 956 | 16 | 1.6 | 4494 | 13 | AF335465  | AF335465 Aspergill  |
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| C 958  | 16 | 1.6 | 4525  | 3  | PFL1233     | V12268 P. fluoresce |
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| C 960  | 16 | 1.6 | 4589  | 7  | RABAB1AG    | M93344 Rabbit acid  |
| C 961  | 16 | 1.6 | 4648  | 63 | AC014057    | AC014057 Drosophi   |
| C 962  | 16 | 1.6 | 4736  | 13 | AF205944    | AF205944 Blastocla  |
| C 963  | 16 | 1.6 | 4746  | 17 | AF034831    | AF034831 Rhizobium  |
| C 964  | 16 | 1.6 | 4756  | 97 | HUMPTPS     | D37781 Human mRNA   |
| C 965  | 16 | 1.6 | 4823  | 89 | AK024484    | AK024484 Homo sapi  |
| C 966  | 16 | 1.6 | 4887  | 5  | AF351187    | AF351187 Drosophi   |
| C 967  | 16 | 1.6 | 4972  | 3  | MAMAMIRM    | X79027 M. ammoniaph |
| C 968  | 16 | 1.6 | 5084  | 3  | SGSTRELMB   | X62567 S. griseus s |
| C 969  | 16 | 1.6 | 5117  | 9  | ARI09903    | ARI09903 Sequence   |
| C 970  | 16 | 1.6 | 5117  | 97 | HSU10886    | U10886 Human dens1  |
| C 971  | 16 | 1.6 | 5282  | 97 | HSY13034    | Y13034 Homo sapien  |
| C 972  | 16 | 1.6 | 5407  | 2  | AF324349    | AF324349 Yersinia   |
| C 973  | 16 | 1.6 | 5591  | 94 | MSMKELINA   | Z22666 M.musculu    |
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| C 975  | 16 | 1.6 | 5645  | 94 | MMU012072   | AJ012072 Mus muscu  |
| C 976  | 16 | 1.6 | 5774  | 94 | AF064748    | AF064748 Mus muscu  |
| C 977  | 16 | 1.6 | 5994  | 3  | SVSNDDE     | Y11547 S. virginiae |
| C 978  | 16 | 1.6 | 6213  | 2  | ASAJ187     | AJ000187 Arthrobac  |
| C 979  | 16 | 1.6 | 6396  | 7  | BTU02285    | U02285 Bos taurus   |
| C 980  | 16 | 1.6 | 6412  | 95 | RNO131902   | AJ131902 Rattus no  |
| C 981  | 16 | 1.6 | 6545  | 2  | ECOMALB     | J01648 E. coli malB |
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| C 983  | 16 | 1.6 | 6676  | 1  | AF031590    | AF031590 Streptomy  |
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| C 986  | 16 | 1.6 | 7581  | 63 | AC014309    | AC014309 Drosophi   |
| C 987  | 16 | 1.6 | 8200  | 93 | STMDNAGR    | L27063 Streptomyce  |
| C 988  | 16 | 1.6 | 8278  | 92 | HS285F3     | AL021452 Human DNA  |
| C 989  | 16 | 1.6 | 8516  | 2  | D88362      | D88362 Arthrobacte  |
| C 990  | 16 | 1.6 | 8813  | 6  | DSXDH       | Y08237 D. subobscur |
| C 991  | 16 | 1.6 | 8832  | 59 | SLVRNAGENN  | M97264 Shalloo vir  |
| C 992  | 16 | 1.6 | 9523  | 2  | AF237894SL1 | AF237894 Streptomy  |
| C 993  | 16 | 1.6 | 9551  | 9  | AR076233    | AR076233 Sequence   |
| C 994  | 16 | 1.6 | 9551  | 10 | I39845      | I39845 Sequence 93  |
| C 995  | 16 | 1.6 | 9551  | 97 | HUMTRHYAL   | L09190 Human trich  |
| C 996  | 16 | 1.6 | 9668  | 64 | AC017387    | AC017387 Lactococc  |
| C 997  | 16 | 1.6 | 9910  | 1  | AE006387    | AE006387 Methanoba  |
| C 998  | 16 | 1.6 | 9956  | 1  | AE000873    | AE000873 Xylella f  |
| C 999  | 16 | 1.6 | 9995  | 1  | AE003891    | AE003891 Xylella f  |
| C 1000 | 16 | 1.6 | 10021 | 1  | AE002537    | AE002537 Neisseria  |

## ALIGNMENTS-

|                       |                                                                                                        |            |     |  |  |  |
|-----------------------|--------------------------------------------------------------------------------------------------------|------------|-----|--|--|--|
| RESULT                | 1                                                                                                      |            |     |  |  |  |
| LOCUS                 | AR047920                                                                                               | 3402 bp    | DNA |  |  |  |
| DEFINITION            | Sequence 1 from patent US 5820864.                                                                     |            |     |  |  |  |
| ACCESSION             | AR047920                                                                                               |            |     |  |  |  |
| VERSION               | AR047920.1                                                                                             | GI:5970263 |     |  |  |  |
| KEYWORDS              |                                                                                                        |            |     |  |  |  |
| SOURCE                | Unknown.                                                                                               |            |     |  |  |  |
| ORGANISM              | Unknown.                                                                                               |            |     |  |  |  |
| REFERENCE             | 1 (bases 1 to 3402)                                                                                    |            |     |  |  |  |
| AUTHORS               | Paranhos-Baccala, G., Lesenechal, M. and Jolivet, M.                                                   |            |     |  |  |  |
| TITLE                 | Trypanosoma cruzi antigen, gene encoding therefor and methods of detecting and treating chagas disease |            |     |  |  |  |
| JOURNAL               | Patent: US 5820864-A 1 13-Oct-1998;                                                                    |            |     |  |  |  |
| FEATURES              | Location/Qualifiers                                                                                    |            |     |  |  |  |
| source                | 1..3402                                                                                                |            |     |  |  |  |
| BASE COUNT            | 888 a 821 c 956 g 737 t                                                                                |            |     |  |  |  |
| ORIGIN                |                                                                                                        |            |     |  |  |  |
| Query Match           | 100.0%; Score 976; DB 9; Length 3402;                                                                  |            |     |  |  |  |
| Best Local Similarity | 100.0%; Pred. No. 0;                                                                                   |            |     |  |  |  |
| Matches               | 976; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                                                   |            |     |  |  |  |

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| OY     | 1      | caagtaacagcgtaacgacctttgtcttaatactcgtacacgccaagcgtaagctcgcttgct | 60          |
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| OY     | 61     | gacatgtcatctgattgaacatcttcacatctccggtccctcccgcaagggnaaacaagag   | 120         |
| Db     | 1292   | GACATGTGATTGCATTGACGATCTTCCATCTCCGGTCTCCCGCAGGAAACACAGAG        | 1351        |
| OY     | 121    | ccagggccaaaaacatcsgtaatgtagcgacgcgaaacccgggtgtgtgttcctcgggcaat  | 180         |
| Db     | 1352   | CCAGGCCAAAAAATCGGGTAGTGGCGACGGCAACCGGGGTGTTGTGCTCGGGCACT        | 1411        |
| OY     | 181    | gaacgsgcgagatgaacatcaataacgaactcttcgcgctgtcgtcgaatccctcgatca    | 240         |
| Db     | 1412   | GACCGGGGAGATTACGTACGTATACCAATACGACTTTCGGCTGCTGTGCATCCCTGCATCA   | 1471        |
| OY     | 241    | ccccctgtcttagcgccaagcgacgcgcgcctccctcgcgcgcgatcgcgtatag         | 300         |
| Db     | 1472   | CCCCCTGTTTAGCGGCCACGCGCAAGCGACGGCCGCTCTCTCGCGCGCGATCGGCTAG      | 1531        |
| OY     | 301    | ccgcacgtlvgggagcaaatcatctgtctaactagtaatcaacgtlvgggtatlaatlcac   | 360         |
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| Db     | 1652   | ACGACTACCGCCCGCGACGCAACAGTCCATACGGGCAATATGGCCGACCTGTGACGGCT     | 1711        |
| OY     | 481    | ggattgtgtgcagctaaatagtggtgcagcgcgcgctcgtctcccaacgcgcgcgcgaa     | 540         |
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| OY     | 541    | ccaacagagaagaagaagcgctccgcgcgcgtggaagaagctccgtgycgaataatgag     | 600         |
| Db     | 1772   | CCAAACGAGAGAAAGAAAGCGCTCCGGCGGCAATGTGAACGACGCTCCGTGGCGAATTAATCG | 1831        |
| OY     | 601    | acaagcccgcgctctcaacaacgcctctcccgcaagcgccaaggaatgagcttttgagcg    | 660         |
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| OY     | 661    | gcagcagataccagctcgcgagggcgaggtcatcagtcgcgtgagcgctgtagtcgctc     | 720         |
| Db     | 1892   | GCAGAGATATACAGTGTGGAGGGGAGAGTTCATCACTGCTGTGAGGCGCTGGAGTCCGCTC   | 1951        |
| OY     | 721    | ataaccaacaagctctcggtcttgaagtgtctcccgaaacatctcgaagagacataaa      | 780         |
| Db     | 1952   | ATAACCAACAGCTCTCGGGTCTGAAATGCTCTCCGTACACCAATTCGAAGAGACCATATAA   | 2011        |
| OY     | 781    | caactctgaatctcgtgtcttagagcgacagatgacagagctgcagacagacgcgtccaca   | 840         |
| Db     | 2012   | CAACTCTGAATCTGGGTTTAGAGGCAACAGTACAGAGCTGCAGAGAGCCGTCCACAA       | 2071        |
| OY     | 841    | ccgcaaacacagccgagagacacaagctccgcgaaatcatccgtgtgttgaagcgtaac     | 900         |
| Db     | 2072   | CCGCAAAACACGCGAGAGACACAGAGCTCCGCCAAATTCATCCGTGTTGAGACGTAACAC    | 2131        |
| OY     | 901    | ctgtttctcatgttggaattccctctcgcgaataatagaaaggggttgaaggtgtgtg      | 960         |
| Db     | 2132   | CTTGTCTCATTTGGGATTTCCCTCTCTCGCAACATACCAAGGGGTGAAGGTGTGTG        | 2191        |
| OY     | 961    | aacgagagccattatgt 976                                           |             |
| Db     | 2192   | AACGAGGCCATTATGT 2207                                           |             |
| RESULT | 2      |                                                                 |             |
| A48910 |        |                                                                 |             |
| LOCUS  | A48910 | 3402 bp                                                         | DNA         |
|        |        |                                                                 | PAT         |
|        |        |                                                                 | 07-MAR-1997 |

|                       |                                                                                                                    |
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| DEFINITION            | Sequence 1 from Patent WO9605312.                                                                                  |
| ACCESSION             | A48910                                                                                                             |
| VERSION               | A48910.1 GI:2302570                                                                                                |
| KEYWORDS              | .                                                                                                                  |
| SOURCE                | Trypanosoma cruzi.                                                                                                 |
| ORGANISM              | Trypanosoma cruzi<br>Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;                                      |
| REFERENCE             | Trypanosoma,<br>Trypanosoma,<br>Schizotrypanum.<br>1 (bases 1 to 3402)                                             |
| AUTHORS               | Paranhos-Baccala,G., Lescenechal,M. and Jolivel,M.                                                                 |
| TITLE                 | NOVEL TRYPANOSOMA CRUZI ANTIGEN, AND GENE CODING THEREFOR; THEIR APPLICATION TO THE DETECTION OF CHAGAS' DISEASE   |
| JOURNAL               | Patient: WO 9605312-A 1 22-FEB-1996;<br>BIO MERIEUX (FR)                                                           |
| COMMENT               | Other publication CA 2173957 960222<br>Other publication AU 3169195 960307<br>Other publication FR 2723589 960216. |
| FEATURES              | location/Qualifiers                                                                                                |
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|                       | /dev_stage="EPIMASTIGOTE"                                                                                          |
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| 1232                  | CAGGTACACCGCTAACGGCTTTGCTTCATCATCTACAACCOCGAGTACTGCCTGGCT 1291                                                     |
| 61                    | gscatgtcatttgatltgaagatcttcatactccggtctcccgaaggaaacaagcaag 120                                                     |
| 1292                  | GACATGTCGAATCGAATTGACGATCTCCATCTCCCGTGCTCCCGCAGGAAGAACAGCAG 1351                                                   |
| 121                   | ccaagccaaaanaaacatcgtagtbgcgcgcgcgcgaacccggggtgtgttcttcggagct 180                                                  |
| 1352                  | CCAGGCCAAAACATTCGGTAAGTAGTGGCAGCGGGCAAAACCGGGGTGTGTCTCGGGCACT 1411                                                 |
| 181                   | gaacgcgcgcagtatagaatcataccaatacgaattctgcgctgtgtgcatctcccttgatca 240                                                |
| 1412                  | GACGCGCGCAGTAGACGATCATACCAATACGACTTTCGCCGTGCTGCATCCCGTCATCA 1471                                                   |
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| 1532                  | CCGCACGTGGGAGCAGACATCTTCTAATCTAGTGAAATCACCTGGGATTAATGTCAAC 1591                                                    |
| 361                   | csaaggaagcgttcagcaacttggagcgcgcgcgcacagcaaggtlctacgcgcgtgacgtcc 420                                                |
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| 421                   | acgactatccgcgcgcgcgcgaacaaagttcatacgggcacaaattggcgcgcgcgttgtagct 480                                               |
| 1652                  | ACGACTACCGCCGCCAGCAGCAAGATCATACGGGGCAAAATGGCCGACCTGTGCGGACT 1711                                                   |
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| 1712                  | GGATTGTGTGCGAGCTAATAAGTGTGTCCAGCGGGCGCTGTCTCCACAGCGCGCGCAAA 1771                                                   |
| 541                   | ccaacaagagaagaagaagcctcgcgcgcgcgttgtaaagaagagctccgttgcatataatgcg 600                                               |
| 1772                  | CCAACAAGGAAGAAGAAAGGCTCTCCGCGCATGTGAAGACACTCCGTGGCATTAATATCG 1831                                                  |
| 601                   | aacagccgcgcgtctcacaaaccctctccgcgcgcgcgcgaacgaatgagcgttttgccg 660                                                   |

Db 1832 ACACGCCGGCGCTTCACACGCCCTCTCTCCGACGAGGCCAACGAGATGGCGTTTGGCG 1891  
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DEFINITION U24190  
ACCESSION U24190.1 GI:790645  
VERSION U24190.1  
KEYWORDS  
SOURCE Trypanosoma cruzi.  
ORGANISM Trypanosoma cruzi.  
Eukaryote; Euglenozoa; Kinetoplastida; Trypanosomatidae;  
Trypanosoma; Schizotrypanum.  
REFERENCE 1 (bases 1 to 3402)  
AUTHORS Lesenechal, M., Duret, L., Cano, M. I., Mortara, R. A., Jolivet, M.,  
Camargo, M. E., da Silveira, J. F., and Paranhos-Baccala, G.  
TITLE Cloning and characterization of a gene encoding a novel  
immunodominant antigen of Trypanosoma cruzi  
Mol. Biochem. Parasitol. 87 (2), 193-204 (1997)  
JOURNAL 97391123  
MEDLINE 2 (bases 1 to 3402)  
REFERENCE Lesenechal, M., Franco Da Silveira, J., Mortara, R. A., Duret, L.,  
AUTHORS Camargo, M. E., Jolivet, M., and Paranhos-Baccala, G.  
TITLE Direct Submission  
JOURNAL Submitted (06-Apr-1995) Mylene Lesenechal, BioMerieux, 22 rue Saint  
Jean de Dieu, Lyon 69007, France  
FEATURES  
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misc\_RNA  
CDS

BASE COUNT 889 a 818 c 958 g 737 t  
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Best Local Similarity 99.8%; Pred. No. 0;  
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Db 1592 CAAAGAGCGGTGTCAGCAGCTGAGCGCGCGGACAGAGAGGTATACGGCGGTGACGTCC 1651  
Qy 421 acgactacgcccgcgcagcgaggaacagtcataagggacaaatgtgcgactgtgagcgct 480  
Db 1652 ACGACTACCGCCCGCCAGCAAGATCCATAAGGGCACAAAGGCGCACCTGTGACGGCTT 1711  
Qy 481 ggaattgtgagcagctaatagtggtgcagcgcgagcgtgctcccaagcgcgcgagaa 540  
Db 1712 GGATTGTGGGACGCTAATAGTGTGTCACAGCGGCGCTGTCTCCACACCGCGCGGCAAA 1771  
Qy 541 ccaacagagagaagaaagcgctcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 600  
Db 1772 CCAACAGAGGAAGAAAGGCGCTCCGCGCATGTGAACGAGCTCGTGCGATTAATGCG 1831  
Qy 601 acaagcccgcgctcacaagcgctcctccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 660  
Db 1832 ACACGCCGGCGCTTCACAAACCCCTCTCCGCGAGGCGCCAAACGATGCGCTTTTGGCG 1891  
Qy 661 gcaagcagatatacagtcggaagggcgaggttcacagtcgctcgagcgagtcgagtcgctc 720  
Db 1892 GCAGAGATATACCACTCGGAGGCGAGGTTCACTGCTGCTGAGCGGCTGAGTCCGTC 1951  
Qy 721 ataaccacaacgctcgcgggttcgaagtgtctccctgaacacatcgaagagacatgaa 780  
Db 1952 ATAAACCAACAGCTCTCGGCTTCTGAAGTTGCTCCCTGACACCATTCGAAGACACATGAA 2011  
Qy 781 caactctgaatctgggttttagagggacagatgacagagctgcaagagccgtccaca 840

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Db 2012 CAACCTTGATCTGGCTTTAGAGGACAGATGACAGAGCTGCAGACGCCGTCACA 2071
QY 841 ccggaacacagccggaagacacaaagctccggaatcatctcgtgtttgagactaac 900
Db 2072 CCGCAACACAGCCGGAAGACACAAAGCTCCGCCAAATCATCCGTTTGGACCTAAC 2131
QY 901 ctgtctcattgcgagatccctctcgcacacatcagaaggggtgaagcgtggtg 960
Db 2132 CTGTCTCATTTGGGATTCCTCTCTCGCAACATCAAGAGGGGTGMAAGCGTGCTG 2191
QY 961 aacgaagccattatgt 976
Db 2192 AACGAGGCATATATGT 2207

RESULT 4
A48918 LOCUS A48918 22 bp DNA PAT 07-MAR-1997
DEFINITION Sequence 9 from Patent WO9605312.
ACCESSION A48918
VERSION A48918.1 GI:2302577
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Paranhos-Baccala,G., Lesenechal,M. and Jolivet,M.
TITLE NOVEL TRYPAOSOMA CRUZI ANTIGEN, AND GENE CODING THEREFOR; THEIR
JOURNAL APPLICATION TO THE DETECTION OF CHAGAS' DISEASE
COMMENT BIO MERIEUX (FR)
Other publication CA 2173957 960222
Other publication AU 3169195 960307
Other publication FR 2723589 960216.
FEATURES
source 1..22
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 3 a 8 c 7 g 4 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 cagccgacggtagctgcgtcct 56
Db 1 CAGCCGACGCTAGCTGCTCCT 22

RESULT 5
AR047927 LOCUS AR047927 22 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 9 from patent US 5820864.
ACCESSION AR047927
VERSION AR047927.1 GI:5970270
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Paranhos-Baccala,G., Lesenechal,M. and Jolivet,M.
TITLE Trypanosoma cruzi antigen, gene encoding therefor and methods of
detecting and treating chagas disease
JOURNAL Patent: US 5820864-A 9 13-OCT-1998;
FEATURES location/Qualifiers
source 1..22
/organism="unknown"
BASE COUNT 3 a 8 c 7 g 4 t
ORIGIN

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Query Match 2.3%; Score 22; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 cagccgacggtagctgcgtcct 56
Db 1 CAGCCGACGCTAGCTGCTCCT 22

RESULT 6
NMA42491 LOCUS NMA42491 331801 bp BCT 04-DEC-2000
DEFINITION Neisseria meningitidis serogroup A strain Z2491 complete genome;
segment 4/7
ACCESSION AL162755
VERSION AL162755.2 GI:7379742
KEYWORDS
SOURCE Neisseria meningitidis Z2491.
ORGANISM Neisseria meningitidis Z2491.
REFERENCE 1 (bases 1 to 331801)
AUTHORS Parkhill,J., Achtman,M., James,K.D., Bentley,S.D., Churcher,C.,
Klee,S.R., Morelli,G., Basham,D., Brown,D., Chillingworth,T.,
Davies,R.M., Davis,P., Devlin,K., Felwell,T., Hamlin,N.,
Holroyd,S., Jagsels,K., Leather,S., Moule,S., Mungall,K.,
Quail,M.A., Rajandream,M.A., Rutherford,K.M., Stammers,M.,
Skellton,J., Whitehead,S., Spratt,B.G. and Barrell,B.G.
TITLE Complete DNA sequence of a serogroup A strain of Neisseria
JOURNAL meningitidis Z2491
MEDLINE Nature 404 (6777), 502-506 (2000)
REFERENCE 2 (bases 1 to 331801)
AUTHORS Parkhill,J.
TITLE Direct Submission
JOURNAL Submitted (30-MAR-2000) Submitted on behalf of the Neisseria
sequencing team, Sanger Centre, Wellcome Trust Genome Campus,
Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk
Notes:
Details of N. meningitidis sequencing at the Sanger Centre are
available on the World Wide Web.
(URL, http://www.sanger.ac.uk/Projects/N_meningitidis/).
FEATURES
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/sstrain="Z2491"
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/note="serogroup: A"
117..1333
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117..1333
/genre="NMA1040"
/note="NMA1040", possible type I restriction-modification
system specificity protein, pseudogene, len: 1217 bp;
N-terminus shows weak similarity to the C-terminal half of
TR:Q50359 (EMBL:L25415), hsdS1B, Mycoplasma pulmonis
restriction-modification enzyme subunit S1B (336 aa),
fasta scores: E(): 2.3e-06, 26.2% identity in 141 aa
overlap and to many hypothetical restriction-modification
subunits. Also similar to NMA1041, fasta scores: E():
4.8e-10, 37.0% identity in 100 aa overlap. C-termnus
similar to part of SW:TI51_ECOLI (EMBL:X13145), hsdS,
Escherichia coli type I restriction enzyme EcoRI2411
specificity protein (410 aa), fasta scores: E(): 1.9e-14,
39.6% identity in 182 aa overlap. Similar to NMA1040, E():
2.9e-09, 38.0% identity in 100 aa overlap. Contains pfam
match to entry PF01420 Methylase_S, type I restriction
modification DNA specificity domain. Contains a C(8) tract
which would allow translation as an intact CDS, if
variable. Lies within a region of unusually low GC
content"
/codon_start=1

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Db 147264 CCAGACTACCGCCCGCAGCG 147285

## RESULT 7

LOCUS A48919 21 bp DNA PAT 07-MAR-1997  
DEFINITION Sequence 10 from Patent WO9605312.  
ACCESSION A48919  
VERSION A48919.1 GI:2302578  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.

REFERENCE 1 (bases 1 to 21)  
AUTHORS Paranhos-Baccala, G., Lesenechal, M. and Jolivet, M.  
TITLE NOVEL TRYPAOSOMA CRUZI ANTIGEN, AND GENE CODING THEREFOR; THEIR APPLICATION TO THE DETECTION OF CHAGAS' DISEASE  
JOURNAL Patent: WO 9605312-A 10 22-FEB-1996;  
BIO MERIEUX (FR)

COMMENT Other publication CA 2173957 960222  
Other publication AU 3169195 960307  
Other publication FR 2723589 960216.  
Location/Qualifiers

FEATURES  
source 1..21  
/organism="unidentified"  
/db\_xref="taxon:32644"

BASE COUNT 6 a 7 c 3 g 5 t  
ORIGIN

Query Match 2.2%: Score 21; DB 9; Length 21;  
Best Local Similarity 100.0%: Pred. No. 9.6;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 956 gtgtgaacgagccattatgt 976

Db 21 GTGTGAACGAGCCATTATGT 1

## RESULT 8

LOCUS A48921 21 bp DNA PAT 07-MAR-1997  
DEFINITION Sequence 12 from Patent WO9605312.  
ACCESSION A48921  
VERSION A48921.1 GI:2302580  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.

REFERENCE 1 (bases 1 to 21)  
AUTHORS Paranhos-Baccala, G., Lesenechal, M. and Jolivet, M.  
TITLE NOVEL TRYPAOSOMA CRUZI ANTIGEN, AND GENE CODING THEREFOR; THEIR APPLICATION TO THE DETECTION OF CHAGAS' DISEASE  
JOURNAL Patent: WO 9605312-A 12 22-FEB-1996;  
BIO MERIEUX (FR)

COMMENT Other publication CA 2173957 960222  
Other publication AU 3169195 960307  
Other publication FR 2723589 960216.  
Location/Qualifiers

FEATURES  
source 1..21  
/organism="unidentified"  
/db\_xref="taxon:32644"

BASE COUNT 9 a 5 c 4 g 3 t  
ORIGIN

Query Match 2.2%: Score 21; DB 9; Length 21;  
Best Local Similarity 100.0%: Pred. No. 9.6;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 766 cgaagagacatgaacaactt 786

Db 1 CGAAGAGACCATGAACAACCTT 21

## RESULT 9

LOCUS AR047928 21 bp DNA PAT 29-SEP-1999  
DEFINITION Sequence 10 from patent US 5820864.  
ACCESSION AR047928  
VERSION AR047928.1 GI:5970271  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 21)  
AUTHORS Paranhos-Baccala, G., Lesenechal, M. and Jolivet, M.  
TITLE Trypanosoma cruzi antigen, gene encoding therefor and methods of detecting and treating chagas disease  
JOURNAL Patent: US 5820864-A 10 13-OCT-1998;  
BIO MERIEUX (FR)

FEATURES  
source 1..21  
/organism="unknown"  
/db\_xref="taxon:32644"

BASE COUNT 6 a 7 c 3 g 5 t  
ORIGIN

Query Match 2.2%: Score 21; DB 9; Length 21;  
Best Local Similarity 100.0%: Pred. No. 9.6;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 956 gtgtgaacgagccattatgt 976

Db 21 GTGTGAACGAGCCATTATGT 1

## RESULT 10

LOCUS AR047930 21 bp DNA PAT 29-SEP-1999  
DEFINITION Sequence 12 from patent US 5820864.  
ACCESSION AR047930  
VERSION AR047930.1 GI:5970273  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 21)  
AUTHORS Paranhos-Baccala, G., Lesenechal, M. and Jolivet, M.  
TITLE Trypanosoma cruzi antigen, gene encoding therefor and methods of detecting and treating chagas disease  
JOURNAL Patent: US 5820864-A 12 13-OCT-1998;  
BIO MERIEUX (FR)

COMMENT Other publication CA 2173957 960222  
Other publication AU 3169195 960307  
Other publication FR 2723589 960216.  
Location/Qualifiers

FEATURES  
source 1..21  
/organism="unknown"

BASE COUNT 9 a 5 c 4 g 3 t  
ORIGIN

Query Match 2.2%: Score 21; DB 9; Length 21;  
Best Local Similarity 100.0%: Pred. No. 9.6;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 766 cgaagagacatgaacaactt 786

Db 1 CGAAGAGACCATGAACAACCTT 21

|           |                                                                      |   |
|-----------|----------------------------------------------------------------------|---|
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;    | * |
| AUTHORS   | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.            | * |
| TITLE     | 1 (bases 1 to 72056)                                                 | * |
| REFERENCE | Bairren,B., Linton,L., Nusbaum,C. and Lander,E.                      | * |
| AUTHORS   | Homo sapiens, clone 12_B.11                                          | * |
| REFERENCE | Unpublished                                                          | * |
| AUTHORS   | 2 (bases 1 to 72056)                                                 | * |
| REFERENCE | Bairren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M., | * |
| AUTHORS   | Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Boukhalter,B.,    | * |
| REFERENCE | Brown,A., Castle,A., Colangelo,M., Collins,S., Collamore,A.,         | * |
| AUTHORS   | Cooke,P., Dearellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,  | * |
| REFERENCE | Ferreira,P., Fitzhugh,W., Forrest,C., Funke,R., Gage,D.,             | * |
| AUTHORS   | Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heatford,A., Horton,L.,  | * |
| REFERENCE | Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,   | * |
| AUTHORS   | Lehoczky,J., Lien,C., Locke,K., MacDonald,P., Marquis,N.,            | * |
| REFERENCE | McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrum,J.,        | * |
| AUTHORS   | Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,        | * |
| REFERENCE | Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,     | * |
| AUTHORS   | Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,        | * |
| REFERENCE | Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,      | * |
| AUTHORS   | Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.                             | * |
| TITLE     | Direct Submission                                                    | * |
| JOURNAL   | Submitted (01-OCF-1999) Whitehead Institute/MIT Center for Genome    | * |
| COMMENT   | Research, 320 Charles Street, Cambridge, MA 02141, USA               | * |
|           | All repeats were identified using RepeatMasker: Smit, A.F.A. &       | * |
|           | Green, P. (1996-1997)                                                | * |
|           | http://ftp.genome.washington.edu/RM/RepeatMasker.html.               | * |
|           | * NOTE: This record contains 80 individual                           | * |
|           | * sequencing reads that have not been assembled into                 | * |
|           | * contigs. Runs of N are used to separate the reads                  | * |
|           | * and the order in which they appear is completely                   | * |
|           | * arbitrary. Low-pass sequence sampling is useful for                | * |
|           | * identifying clones that may be gene-rich and allows                | * |
|           | * overlap relationships among clones to be deduced.                  | * |
|           | * However, it should not be assumed that this clone                  | * |
|           | * will be sequenced to completion. In the event that                 | * |
|           | * the record is updated, the accession number will                   | * |
|           | * be preserved.                                                      | * |
|           | 1                                                                    | * |
|           | 898: contig of 898 bp in length                                      | * |
|           | gap of unknown length                                                | * |
|           | 899                                                                  | * |
|           | 1785: contig of 887 bp in length                                     | * |
|           | gap of unknown length                                                | * |
|           | 1786                                                                 | * |
|           | 2678: contig of 893 bp in length                                     | * |
|           | gap of unknown length                                                | * |
|           | 2679                                                                 | * |
|           | 3566: contig of 888 bp in length                                     | * |
|           | gap of unknown length                                                | * |
|           | 3567                                                                 | * |
|           | 4474: contig of 908 bp in length                                     | * |
|           | gap of unknown length                                                | * |
|           | 4475                                                                 | * |
|           | 5394: contig of 920 bp in length                                     | * |
|           | gap of unknown length                                                | * |
|           | 5395                                                                 | * |
|           | 6335: contig of 941 bp in length                                     | * |
|           | gap of unknown length                                                | * |
|           | 6336                                                                 | * |
|           | 7293: contig of 958 bp in length                                     | * |
|           | gap of unknown length                                                | * |
|           | 7294                                                                 | * |
|           | 8172: contig of 878 bp in length                                     | * |
|           | gap of unknown length                                                | * |
|           | 8173                                                                 | * |
|           | 9058: contig of 886 bp in length                                     | * |
|           | gap of unknown length                                                | * |
|           | 9059                                                                 | * |
|           | 9962: contig of 904 bp in length                                     | * |
|           | gap of unknown length                                                | * |
|           | 9963                                                                 | * |
|           | 10708: contig of 746 bp in length                                    | * |
|           | gap of unknown length                                                | * |
|           | 10709                                                                | * |
|           | 11617: contig of 909 bp in length                                    | * |
|           | gap of unknown length                                                | * |
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|           | 12521: contig of 904 bp in length                                    | * |
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|           | 16096: contig of 876 bp in length                                    | * |
|           | gap of unknown length                                                | * |
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|           | 17964: contig of 926 bp in length                                    | * |
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|           | 20736: contig of 894 bp in length                                    | * |
|           | gap of unknown length                                                | * |
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|           | 21598: contig of 862 bp in length                                    | * |
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|           | 23395: contig of 887 bp in length                                    | * |
|           | gap of unknown length                                                | * |
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|           | 24301: contig of 906 bp in length                                    | * |
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|           | 25201: contig of 900 bp in length                                    | * |
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|           | 26120: contig of 919 bp in length                                    | * |
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|           | gap of unknown length                                                | * |
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|           | 29667: contig of 911 bp in length                                    | * |
|           | gap of unknown length                                                | * |
|           | 29668                                                                | * |
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|           | gap of unknown length                                                | * |
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|           | 31490                                                                | * |
|           | 32445: contig of 956 bp in length                                    | * |
|           | gap of unknown length                                                | * |
|           | 32446                                                                | * |
|           | 33362: contig of 917 bp in length                                    | * |
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|           | 34289                                                                | * |
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|           | 35196                                                                | * |
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|           | gap of unknown length                                                | * |
|           | 36091                                                                | * |
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|           | gap of unknown length                                                | * |
|           | 36977                                                                | * |
|           | 37702: contig of 726 bp in length                                    | * |
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|           | 37703                                                                | * |
|           | 38398: contig of 636 bp in length                                    | * |
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|           | 39314: contig of 916 bp in length                                    | * |
|           | gap of unknown length                                                | * |
|           | 39315                                                                | * |
|           | 40226: contig of 912 bp in length                                    | * |
|           | gap of unknown length                                                | * |
|           | 40227                                                                | * |
|           | 41133: contig of 907 bp in length                                    | * |
|           | gap of unknown length                                                | * |
|           | 41134                                                                | * |
|           | 42015: contig of 882 bp in length                                    | * |
|           | gap of unknown length                                                | * |
|           | 42016                                                                | * |
|           | 42879: contig of 864 bp in length                                    | * |
|           | gap of unknown length                                                | * |
|           | 42880                                                                | * |
|           | 43787: contig of 908 bp in length                                    | * |
|           | gap of unknown length                                                | * |
|           | 43788                                                                | * |
|           | 44732: contig of 945 bp in length                                    | * |
|           | gap of unknown length                                                | * |
|           | 44733                                                                | * |
|           | 45645: contig of 913 bp in length                                    | * |
|           | gap of unknown length                                                | * |
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|           | 46606: contig of 961 bp in length                                    | * |
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|           | 46607                                                                | * |
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|           | gap of unknown length                                                | * |
|           | 47528                                                                | * |
|           | 48457: contig of 930 bp in length                                    | * |
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* 50301 51179: contig of 879 bp in length
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* 51180 52130: contig of 951 bp in length
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* 52131 53074: contig of 944 bp in length
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* 53075 54010: contig of 936 bp in length
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* 54011 54906: contig of 896 bp in length
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* 54907 55797: contig of 891 bp in length
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* 56688 57579: contig of 892 bp in length
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* 58444 59345: contig of 902 bp in length
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* 59346 60251: contig of 906 bp in length
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* 60252 61197: contig of 946 bp in length
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* 61198 62066: contig of 869 bp in length
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* 62067 62960: contig of 894 bp in length
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* 62961 63871: contig of 911 bp in length
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* 63872 64769: contig of 898 bp in length
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* 64770 65714: contig of 945 bp in length
*      gap of unknown length
* 65715 66596: contig of 882 bp in length
*      gap of unknown length
* 66597 67499: contig of 903 bp in length
*      gap of unknown length
* 67500 68408: contig of 909 bp in length
*      gap of unknown length
* 68409 69331: contig of 923 bp in length
*      gap of unknown length
* 69332 70264: contig of 933 bp in length

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Query Match 2.0%; Score 20; DB 62; Length 72056;  
 Best local similarity 100.0%; Pred. No. 10;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 538 aaacacacagagagaagaaa 557  
 |||||  
 Db 39898 AACCAACAGAGACAGAAA 39917

RESULT 12  
 AC011438/C AC011438 91470 bp DNA PLN 11-OCT-2000  
 DEFINITION Genomic sequence for Arabidopsis thaliana BAC T23G18 from  
 chromosome I, complete sequence.  
 AC011438 AC011438 GI:6289106  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

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 Arabidopsis thaliana  
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 Magnoliophyta: eudicotyledons, core eudicots, Rosidae, eurosids II;  
 Brassicales: Brassicaceae: Arabidopsis.  
 1 (bases 1 to 91470)  
 Shin,P., Brooks,S., Buehler,E., Chao,Q., Johnson-Hopson,C.,  
 Khan,S., Kim,C., Altafi,H., Bel,Q., Chin,C., Chlou,J., Choi,E.,  
 Khan,S., Kim,C., Altafi,H., Bel,Q., Chin,C., Chlou,J., Choi,E.,

Comm,L., Conway,A., Gonzales,A., Hansen,N., Howing,B., Koo,T.,  
 Lam,B., Lee,J., Lenz,C., Li,J., Liu,A., Liu,K., Liu,S.,  
 Mukharisky,N., Nguyen,M., Palm,C., Pham,P., Sakano,H., Schwartz,J.,  
 Southwick,A., Thaveri,A., Toriumi,M., Vaysberg,M., Yu,G.,  
 Federspiel,N.A., Theologis,A. and Ecker,J.R.  
 Genomic sequence for Arabidopsis thaliana BAC T23G18 from  
 chromosome I  
 Unpublished

TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL

2<(bases 1 to 91470)  
 Ecker,J.R.  
 Direct Submission  
 Submitted (07-OCT-1999) Arabidopsis thaliana Genome Center,  
 Department of Biology, University of Pennsylvania, 38th Street and  
 Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA  
 3 (bases 1 to 91470)  
 Ecker,J.R.  
 Direct Submission  
 Submitted (09-NOV-1999) Arabidopsis thaliana Genome Center,  
 Department of Biology, University of Pennsylvania, 38th Street and  
 Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA  
 4 (bases 1 to 91470)

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL

Chao,Q., Brooks,S., Buehler,E., Johnson-Hopson,C., Khan,S., Kim,C.,  
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 Conway,A., Gonzalez,A., Hansen,N., Howing,B., Koo,T., Lam,B.,  
 Lee,J., Lenz,C., Li,J., Liu,A., Liu,J., Liu,S., Mukharisky,N.,  
 Nguyen,M., Palm,C., Pham,P., Sakano,H., Schwartz,J., Southwick,A.,  
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 Federspiel,N., Theologis,A. and Ecker,J.  
 Direct Submission  
 Submitted (15-DEC-1999) Arabidopsis thaliana Genome Center,  
 Department of Biology, University of Pennsylvania, 38th and  
 Hamilton Walk, Philadelphia, PA 19104-6018, USA  
 5 (bases 1 to 91470)

TITLE  
 JOURNAL

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 JOURNAL

Chen,K., Brooks,S., Buehler,E., Chao,Q., Johnson-Hopson,C.,  
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 Direct Submission  
 Submitted (28-JUN-2000) Arabidopsis thaliana Genome Center,  
 Department of Biology, University of Pennsylvania, 38th and  
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 6 (bases 1 to 91470)

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL

Chao,Q., Brooks,S., Buehler,E., Johnson-Hopson,C., Khan,S., Kim,C.,  
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 Direct Submission  
 Submitted (11-OCT-2000) Arabidopsis thaliana Genome Center,  
 Department of Biology, University of Pennsylvania, 38th and  
 Hamilton Walk, Philadelphia, PA 19104-6018, USA  
 On Nov 9, 1999, this sequence version replaced gi:6139057.  
 Location/Qualifiers

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complement(20859, 21590)

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| DB 42747 CTTCTGCGCGCTGCTCATCC 42728                         |                       |                                      |
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| RESULT 13                                                   |                       |                                      |
| AL157771                                                    |                       |                                      |
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| DEFINITION                                                  |                       |                                      |
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| KEYWORDS                                                    |                       |                                      |
| SOURCE                                                      |                       |                                      |
| ORGANISM                                                    |                       |                                      |
| REFERENCE                                                   |                       |                                      |
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corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL, Sw: SWISSPROT, Tr: TREMBL, Wp: WORMPEP; Information on the WORMPEP database can be found at <http://www.sanger.ac.uk/Projects/C.elegans/wormpep> This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr13> RP11-67J18 is from the library RPc1-11.1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/Bacpac/home.htm> VECTOR: pBAC3.6

IMPORTANT: This sequence is not the entire insert of clone RP11-67J18. It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP11-67J18 is at 1 in this sequence. The true left end of clone RP11-141M24 is at 115144 in this sequence. The true right end of clone RP11-465C24 is at 93228 in this sequence.

## FEATURES

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DEFINITION sequence.
AC087859
VERSION AC087859.1 GI:12656789
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SOURCE human.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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1 (bases 1 to 153259)
Zhang,L., Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C.,
Chen,J., Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q.,
Gu,X., Guo,D., Guo,Z., He,L., Hu,S., Huang,F., Jin,Y., Kang,N.,
Li,C., Li,C., Li,F., Li,G., Li,J., Li,L., Li,S., Li,T., Liu,Y.,
Liu,N., Liu,B., Liu,Y., Li,W., Li,W., Li,Y., Luo,C., Luo,J.,
Niu,Y., Qi,Q., Qi,X., Song,L., Song,S., Sun,M., Sun,W., Sun,Y.,
Tan,X., Tao,R., Wang,H., Wang,J., Wang,J., Wang,J., Wang,L.,
Wang,L., Wang,R., Wang,X., Wang,X., Wang,Y., Wu,D., Wu,Q., Xie,F.,
Xuan,Z., Xue,Y., Yan,C., Yang,X., Yu,B., Zeng,Y., Zhang,G.,
Zhang,H., Zhang,H., Zhang,M., Zhang,X., Zhang,Y., Zhang,Y.,
Zhang,Y., Zhang,Z., Zhu,B., Zhu,N., Yu,J. and Yang,H.
Chromosome 3p genomic sequence
Unpublished
TITLE
JOURNAL
REFERENCE 2 (bases 1 to 153259)
AUTHORS Chen,L., Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C.,
Zhang,L., Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q.,
Gu,X., Guo,D., Guo,Z., He,L., Hu,S., Huang,F., Jin,Y., Kang,N.,

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Li,C., Li,C., Li,F., Li,G., Li,J., Li,L., Li,S., Li,T., Liu,Y.,
Liu,N., Liu,B., Liu,Y., Li,W., Li,W., Li,Y., Luo,C., Luo,J.,
Niu,Y., Qi,Q., Qi,X., Song,L., Song,S., Sun,M., Sun,W., Sun,Y.,
Tan,X., Tao,R., Wang,H., Wang,J., Wang,J., Wang,J., Wang,L.,
Wang,L., Wang,R., Wang,X., Wang,X., Wang,Y., Wu,D., Wu,Q., Xie,F.,
Xuan,Z., Xue,Y., Yan,C., Yang,X., Yang,X., Yu,B., Zeng,Y., Zhang,G.,
Zhang,H., Zhang,H., Zhang,M., Zhang,X., Zhang,X., Zhang,Y.,
Zhang,Y., Zhang,Z., Zhu,B., Zhu,N., Yu,J. and Yang,H.
Direct Submission
Submitted (02-FEB-2001) Human Genomic Center, Institute of
Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
100101, P.R.China
-----Genome Center
Center:Beijing Center
Center code:Beijing
Website:http://hg.igtp.ac.cn
http://www.genomics.org.cn
Contact:hgct@igtp.ac.cn
----- Project Information
Center project name:1% project
Center clone name: RP11-34L16
----- Summary Statistics
Sequencing vector: pUC18; 100% of reads
Chemistry: Dye-terminator; ET 55% of reads
Chemistry: Dye-terminator Big Dye; 45% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 952 bases at least Q40
Consensus quality: 1082 bases at least Q30
Insert size: 1160; sum-of-contigs
Quality coverage: 1.59x in Q20 bases;sum-of-contigs
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Location/Qualifiers
1..153259
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"
/map="3p"
/clone="RP11-34L16"
BASE COUNT 41764 a 33139 c 34151 g 44205 t
ORIGIN

```

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FEATURES
source
1..153259
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"
/map="3p"
/clone="RP11-34L16"
BASE COUNT 41764 a 33139 c 34151 g 44205 t
ORIGIN
Query Match 2.0% Score 20: DB 88: Length 153259;
Best Local Similarity 100.0%; Pred. NO. 9.3;
Matches 20: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 813 gacagagctgcagcagacc 832
|||||
Db 3666 GACAGAGCTGCAGCAGACC 3647

```

```

RESULT 15
AC018355/c 155075 bp DNA HTG 07-SEP-2000
LOCUS Homo sapiens chromosome 3 clone RP11-34L16, WORKING DRAFT SEQUENCE,
DEFINITION 12 unordered pieces.
AC018355
VERSION AC018355.14 GI:9966753
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 155075)
Muzny,D.M., Adams,C., Bailey,M., Barbarta,J., Blankenburg,K.,
Booth,B., Bouck,J., Bowie,S., Brooks,A., Buhay,C., Bunc,C.,
Burkett,C., Burrows,J., Carter,M., Chacko,J., Chen,Z., Cox,C.,
David,R., Delgado,O., Deshazo,D., Ding,Y., Donah-Rashid,N.,
Dugan-Rocha,S., Durbin,K.J., Fernandez,C., Ferraguto,D.,
Forcum-Tansey,J., Frantz,P., Ganesha,R., Gorrell,J.H., Gorrell,L.L.,
Guevara,W., Harris,K., Hernandez,J., Hodgson,A., Hughes,M.,
Holloway,C., Hosak,H., Jackson,L.E., Jackson,L., Jia,Y., Jones,M.,

```

Kelly, S., Kondejewski, N., Kong, Y., Kovar, C., Leal, B., Li, Z., Licharge, O., Liu, J., Liu, W., Logan, O., Lozano, R.J., Lu, J., Luchter, R., Martin, R., Martinez, C., McLeod, M.P., Mei, G., Morgan, M., Morris, S., Nash, S., Nelson, A., Nguyen, R., Nguyen, N., Nguyen, S., Oswal, G., Parish, B., Paxton, S., Payton, B., Perez, L., Pu, L.L., Quiles, M., Reiter, D., Rives, M., Samuel, S., Say, J., Scherer, S., Shah, E., Shen, H., Simon, M., Sparks, A., Stamps, A., Suqanq, R., Taber, P., Taylor, T., Vasquez, L., Vinsion, R., Vo, O., Wahab, M., Watlington, S., Weinstein, G., Weinstein, I.R., Williamson, A., Worley, K., Wren, J., Wrenford, G., Yu, W., Zhou, X., Nelson, D. and Gibbs, R.

Direct Submission  
Unpublished  
2 (bases 1 to 155075)  
Worley, K.C.

Direct Submission  
Submitted (10-DEC-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
On Sep 5, 2000 this sequence version replaced gi:8493479.

----- Genome Center -----  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information -----  
Center project name: HMYJ  
Center clone name: RP11-3416  
----- Summary Statistics -----  
Sequencing vector: M13; L08821  
Assembly program: Phrap; version 0.990329  
Consensus quality: 13865 bases at least Q40  
Consensus quality: 147372 bases at least Q30  
Consensus quality: 149805 bases at least Q20  
Estimated insert size: 150288; sum-of-coverage estimation  
Estimated insert size: 151640; agarose-fp estimation  
Quality coverage: 4.3x in Q20 bases; agarose-fp estimation  
Quality coverage: 4.6x in Q20 bases; sum-of-coverage estimation  
-----  
\* NOTE: Estimated insert size may differ from sequence length  
\* (see <http://www.hgsc.bcm.tmc.edu/docs/genbank-draft-data.html>).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 12 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
\*  
\* 1 48839: contig of 48839 bp in length  
\* 48840 48939: gap of unknown length  
\* 48940 81367: contig of 32428 bp in length  
\* 81368 81467: gap of unknown length  
\* 81468 93764: contig of 12297 bp in length  
\* 93765 93864: gap of unknown length  
\* 93865 107706: contig of 13842 bp in length  
\* 107707 107806: gap of unknown length  
\* 107807 120074: contig of 12268 bp in length  
\* 120075 130823: contig of 10649 bp in length  
\* 130824 130923: gap of unknown length  
\* 130924 137196: contig of 6273 bp in length  
\* 137197 137296: gap of unknown length  
\* 137297 143104: contig of 5808 bp in length  
\* 143105 143204: gap of unknown length  
\* 143205 146435: contig of 3231 bp in length  
\* 146436 146535: gap of unknown length  
\* 146536 149751: contig of 3116 bp in length  
\* 149752 153787: contig of 4036 bp in length  
\* 153788 153887: gap of unknown length  
\* 153888 155075: contig of 1188 bp in length.

FEATURES  
source 1. 155075 Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="3"  
/clone="RP11-3416"

BASE COUNT 42142 a 33789 c 3367 g 44018 t 1159 others  
ORIGIN

Query Match: 2.0%; Score 20; DB 65; Length 155075;  
Best Local Similarity 100.0%; Pred. No. 9.3;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 813 gacagagctcagcagagcc 832  
|||||  
Db 134584 GACAGAGCTCAGCAGAGCC 134565

RESULT 16  
AC034187/c 171714 bp DNA PRI 09-OCT-2000  
LOCUS Homo sapiens chromosome 3 clone RP11-202A21 map 3p, complete  
DEFINITION sequence.  
ACCESSION AC034187  
VERSION AC034187.4 GI:10719838  
KEYWORDS HTG.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 171714)  
Zhang, L., Bao, J., Bao, Q., Bao, W., Bian, X., Cao, T., Chen, C., Chen, J., Ding, H., Dong, W., Fan, H., Feng, X., Gong, J., Guan, Q., Gu, X., Guo, D., He, L., Hu, S., Huang, F., Jin, Y., Kang, N., Li, C., Li, C., Li, G., Li, J., Li, L., Li, S., Li, T., Liu, Y., Liu, N., Liu, B., Liu, Y., Li, W., Li, W., Li, Y., Luo, J., Niu, Y., Qi, Q., Qi, X., Song, L., Song, S., Sun, M., Sun, W., Sun, Y., Tan, X., Tao, R., Wang, H., Wang, J., Wang, J., Wang, L., Wang, L., Wang, R., Wang, X., Wang, X., Wang, Y., Wu, D., Wu, Q., Xie, F., Xuan, Z., Xue, Y., Yan, C., Yang, X., Yu, B., Zeng, Y., Zhang, G., Zhang, H., Zhang, H., Zhang, L., Zhang, M., Zhang, X., Zhang, X., Zhang, Y., Zhang, Y., Zhang, Z., Zhu, B., Zhu, N., Yu, J. and Yang, H.  
Chromosome 3p genomic sequence  
Unpublished

JOURNAL 2 (bases 1 to 171714)  
Li, G., Hu, S., Dong, W., Wang, J., Zhang, Y., Zhang, H., Liu, B., Bao, W., Sun, Y., Wu, Q., Wang, H., Yang, X., Cheng, C., Wang, Y., Niu, Y., Qi, X., Li, T., Zhang, H., Liu, N., Wu, D., Yu, B., Fan, H., Liu, Y., Li, G., Li, C., Bao, Q., Bao, J., Wang, X., Song, L., Zhang, L., Guo, D., Huang, F., Zhang, G., Li, J., Bian, X., Zhang, M., Li, L., Feng, X., Yu, J. and Yang, H.  
Direct Submission  
Submitted (05-APR-2000) Human Genomic Center, Institute of Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing 100101, P.R.China

JOURNAL 3 (bases 1 to 171714)  
Zhang, L., Bao, J., Bao, Q., Bao, W., Bian, X., Cao, T., Chen, C., Chen, J., Ding, H., Dong, W., Fan, H., Feng, X., Gong, J., Guan, Q., Gu, X., Guo, D., He, L., Hu, S., Huang, F., Jin, Y., Kang, N., Li, C., Li, C., Li, G., Li, J., Li, L., Li, S., Li, T., Liu, Y., Liu, N., Liu, B., Liu, Y., Li, W., Li, W., Li, Y., Luo, J., Niu, Y., Qi, Q., Qi, X., Song, L., Song, S., Sun, M., Sun, W., Sun, Y., Tan, X., Tao, R., Wang, H., Wang, J., Wang, J., Wang, L., Wang, L., Wang, R., Wang, X., Wang, X., Wang, Y., Wu, D., Wu, Q., Xie, F., Xuan, Z., Xue, Y., Yan, C., Yang, X., Yu, B., Zeng, Y., Zhang, G., Zhang, H., Zhang, H., Zhang, L., Zhang, M., Zhang, X., Zhang, X., Zhang, Y., Zhang, Y., Zhang, Z., Zhu, B., Zhu, N., Yu, J. and Yang, H.  
Direct Submission  
Submitted (09-OCT-2000) Human Genomic Center, Institute of Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing 100101, P.R.China  
On Oct 9, 2000 this sequence version replaced gi:9858933.

-----Genome Center  
Center:Beijing Center  
Center code:Beijing  
Website:http://hgc.igtp.ac.cn  
http://www.genomics.org.cn  
Contact:hgc@igtp.ac.cn  
----- Project Information  
Center project name:1% project  
Center clone name: RP11-202A21  
----- Summary Statistics  
Sequencing vector: pUC18; 100% of reads  
Chemistry: Dye-terminator; ET 55% of reads  
Chemistry: Dye-terminator Big Dye; 45% of reads  
Assembly program: Phrap; version: 0.990329  
Consensus quality: 832 bases at least Q40  
Consensus quality: 1233 bases at least Q30  
Consensus quality: 1299 bases at least Q20  
Insert size: 1280; sum-of-contigs  
Quality coverage: 1.10x in Q20 bases;sum-of-contigs  
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FEATURES  
source  
1. 171714  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="3"  
/map="3p"  
/clone="RP11-202A21"

BASE COUNT 44183 a 38235 c 40748 g 48547 t 1 others  
ORIGIN

Query Match 2.0%; Score 20; DB 88; Length 171714;  
Best Local Similarity 100.0%; Prid. NO. 9.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 813 gacagagctgcagcagacc 832  
|||||  
Db 136257 GACGAGCTGCAGCAGACC 136238

RESULT 17  
AC017643 177816 bp DNA HTG 10-DEC-1999  
LOCUS Drosophila melanogaster, \*\*\* SEQUENCING IN PROGRESS \*\*\*, in ordered  
DEFINITION pieces.  
AC017643  
AC017643.1 GI:6554354  
VERSION HTG; HTGS\_PHASE2.  
KEYWORDS fruit fly  
SOURCE Drosophila melanogaster  
ORGANISM Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
1 (bases 1 to 177816)  
Adams, M. and Venter, J.C.  
REFERENCE  
AUTHORS  
TITLE Direct Submission  
JOURNAL Submitted (10-DEC-1999) Celera Genomics, 45 West Gude Drive,  
Rockville, MD, USA  
COMMENT  
This sequence was identified as CDM:10211585 by the submitter.  
For more information on this record e-mail to fly@celera.com.  
\* NOTE: This is a 'working draft' sequence.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.  
Location/Qualifiers  
1. 177816  
/organism="Drosophila melanogaster"  
/db\_xref="taxon:7227"  
/chromosome="3"

FEATURES  
source  
1. 177816  
/organism="Drosophila melanogaster"  
/db\_xref="taxon:7227"  
/chromosome="3"

BASE COUNT 50527 a 38300 c 39085 g 49904 t  
ORIGIN  
Query Match 2.0%; Score 20; DB 65; Length 177816;

Best Local Similarity 100.0%; Prid. NO. 9.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 50 ggcctcgtgcacatgctg 69  
|||||  
Db 164707 GCGCTCTGGCTGACATGTCG 164726

RESULT 18  
AL512648 182365 bp DNA HTG 08-APR-2001  
LOCUS Homo sapiens chromosome 13 clone RP11-465C24, \*\*\* SEQUENCING IN  
DEFINITION PROGRESS \*\*\*, 7 unordered pieces.  
AL512648  
AL512648.6 GI:13568246  
VERSION HTG; HTGS\_PHASE1; HTGS\_ACTIVEFIN; HTGS\_DRAFT; HTGS\_FULLTOP.  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 182365)  
Submitted (08-APR-2001) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk  
On April 9, 2001 this sequence version replaced gi.13396721.  
----- Genome Center  
Center: Sanger Centre  
Center code: SC  
Web site: http://www.sanger.ac.uk  
Contact: humquery@sanger.ac.uk  
----- Project Information  
Center project name: ba465C24  
----- Summary Statistics  
Assembly program: XGAP4; version 4.5  
Sequencing vector: plasmid; L08752; 100% of reads  
Chemistry: Dye-terminator Big Dye; 98% of reads  
Chemistry: Dye-terminator Big Dye; 0% of reads  
Consensus quality: 180306 bases at least Q40  
Consensus quality: 181081 bases at least Q30  
Consensus quality: 181448 bases at least Q20  
Insert size: 181765; sum-of-contigs  
Insert size: 165725; 8.2% error; agarose-fp  
Quality coverage: 9.90x in Q20 bases; sum-of-contigs Quality  
coverage: 11.02x in Q20 bases; agarose-fp  
-----

COMMENT  
REFERENCE  
AUTHORS  
TITLE Direct Submission  
JOURNAL Submitted (08-APR-2001) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk  
On April 9, 2001 this sequence version replaced gi.13396721.  
----- Genome Center  
Center: Sanger Centre  
Center code: SC  
Web site: http://www.sanger.ac.uk  
Contact: humquery@sanger.ac.uk  
----- Project Information  
Center project name: ba465C24  
----- Summary Statistics  
Assembly program: XGAP4; version 4.5  
Sequencing vector: plasmid; L08752; 100% of reads  
Chemistry: Dye-terminator Big Dye; 98% of reads  
Chemistry: Dye-terminator Big Dye; 0% of reads  
Consensus quality: 180306 bases at least Q40  
Consensus quality: 181081 bases at least Q30  
Consensus quality: 181448 bases at least Q20  
Insert size: 181765; sum-of-contigs  
Insert size: 165725; 8.2% error; agarose-fp  
Quality coverage: 9.90x in Q20 bases; sum-of-contigs Quality  
coverage: 11.02x in Q20 bases; agarose-fp  
-----

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 7 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
1 10549: contig of 10549 bp in length  
10550 10649: gap of 100 bp  
10650 30196: contig of 19547 bp in length  
30197 30296: gap of 100 bp  
30297 32343: contig of 2047 bp in length  
32344 32443: gap of 100 bp  
32444 32443: gap of 100 bp  
32444 35679: contig of 3236 bp in length  
35680 35779: gap of 100 bp  
35780 53912: contig of 18133 bp in length  
53913 54012: gap of 100 bp  
54013 79432: contig of 25420 bp in length  
79433 79532: gap of 100 bp  
79533 182365: contig of 102833 bp in length.  
Location/Qualifiers  
1. 182365  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="13"

FEATURES  
source  
1. 182365  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="13"



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misc_feature      /clone="RP11-465C24"
                  /clone_lib="RP11-11.2"
                  1..10549
                  /note="assembly_fragment:04706
                  fragment_chain:1"
                  10650..30196
                  /note="assembly_fragment:04716
                  fragment_chain:1"
                  30297..32343
                  /note="assembly_fragment:04843"
                  32444..35679
                  /note="assembly_fragment:04853"
                  35780..53912
                  /note="assembly_fragment:02763
                  fragment_chain:2"
                  54013..79432
                  /note="assembly_fragment:04938
                  fragment_chain:2"
                  79533..182365
                  /note="assembly_fragment:04959
                  fragment_chain:2
                  clone_end:77
                  vector_side:right"
BASE COUNT      53190 a 34137 c 35417 g 59008 t 613 others
ORIGIN
Query Match      2.0%; Score 20; DB 81; Length 182365;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 719 tcataccacacgctctcg 738
|||||
Db 165448 TCATACCAACACGCTCTCG 165467

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RESULT 19
LOCUS      AC007697
DEFINITION Drosophila melanogaster, chromosome 2R, region 54D4-54E7, BAC clone
ACCESSION AC007697
VERSION    AC007697.5 GI:13270541
KEYWORDS   HTG.
SOURCE     fruit fly.
ORGANISM   Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1 (bases 1 to 194897)
AUTHORS    Celiker,S.E., Adams,M.D., Krommiller,B., Tyler,D., Wan,K.H.,
            Holt,R.A., Evans,C.A., Gocayne,J.D., Amanatides,P.G., Brandon,R.C.,
            Rogers,J., An,H., Baldwin,D., Bonzon,J., Beeson,K.Y., Busam,D.A.,
            Carlson,J.W., Center,A., Champe,M., Davenport,L.B., Dietz,S.M.,
            Dodson,K., Dorsett,V., Doup,L.E., Doyle,C., Dresnek,D., Farfan,D.,
            Ferris,S., Frise,E., Galle,R.F., Garg,N.S., George,R.A.,
            Gonzalez,M., Houch,J., Hoskins,R.A., Hostin,D., Howland,T.J.,
            Ibegwam,C., Jalali,M., Kruse,D., Li,P., Mattei,B., Moshrefi,A.,
            McIntosh,T.C., Moy,M., Murphy,B., Nelson,C., Nelson,K.A., Nunoo,J.,
            Pacleb,J., Paragas,V., Park,S., Patel,S., Pfeiffer,B.,
            Phouanavong,S., Piltman,G.S., Puri,V., Richards,S., Scheeler,F.,
            Stapleton,M., Strong,R., Svirskaas,R., Tector,C., Williams,S.M.,
            Zaveri,J.S., Smith,H.O., Rubin,G.M. and Venter,J.C.
            Sequencing of Drosophila chromosome 2R, region 54D4-54E7
TITLE      2 (bases 1 to 194897)
JOURNAL    Unpublished
REFERENCE   2 (bases 1 to 194897)
AUTHORS    Celiker,S.E., Agapayni,A., Arcaina,T.T., Baxter,E., Blazef,R.G.,
            Butenhoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L.,
            Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L.,
            Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karris,K., Kearney,L.,
            Kim,E., Lee,B., Lewis,S., Li,P., Lomocan,M.A., Mazda,P.,
            Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S.,
            Pfeiffer,B., Poon,L., Sequeira,A., Sethi,H., Snir,E.,

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TITLE      Submitted Submission
JOURNAL    Submitted (02-JUN-1999) Drosophila Genome Center, Lawrence Berkeley
            Laboratory, MS 64-121, Berkeley, CA 94720, USA
COMMENT    On Mar 10, 2001 this sequence version replaced g1:5670564.
            Sequence submitted by:
            Berkeley Drosophila Genome Project
            Lawrence Berkeley National Laboratory, MS 64-121
            Berkeley, CA 94720
            This sequence was assembled using end sequences from a whole genome
            shotgun and from subclones of this BAC and its neighboring clones.
            For further information about this sequence, including its location
            and relationship to other sequences, please visit our sequence
            archive Web site (http://www.fruitfly.org/sequence/) or send email
            to bdg@fruitfly.berkeley.edu.
            Location/Qualifiers:
            1..194897
               /organism="Drosophila melanogaster"
               /strain="y: cn bw sp"
               /db_xref="taxon:7227"
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               Drosophila melanogaster BAC library, partial Ecom1 in
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 50 ggcgtcgtgctgacatgctg 69
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Db 128453 GCGTCCTGGCGACATGTCG 128472

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RESULT 20
LOCUS      AC022297/c
DEFINITION AC022297 203195 bp DNA HTG 10-NOV-2000
ACCESSION AC022297
VERSION    AC022297.9 GI:11128306
KEYWORDS   HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE     Mus musculus
            house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 203195)
REFERENCE   1 (bases 1 to 203195)
AUTHORS    Metzger,M.L., Lewis,L.R., Hume,J., Edwards,C., Harris,C.,
            Dederich,D., Thomas,S., Okwuonu,G., Carlock,C., Garner,T.,
            Addison,S., Pace,A., Williams,G., Bonnin,D., Brooks,A., Brown,J.,
            Buhray,C., Bunac,C., Burkett,C., Chacko,J., Chen,G., Chen,Z.,
            Cox,C., Davis,C., Delgado,O., Ding,Y., Dugan-Rocha,S.,
            Fernandez,C., Ferraguto,D., Fortum-Tansey,J., Gill,R.,
            Gorrell,J.H., Gunaratne,P., Haller,G., Hernandez,J., Hogues,M.,
            Hosak,H., Hou,X., Huber,J., Jackson,L., Jia,Y., Kelly,J., Kelly,S.,
            Kovar,C., Liu,J., Liu,W., Louised,H., Lozado,R.J., Martin,R.,
            Massay,E., McLeod,M.P., Mel,G., Moore,S., Morgan,M., Morris,S.,
            Neal,D., Nelson,A., Nguyen,R., Nguyen,N., Ogun,M., Parish,B.,
            Perez,L., Reiter,D., Say,J., Shen,H., Vasquez,L., Wallington,S.,
            Williamson,A., Wrensford,G., Zhou,X., Bouck,J., Hodgson,A.,
            Muzny,D.M., Rives,M., Scherer,S., Sodergren,E., Weinstock,G.,
            Morley,K. and Gibbs,R.
            Direct Submission
TITLE      2 (bases 1 to 203195)
JOURNAL    Unpublished
REFERENCE   2 (bases 1 to 203195)
AUTHORS    Morley,K.C.
TITLE      Direct Submission

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|           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |                           |
|-----------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------|
| ACCESSION | AE003802 AE002787                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | of 52, complete sequence. |
| VERSION   | AE003802.2 GI:10727480                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |                           |
| KEYWORDS  | HTG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |                           |
| SOURCE    | fruit fly.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                           |
| ORGANISM  | Drosophila melanogaster                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |                           |
| REFERENCE | Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |                           |
| AUTHORS   | 1 (bases 1 to 262395)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |                           |
|           | Adams,M.D., Celisner,S.E., Holt,R.A., Evans,C.A., Gocayne,J.D., Amaratunga,P.G., Scherer,S.E., Li,P.W., Hoskins,R.A., Galle,R.F., George,K.A., Lewis,S.E., Richards,S., Ashburner,M., Henderson,S.N., Sutton,G.G., Wortman,J.R., Yandell,M.D., Zhang,Q., Chen,L.X., Brandon,R.C., Rogers,Y.H., Blazer,J.R., Champe,M., Pfeiffer,B.D., Wan,K.H., Doyle,C., Baxter,E.G., Helt,G., Nelson,C.R., Gabor Milos,G.L., Abril,J.F., Agbayani,A., An,H.J., Andrews-Frankoch,C., Baldwin,D., Ballew,R.M., Basu,A., Benos,P.V., Berman,B.P., Bhandari,D., Bolshakov,S., Borkova,D., Botchan,M.R., Bouck,J., Brokstein,P., Brothier,P., Butts,K.C., Busam,D.A., Butler,H., Cadieu,E., Center,A., Chandra,I., Cherry,J.M., Cawley,S., Dahlke,C., Davenport,L.B., Davies,P., de Pablos,B., Delcher,A., Deng,Z., Mays,A.D., Dew,I., Dietz,S.M., Dodson,K., Doup,L.E., Downes,M., Dugan-Rocha,S., Dunkov,B.C., Dunn,P., Durbin,K.J., Evangelista,C.C., Ferraz,C., Ferrieres,S., Fleischmann,W., Foster,C., Gabrielian,A.E., Garg,N.S., Gelbart,W.M., Glasser,K., Glodek,A., Gong,F., Gorrell,J.H., Gu,Z., Guan,P., Harris,M., Harris,N.L., Harvey,D., Heiman,T.J., Hernandez,J.R., Houck,J., Hostin,D., Houston,K.A., Howland,T.J., Wel,M.H., Ibeagwam,C., Jaielli,M., Kalish,F., Karpen,G.H., Ke,Z., Kennison,J.A., Ketchum,K.A., Kimmel,B.E., Kodira,C.D., Kraft,C., Kravitz,S., Kulp,D., Lai,Z., Lasko,P., Lei,Y., Levitsky,A.A., Li,J., Li,Z., Liang,Y., Lin,X., Liu,X., Mattei,B., McIntosh,T.C., McCreel,M.P., McPherson,D., Merkulov,G., Milshina,N.V., Mobarry,C., Morris,J., Moshrefi,A., Mount,S.M., Moy,M., Murphy,B., Murphy,L., Muzny,D.M., Nelson,D.L., Nelson,D.R., Nelson,K.A., Nixon,K., Nusser,D.R., Pacled,J.M., Palazolo,M., Pltman,G.S., Pan,S., Pollard,J., Puri,V., Reese,M.G., Reinert,K., Remington,K., Sanders,R.D., Scheeler,F., Shen,H., Shue,B.C., Siden-Kiamos,I., Simpson,M., Skupski,M.P., Smith,T., Spier,E., Spreading,K.A.C., Stapleton,M., Strong,R., Sun,E., Svrtkas,R., Tector,C., Turner,R., Venter,E., Wang,A.H., Wang,X., Wang,Z.Y., Wasserman,D.A., Weinstein,G.M., Weissbach,J., Williams,S.M., Woodage,T., Worley,K.C., Wu,D., Yang,S., Yao,Q.A., Ye,J., Yeh,R.F., Zaveri,J.S., Zhang,M., Zhang,G., Zhao,Q., Zheng,L., Zheng,X.H., Zhong,F.N., Zhong,W., Zhou,X., Zhu,S., Zhu,X., Smith,H.O., Gibbs,R.A., Myers,E.W., Rubin,G.M., and Venter,J.C. |                           |
| TITLE     | The genome sequence of Drosophila melanogaster                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |                           |
| JOURNAL   | Science 287 (5461), 2185-2195 (2000)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                           |
| MEDLINE   | 20196006                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |                           |
| REFERENCE | 2 (bases 1 to 262395)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |                           |
| AUTHORS   | Adams,M.D., Celisner,S.E., Gibbs,R.A., Rubin,G.M. and Venter,C.J.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                           |
| TITLE     | Direct Submission                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                           |
| JOURNAL   | Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |                           |
| COMMENT   | On Oct 9, 2000 this sequence version replaced gi:7302706.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |                           |
| FEATURES  | Location/Qualifiers                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |                           |
| SOURCE    | 1. 262395                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |                           |
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| mrna      | <1. 27                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |                           |
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|           | <1. 27                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |                           |
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| gene      | <1. .>27                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |                           |

|      |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |                                |
|------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------|
| mrna | /gene="CG4878"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | /map="54C10-54C12"             |
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|      | join(<2926. 3204,3268. .3993,4054. .4292,4416. .>4506)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |                                |
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|      | /evidence=not_experimental                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |                                |
|      | join(<2926. 3204,3268. .3993,4054. .4292,4416. .4506)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                |
|      | /gene="CG18631"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |                                |
|      | /note="CG18631 gene product"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                |
|      | /codon_start=1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |                                |
|      | /db_xref="FLYBASE:FBan0018631"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |                                |
|      | /db_xref="FLYBASE:FBgn0034239"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |                                |
|      | /evidence=not_experimental                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |                                |
|      | protein_id="AAF57840.1"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |                                |
|      | /db_xref="GI:7302762"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                |
|      | /translation="MYSNVRPFTVLTSGQRLCRSRTAEGSNPTNNEOLOLOIQSGFCDLRDLKISLFDLIEQOYSDASDVQVQCNWMLGEFRVPIINSLASTFTGCTELAMPKVLGVKRRPLIDSVTNMPTDOYVEFEKAVHAWLYLSIEPGGLAPLHSCALCAEKPELOOYIDERLELQQLPQPORYVEPFAVCAQGRVCLTFLMPDVLPPAAVSGENPLEICIRVSLSHLSRSDPCQGRGWLWDSLLSDSWCSVKDGLVLCNVMISLGLKCMILICVYSCPHGSGSVLFRQPEPAELFLVDSPATGRYOLODVHCPRLRYCVVGGONITFNIOTETRVSTHNLQDQACWPFPRRRYAPQSGVCKLDYATKRSLELOLOKHIERKIKKISAMWTRKTIWNRGRITDPTSEQDERFPYRVSALAFRKK"                                                                                                                                                                                                                                                                                                                        |                                |
|      | join(<6206. 6413,6478. .6861,6918. .7090,7164. .>7308)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |                                |
|      | /gene="cyp33"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |                                |
|      | /note="Nucleotide sequence of the Celera sequence differs from the published sequence for this transcript."                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |                                |

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gene
  /product="CT15697"
  /db_xref="FLYBASE:FBgn0004886"
  /db_xref="FLYBASE:FBgn0028382"
  <6206..>7308
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  /note="CG4886"
  /map="54C11-54D1"
  /db_xref="FLYBASE:FBgn0004886"
  /db_xref="FLYBASE:FBgn0028382"
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  /gene="cyp33"
  /note="cyp33 gene product; Nucleotide sequence of the
  Celera sequence differs from the published sequence for
  this transcript"
  /codon_start=1
  /db_xref="FLYBASE:FBgn0004886"
  /db_xref="FLYBASE:FBgn0028382"
  /protein_id="AAF57839.1"
  /db_xref="GI:7302761"
  /translation="MSNDRRTIYVGLADEVTERLNNAPFPGDIADIOMPADYESO
  RHRGAFIEEESSEDAADIDNNSELCGRTRVNLAKPVKEDSFPIAADDMVL
  ORHAGATLOPEGEPEAEKVEYPTSTGPATVEKAEKRPQVFEDIRIGNDAGRIVMLLR
  AVVPTAEFRQLCTHEQGYGKGSFHRVLPFCGGDFTNNNGTSGKSLDGLFE
  NDENFLKHNSEGLTSMANGSANTNGSQFICTTKTDMDLNKHVFGHVISGAEVVRK
  MERCGSKGTPSQKIVIVSGELK"
  complement(join(7324..7910,8333..8405))
  /gene="RPL18A"
  /note="Nucleotide sequence of the Celera sequence differs
  from the published sequence for this transcript."
  /product="CT20271"
  /db_xref="FLYBASE:FBgn0006510"
  /db_xref="FLYBASE:FBgn0010409"
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  /note="CG6510"
  /map="54C11-54D1"
  /db_xref="FLYBASE:FBgn0006510"
  /db_xref="FLYBASE:FBgn0010409"
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  /gene="RPL18A"
  /note="RPL18A gene product; Nucleotide sequence of the
  Celera sequence differs from the published sequence for
  this transcript"
  /codon_start=1
  /db_xref="FLYBASE:FBgn0006510"
  /db_xref="FLYBASE:FBgn0010409"
  /protein_id="AAF57838.1"
  /db_xref="GI:7302760"
  /translation="MRAGKILKEVEYVGRKLPESEKPEQTPLYKMRIFAPDNIYAKSRF
  WFLRLTKKFKTGTGEIVSIKOYERSPKIKFGLWLDSDSGTHNNHREYRLTV
  GGAVTQCYRDMGARHRAHSHIOIIVDSIPAKTRRVHVKPHDSKIKFPLVQRVHH
  KGRKLFSEFRKPRFTFQ"

CDS
  Query Match      2.0%; Score 20; DB 5; Length 262395;
  Best Local Similarity 100.0%; Pred. No. 8.6;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 ggcctcgtgcacatcgtcg 69
  |||
  Db 140906 GCGTCTGGCTGACATGTCG 140925

RESULT 23
D89210/c  D89210      1152 bp      mRNA      PLN      13-MAR-1998
LOCUS     Schizosaccharomyces pombe mRNA, partial cds, clone: SY 1164.
ACCESSION D89210
VERSION   D89210.1 GI:1749627
KEYWORDS
SOURCE    Schizosaccharomyces pombe (strain:PR745) cDNA to mRNA,
           clone_11b:library of H. Nojima clone:SY1164.
ORGANISM  Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

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REFERENCE
AUTHORS   Schizosaccharomycetales; Schizosaccharomycetales;
           Schizosaccharomycetes.
TITLE     1 (bases 1 to 1152)
JOURNAL   Yoshioaka,S.
          Direct Submission
          Submitted (15-NOV-1996) to the DDBJ/EMBL/GenBank databases. Sachio
          Yoshioaka, Tsukita Cell Axis Project ERATO JST, Kyoto Research Park;
          17 Chudouji Minamimachi, Shimokyo-ku, Kyoto, Kyoto 600, Japan
          (E-mail: syoshio@cell.tsukita.jst.go.jp, Tel:+81-75-315-7913,
          Fax:+81-75-315-6420)
          2 (sites)
AUTHORS   Yoshioaka,S., Kato,K., Nakai,K., Okayama,H. and Nojima,H.
TITLE     Identification of open reading frames in Schizosaccharomyces pombe
          cDNAs
JOURNAL   DNA Res. 4 (6), 363-369 (1997)
MEDLINE   96162722
FEATURES
Source    Location/Qualifiers
          1..1152
            /organism="Schizosaccharomyces pombe"
            /strain="PR745"
            /db_xref="taxon:4896"
            /clone="SY1164"
            /clone_11b="library of H. Nojima"
            <1..522
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              EMBL Accession Number Z72658"
            /codon_start=1
            /protein_id="BAA13871.1"
            /db_xref="GI:1749628"
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            LSEMLCASALHVALVFLKSGSTICKFYMDDEDADIDNLKSHFRVQVWKPKASLKE
            SRKATVYCLERK"

BASE COUNT      325 a      211 c      257 g      359 t
ORIGIN

Query Match      1.9%; Score 19; DB 14; Length 1152;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 233 ctgcataccaccctcgttc 251
  |||
  Db 853 CTGCATCACCCCTGTTTC 835

RESULT 24
AF273691      1279 bp      mRNA      ROD      22-FEB-2001
LOCUS     Mus musculus ribosome receptor isoform mRrp2 mRNA, complete cds,
          alternatively spliced.
DEFINITION AF273691
ACCESSION  AF273691.1 GI:13094692
VERSION
KEYWORDS
SOURCE     house mouse.
ORGANISM   Mus musculus.
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 1279)
AUTHORS   Kim,Y.-J., Lee,M.-C., Kim,S. and Chun,J.-Y.
TITLE     Identification and characterization of multiple isoforms of a mouse
          ribosome receptor
JOURNAL   Gene 261 (2), 337-344 (2000)
PUBMED    11167022
REFERENCE  2 (bases 1 to 1279)
AUTHORS   Kim,Y.-J., Lee,M.-C., Kim,S. and Chun,J.-Y.
TITLE     Direct Submission
JOURNAL   Submitted (01-JUN-2000) Kumbo life and Environmental Science
          Laboratory, 572 Sangam-Dong, Kwangsan-Gu, Kwangju 506-712, Korea
          1..1279
          Location/Qualifiers
            /organism="Mus musculus"
            /strain="ICR"

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gene complement(4315. .5418)
/ gene="VNG0789C"
/ complement(4315. .5418)
CDS / gene="VNG0789C"
/ note="conserved hypothetical protein"
/ codon_start=1
/ transl_table=11
/ product="Vng0789c"
/ protein_id="AAG19255.1"
/ db_xref="GI:10580363"
/ translation="MATIGRSSNDSDGVRDVAGVSGAEFVRYTAAPGCGVVAAGLL
AGVCDGVGVSQVRRVSEPPSHSGADGSOAAPTASHYVGC EAANAASVGVADA
FALAREVGTHPDPVTAGAVADGVEPPADVRAAAGAWTRRPGVPTDLAAGLASH
TLVHASFSGDEOGAFAELGLPPEPDAAARRRLASVALDPTADAPPCADAVHDA
LRRPATPDGMMATVEGADVINAAMAAHGHGALGLTGLDADRTAVLAAMAHAPSHA
AVRAASLARHRCVYADVPTASTFVARLLRDYATATPAVLAVETETALATTTADAH
VLEGSVTRRAATTLGSSSDADAVIEIVRGGL"
gene complement(5423. .5890)
/ gene="rps15p"
/ note="VNG0790G"
/ complement(5423. .5890)
CDS / gene="rps15p"
/ note="rps15p"
/ codon_start=1
/ transl_table=11
/ product="30S ribosomal protein S15p"
/ protein_id="AAG19256.1"
/ db_xref="GI:10580364"
/ translation="MARHTRRRSGSSGDRPTADEPPESDVEDADEEERVELAEQG
HDSQIGLRDEGVGTVPDVKATGKVEILPAHDAPELPDPFRNLLEKAVRL
HEHEVAMGODHNRKRALQNTQSKIRRLADYRGDKLDEFAFYSYETARETIEE"
6115. .6186
/ gene="trn11"
/ product="trnA-Ala"
6115. .6186
/ gene="trn11"
/ complement(6477. .8846)
gene / gene="trn11"
/ complement(6477. .8846)
CDS / gene="trn11"
/ complement(6477. .8846)
/ note="VNG0793G"
/ complement(6477. .8846)
/ gene="trn6"
/ note="trn6"
/ codon_start=1
/ transl_table=11
/ product="trn6 transducer"
/ protein_id="Htr6_19257.1"
/ db_xref="GI:10580365"
/ translation="MSDGIITGALRNAASVAVAPAIRRGAKFAVFIIVLVYIAGAG
VFAFQSTETVEHOTTRQLAESNLEADAGAMEGOQTHARSVODEALRODRRAP
YTLKDQLPADVSMHLVNETRGTVASTELAIEGRSLAELDAPMTTAAVPGPCND
SAVMATEQSYRSPVLEDERVMAFASVPRREGHLLVYTRIQVPRLSANSTRRTT
ILNTGDEPVLDSNSRFDAGALDSTIAVRNDTAAVTVVTRISNGVYALASATPHDWTY
TSVDTGEAFVADVTGQTVTVLVAVLISLAIAGLGRHTVPLRLARRADIDISG
TFDVIDLSTRIDIEVGRLYGSFDMRVSLDRIQEAFAVEANAARAEELTDED
AQAEEARAKATAEAERLOERADYSSEVMAVAADDLERLEDEDEEMRVAEEF
NAMLGLEATIAOVAGEFADVADTQVATGETTSQTSERIOELTADAGLIOOH
DLERAGEMDELASQVVAASATYAEFAAABVEGEGRDAESALIDMATESIS
ADAVDOIILQERMSDIDITIEITDIACTNMLANANLEANRARKDGGFVAVNE
VVDLAETKQAAADIESEIQAVQETDETVADIRATSEIHDDGVSTVERAAAIEDTV
DAIEDANNDGLOEISDATEDOADATQSVVRVDVADISQHVTEADAOVSAAAEQAS
VAIEARSADDLRBDALATVNOFETRADADEPDADTTVDASADDTGD"
complement(8843. .9611)
gene / gene="yu1f"
/ note="VNG0794G"
/ complement(8843. .9611)
CDS / gene="yu1f"
/ note="yu1f"
/ codon_start=1
/ transl_table=11
/ product="ABC transporter (lipoprotein)"
/ protein_id="AAG19258.1"
/ db_xref="GI:10580366"
/ translation="WYVALGGLDRSFNDANRGAQRARLDHGIAVTNHEPDSIAELG
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EQOATLAASNPAVDLVCYGFROADGLESAANAAPDOOFMIVDTAVDASNVAAYEE
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TASDIDVLAAYTGDPEDEVEAPAAANAAMDAGADITYHAAGCGVGYLQAAQNGRYA
IGVSDOSRNPRTADVVLASMKRITDITAVDITAEATIDBDLPGADVSLGLATNGVS
VOYGTQDGPAPVAVDVALGETREVALVAGDITVTPRPOSAGGGG"
BASE COUNT 1353 a 3628 c 3425 g 1722 t
ORIGIN

Query Match 1.98; Score 19; DB 1; Length 10128;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 386 CGCGGCGCAGCAGGATC 404
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Db 574 CGCGGCGCAGCAGGATC 556

RESULT 26
AR083116/c 11873 bp DNA PAT 01-SEP-2000
LOCUS AR083116
DEFINITION Sequence 32 from patent US 5976803.
ACCESSION AR083116
VERSION AR083116.1 GI:10009906
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11873)
AUTHORS Meek, K.D.
TITLE Genetic test for equine severe combined immunodeficiency disease
JOURNAL Patent: US 5976803-A 32 02-NOV-1999;
FEATURES
source Location/Qualifiers
1..11873
/organism="unknown"
BASE COUNT 3585 a 2320 c 2669 g 3299 t
ORIGIN

Query Match 1.98; Score 19; DB 9; Length 11873;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 211 actctgcgcgtgctgat 229
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Db 6446 ACTTCTGCCGCTGCTGAT 6428

RESULT 27
AR083115/c 11878 bp DNA PAT 01-SEP-2000
LOCUS AR083115
DEFINITION Sequence 31 from patent US 5976803.
ACCESSION AR083115
VERSION AR083115.1 GI:10009905
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11878)
AUTHORS Meek, K.D.
TITLE Genetic test for equine severe combined immunodeficiency disease
JOURNAL Patent: US 5976803-A 31 02-NOV-1999;
FEATURES
source Location/Qualifiers
1..11878
/organism="unknown"
BASE COUNT 3586 a 2323 c 2668 g 3301 t
ORIGIN

Query Match 1.98; Score 19; DB 9; Length 11878;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      211 actctgcgcgtcgtcat 229
Db      6446 ACTTCTGCCGCTGTCAT 6428

RESULT 28
AR083114/c 11883 bp DNA PAT 01-SEP-2000
DEFINITION Sequence 28 from patent US 5976803.
ACCESSION AR083114
VERSION AR083114.1 GI:10009904
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11883)
AUTHORS Meek,K.D.
TITLE Genetic test for equine severe combined immunodeficiency disease
JOURNAL Patent: US 5976803-A 28 02-NOV-1999;
FEATURES
source 1. 11883
location/Qualifiers
BASE COUNT 3588 a 2324 c 2669 g 3302 t
ORIGIN

Query Match 1.9%; Score 19; DB 9; Length 11883;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      211 actctgcgcgtcgtcat 229
Db      6449 ACTTCTGCCGCTGTCAT 6431

RESULT 29
SPBC262 36493 bp DNA PLN 23-MAY-1999
LOCUS S.pombe chromosome II cosmid c262.
DEFINITION AL022103
ACCESSION AL022103.1 GI:2956767
VERSION
KEYWORDS 608 ribosomal protein l16-c; beta transducin; beta-adaptin; cell
division protein l16; homolog; deoxycytidylate deaminase;
glycylpeptide n-tetradecanoyltransferase; histidyl-trna synthetase;
l12lp; mannose-6-phosphate isomerase; phosphatidylinositol
phosphate phosphatase; popl; protein transport protein; rpl16c; sun
family protein; tetrahydrofolate synthase; transmembrane
transporter; WD repeat protein; WD-40 repeat.
fission yeast.
SOURCE Schizosaccharomyces pombe
ORGANISM Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomycetes.
1 (bases 1 to 36493)
Wood,V., Rajandream,M.A., Barrell,B.G., Devlin,K. and Churcher,C.M.
Direct Submission
Submitted (04-MAR-1998) European Schizosaccharomyces genome
sequencing project, Sanger Centre, The Wellcome Trust Genome
Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk
Notes:
Details of yeast sequencing at the Sanger Centre are available on
the World Wide Web.
(URL, http://www.sanger.ac.uk/projects/S.pombe/)
During 1995 to 1996 about 80% of S. pombe chromosome I was
sequenced by the Sanger Centre. The sequencing of the S. pombe
genome is now being continued with funding from The European
Commission. Fourteen European sequencing laboratories, including
the Sanger Centre, are participating in the project.
Computer coding regions (CDS) have been predicted with the help of
protein analysis using the Genefinder program in Pombase (an ACEDB
database) with additional predictions for the branch-acceptor sites
supplied by the program Spsplice. CAUTION: It is possible that for
any individual CDS we may have underestimated or overestimated the

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number of introns/exons or we may not have chosen the correct
splice donor/acceptor sites.
CDS are numbered using the following system eg SPBC25H2.01c. SP (S.
pombe), B (chromosome 2), c25H2 (cosmid name), .01 (first CDS), c
(complementary strand).
The more significant matches with motifs in the PROSITE database
are also included but some of these may be fortuitous.
The length in codons is given for each CDS.
IMPORTANT: This sequence MAY NOT be the entire insert of the
sequenced clone. It may be shorter because we only sequence
overlapping sections once, or longer, because we arrange for a
small overlap between neighbouring submissions.
Cosmid c262 overlaps 5' with c4B4.
location/Qualifiers
source 1. 36493
/organism="Schizosaccharomyces pombe"
/strain="972h-"
/db_xref="taxon:4896"
/chromosome="II"
/clone="cosmid c262"
/map="IIR"
complement(1..1156)
/gene="SPBC262.01c"
/note="1121"
1..1709
/note="9nominal overlap with SPBC4B4 S. pombe chromosome
2"
complement(1..1156)
/partial
/gene="SPBC262.01c"
/function="transmembrane transporter; affects cell cycle
progression"
/note="SPBC262.01c, len:>383"
/codon_start=1
/label=1121
/product="transmembrane transporter l12lp."
/protein_id="CA17881.1"
/db_xref="GI:2956768"
/db_xref="SPTREMBL:O43000"
/translation="MALNRLAKTFSPYGLNKVEOKLIKIDMFILSCCVSEFINV
LRRSINNAVYSGMGEDEKMGNEFDODINVTGCIITIGLPGSYALORVAPRMEFV
NMLLGLMTITSPFAVSHVRLALITREFPAVAEASTFACHTITLAWKESLCKRAGI
FSAAGLVTPMAGLIQTAVHSSLNKGGSLMRKFTIDGLITPLSLGLELPDPV
ETTKAPKPTFDEKEISFKRLPARPKKPLTKAIKDIVSRWITGLCLTWLFEETQA
IAVWLMQOMKMKNSKFSVAQINNPVTAVGVSTLGASVIDSKLAGNPRWFGFLR
LCVITVATITLLAMWNPDAKFPAYFASCTYAGQAVWFSMANDICHDND"
2337..5567
/gene="SPBC262.02"
2337..5567
/note="SPBC262.02"
/gene="SPBC262.02, len:1075, SIMILARITY: Saccharomyces
cerevisiae, Q12271, YOR109y, phosphatidylinositol
phosphate phosphatase (1107 aa), fasta scores: opt: 1630,
E(-):0, (39.0% identity in 1100 aa)"
/codon_start=1
/label=SPBC262.02
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synaptojanin-like"
/synpjojanin_id="CA17882.1"
/db_xref="GI:2956769"
/db_xref="SPTREMBL:O43001"
/translation="WQCLLRKPNLSALVNKDHALMHSVPQNKNSLVCVAEFTALS
EKLPEGRKISSHRYGTGLILEGSNPLCVISGASVAVRKRERFRTMEVCFYS
VNRSMWHIROENSPDIDGVDTGDSYKYAAEPSSLRLKLTNGSFYSIDPD
ITTRLQRLSTQMTPEPOYDSMHTQPMNRMFLROLIKRSHLNGDEKSGALDGRFTC
AIRGPASTREOKLIGQTRLSLSTLSLACTRPLSGRDDGNAVFETRTLDS
SKVCSTQVKGSTITFEWEGVQVFGKIDITNSLEATRAAFERHFTSLIEBGPVH
IINLGTSGERSLSERLROIQLSPEDLIHLETFDHOIRSEEDNKRTPMITYSD
AETFGYFENNNGOSIVQDVFPTNCDICDRTVONLVSRLFLEQVMYTRNAG
YDEMVOVHSTIVANNGDALARTYGTGALCKSRFGKLSIGALMLDLSVGRIMN
FODKGRQETIDLLGLRIDHPVLLYDPIHVVNHELRKRENESEHKNIEPIASVY
LNGCSATTKLENMLFPEPTPLADITVYVGFQETVQITPQVTSADPAKREMEVCYKL
LNGKCTSGPIGVQLRSGLVGTALVITFKESCLPSINKVEGTAKTKGLGVSQNGKAV

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GDIYDTSOKHVPAMTDRIYGLVPLHSYGSPVLYSHRPIVATVATYKIVRE
KKKILFEELYNORKOEVRDASQSTYLLIDAGSVACKPNI.IPLPANGKDIKPSSE
RKMWFDDGICPAKSIAPAPPEYRILNPSRINFPEPTAEIDMISNTKOSDKKSLID
STPASPAPSSILARSSVSORSSTSIILPIKPNPTPDHLVAVRVPPLPRSGSSSS
GVPAPMITPVNPPPTPPKSSASORSGLDLPRESSISMKPLV"
complement(join(5906..6005,6056..6187,6252..6313,
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complement(join(5906..6005,6056..6187,6252..6313,
6364..6378))
/gene="SPBC262.03c"
/note="SPBC262.03c, len:101, SIMILARITY: Saccharomyces
cerevisiae, S6B2_YEAST, protein transport protein sec61
beta 2 subunit, (88 aa), fasta scores: opt: 242,
E():2.1e-09, (46.38 identity in 82 aa)"
/codon_start=1
/label="SPBC262.03c
/product="putative protein transport protein; yeast sec61
beta 2 subunit-like"
/protein_id="CAI17883.1"
/db_xref="GI:2956770"
/translation="MSSTKASGSKNSAASAPGPKSQIRRAAVEKNTKESGPG
ARAAGAPGSTPLIKLYTDEAGCFKVDPVVWVLSVGLASVFLHIVARILKKFASE
"
misc_feature
complement(6006..6020)
/note="ctaacgtatctaag, splice branch and acceptor"
complement(6050..6055)
/note="gtaacg, splice donor sequence"
complement(6188..6210)
/note="ctaacctttgtgtgtgttg, splice branch and
acceptor"
complement(6246..6251)
/note="gttcgt, splice donor sequence"
complement(6314..6324)
/note="ctaacatagtag, splice branch and acceptor"
complement(6358..6363)
/note="gtaacg, splice donor sequence"
complement(6975..7463)
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complement(6975..7463)
/note="SPBC262.04c, len:161, SIMILARITY: Saccharomyces
cerevisiae, Y1P1_YEAST, required for maintenance of
mitochondrial DNA, (145 aa), fasta scores: opt: 357,
E():7.5e-17, (44.08 identity in 141 aa)
sequence possibly needs truncating to second met"
/codon_start=1
/label="SPBC262.04c
/product="hypothetical protein"
/protein_id="CAI17884.1"
/db_xref="GI:2956771"
/translation="MLRALGSRLLVASRPAARYSFOOSLRPREFIHKMSKTPINS
PKSSAGPYNOATKANGVIYSGOIVANGKVEGTGDTROCLINLQEVLEAASS
LKTIYKVNIFLADMDFPAVANKYTYEVLDPKPARSCVAVKTYPLSTOGVKIETCIA
LE"
gene
join(8051..8091,8150..8702)
/gene="SPBC262.05"
/note="rp116c"
join(8051..8091,8150..8702)
/gene="SPBC262.05"
/note="SPBC262.05, len:196"
/codon_start=1
/label="rp116c
/product="60s ribosomal protein 116-c."
/protein_id="CAI17885.1"
/db_xref="GI:2956772"
/translation="MSEFQKLVIIIDAKGHLMGLASTVAKOLLAGQVVVRCETINI
SCHFFRNKLKYLALRRACRYNPSRGAFHFRAPSRIPTAVRGMPLPKTTFGIATLKN

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```

LQALEGIPPEFDKRLVPAALRVLRKPSRYCTIGRLSEVGMKYNKIVSKLEER
RKIKSAFYAKCANQKHIVAKTKSSVNEKLAVFG"
8092..8097
/note="gtatga, splice donor sequence"
8135..8149
/note="ctaacgtatctaag, splice branch and acceptor"
8361..8432
/gene="SPBC262.05"
/note="P500783 Ribosomal protein L13 signature"
complement(join(8859..10245,10290..10408,10453..10698,
10752..10797,10835..11043,11090..11116))
/gene="SPBC262.06c"
complement(join(8859..10245,10290..10408,10453..10698,
10752..10797,10835..11043,11090..11116))
/gene="SPBC262.06c"
/note="SPBC262.06c, len:676, SIMILARITY: Drosophila
melanogaster, Q24253, beta-adaptin drosophila 1., (921
aa), fasta scores: opt: 1724, E():0, (45.28 identity in
aa)
Query Match 1.9% Score 19; DB 15; Length 36493;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 233 ctgcatacaccctcgtttc 251
|||||
Db 27668 CTCGATCACCCCGCTTTC 27686
RESULT 30
AC015691
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
JOURNAL
TITLE
JOURNAL
REFERENCE
2 (bases 1 to 67442)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Batra,N., Beckerly,R., Boguslavsky,L., Bouckgalter,B.,
Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
Cooke,P., Dearrellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
Galagan,J., Gardyna,S., Grant,G., Hages,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Lehoczky,J., Liu,C., Locke,K., MacDonald,P., Marquis,N.,
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrum,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Strange-Rhmann,N., Stojanovic,N., Subramanian,A., Telamas,J.,
Testaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
Project Information
Center project name: L1351
Center clone name: 54_F_1
* NOTE: This record contains 78 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely

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LOCUS AC068952 95292 bp DNA 18-AUG-2000  
DEFINITION Mus musculus chromosome 2 clone ct7-254f1 strain 129/Sv ES cell  
line C37, complete sequence.  
ACCESSION AC068952  
VERSION AC068952.10 GI:9845112  
KEYWORDS HTG.  
SOURCE house mouse.  
ORGANISM Mus musculus.  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
AUTHORS Shull, S., Rahhal, R., Yao, Z., Ritchiech, K. and ROE, B.A.  
TITLE Mus musculus Chromosome 2 BAC Clone c1b-254f1  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 95292)  
AUTHORS Shull, S., Rahhal, R., Yao, Z., Ritchiech, K. and ROE, B.A.  
TITLE Direct Submission  
JOURNAL Submitted (13-MAY-2000) Department of Chemistry and Biochemistry,  
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,  
OK 73019, USA  
COMMENT On Aug 18, 2000 this sequence version replaced gi:9795634.  
FEATURES  
source Location/Qualifiers  
1..95292  
/organism="Mus musculus"  
/strain="129/Sv ES cell line C37"  
/db\_xref="taxon:10090"  
/chromosome="2"  
/clone="ct7-254f1"  
/clone\_11b="CalTech CTFB-BAC library"  
BASE COUNT 28084 a 18825 c 18104 g 30279 t  
ORIGIN  
Query Match 1.9%; Score 19; DB 94; Length 95292;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 537 gaaccacacagagaaga 555  
|||||  
Db 76659 GAACCAACAGGAGAGAA 76641.  
|||||  
RESULT 34  
AL354832.1  
WPCOMMENT  
Sequence split into 4 fragments LOCUS AL354832 Accession AL354832  
Fragment Name Begin End  
AL354832\_0 1 110000  
AL354832\_1 100001 210000  
AL354832\_2 200001 310000  
AL354832\_3 300001 372955  
Continuation (2 of 4) of AL354832 from base 100001 (AL354832 Homo sapiens chromosome 20  
Query Match 1.9%; Score 19; DB 79; Length 110000;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 215 ctgcgcctgcacccc 233  
|||||  
Db 66912 CTGCCGCTGCTGATCCCC 66930  
|||||  
RESULT 35  
AC024591 111071 bp DNA HTG 18-JUL-2000  
LOCUS AC024591/c  
DEFINITION Homo sapiens chromosome 16 clone RP11-511G21, WORKING DRAFT

SEQUENCE, 13 ordered pieces.  
AC024591  
VERSION AC024591.3 GI:9256450  
KEYWORDS HTG; HTGS\_PHASE2; HTGS\_DRAFT.  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
AUTHORS 1 (bases 1 to 111071)  
TITLE DOE Joint Genome Institute.  
JOURNAL Sequencing of Human Chromosome 16  
REFERENCE 2 (bases 1 to 111071)  
AUTHORS DOE Joint Genome Institute.  
TITLE Direct Submission  
JOURNAL Submitted (29-FEB-2000) Production Sequencing Facility, DOE Joint  
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
On Jul 18, 2000 this sequence version replaced gi:7705016.  
-----Genome Center  
Center: Joint Genome Institute  
Center Code: JGI  
Web site: <http://www.jgi.doe.gov>  
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Project Information  
Center Project Name: 602754  
Center clone name: RPCI-11\_511G21  
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Summary Statistics  
Consensus quality: 104021 bases at least Q40  
Consensus quality: 108348 bases at least Q30  
Consensus quality: 109319 bases at least Q20  
Estimated insert size: 118930; agarose-fp estimation  
Estimated insert size: 110521; sum-of-ctrls estimation  
Quality coverage: 8.44 in Q20 bases; agarose-fp estimation  
Quality coverage: 9.08 in Q20 bases; sum-of-ctrls estimation.  
\* NOTE: This is a "working draft" sequence. It currently  
\* consists of 13 contigs. Gaps between the contigs  
\* are represented as runs of N. The order of the pieces  
\* is believed to be correct as given, however the sizes  
\* of the gaps between them are based on estimates that have  
\* provided by the submitter.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.  
1  
4000 3999: contig of 3999 bp in length  
4099: gap of unknown length  
4100 6224: contig of 2125 bp in length  
6225 6325: gap of unknown length  
6325 14602: contig of 8278 bp in length  
14603 14703: gap of unknown length  
14703 54245: contig of 39543 bp in length  
54246 54345: gap of unknown length  
54346 58569: contig of 4224 bp in length  
58570 58670: gap of unknown length  
58670 59481: contig of 811 bp in length  
59481 59580: gap of unknown length  
59580 60683: contig of 1103 bp in length  
60683 60784: gap of unknown length  
60784 62950: contig of 2167 bp in length  
62950 63050: gap of unknown length  
63050 63051: gap of unknown length  
63051 64092: contig of 1042 bp in length  
64093 64192: gap of unknown length  
64192 85067: contig of 20875 bp in length  
85068 85167: gap of unknown length  
85168 91149: contig of 5982 bp in length  
91150 91249: gap of unknown length  
91250 108236: contig of 16987 bp in length  
108237 108336: gap of unknown length  
108337 111071: contig of 2735 bp in length.  
Location/Qualifiers  
1..111071  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"



**AUTHORS** Jia, H., Lin, S., Rithideck, K. and Roe, B.A.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (24-AUG-2000) Department of Chemistry And Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA  
**COMMENT** On Aug 4, 2000 this sequence version replaced gi:9280733.  
**FEATURES** Location/Qualifiers  
 source  
 1. 130734  
 /organism="Mus musculus"  
 /strain="129/SV3S Cell Line C17"  
 /db\_xref="taxon:10090"  
 /chromosome="2"  
 /clone="CT-305f12"  
 /clone\_lib="Caltech C17B-BAC library"  
**BASE COUNT** 41025 a 25364 c 26653 g 37692 t  
**ORIGIN**

Query Match 1.9%; Score 19; DB 94; Length 130734;  
 Best Local Similarity 100.0%; Pred. No. 34;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 537 gaaccacagagaaga 555  
 ||||||||||||||||  
 Db 65070 GAACCAACAGAGAGAA 65088

**RESULT** 38  
**LOCUS** HSJ1057D4 131888 bp DNA PRI 01-MAR-2001  
**DEFINITION** Human DNA sequence from clone RP5-1057D4 on chromosome 20 contains a spermidine synthase (SPDSY) pseudogene, a CpG island, ESTs, STSS and GSSs, complete sequence.  
**ACCESSION** AL121777  
**VERSION** AL121777.39 GI:10862842  
**KEYWORDS** HTG; CpG island; spermidine synthase.  
**SOURCE** human.  
**ORGANISM** Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homimidae; Homo.  
**REFERENCE** 1 (bases 1 to 131888)  
**AUTHORS** Blakey, S.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (26-FEB-2001) Sanger, Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk  
**COMMENT** On Oct 17, 2000 this sequence version replaced gi:10716550. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.  
 The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:  
 Em, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at  
 http://www.sanger.ac.uk/Projects/C\_elegans/wormpep This sequence was generated from part of bacterial clone configs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at  
 http://www.sanger.ac.uk/HGP/Chr20  
 This sequence is the entire insert of clone RP5-1057D4 The true right end of clone RP1-73E16 is at 71240 in this sequence. The true left end of clone CTD-2653D5 is at 84358 in this sequence. This region was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RP5-1057D4 is from the library RPI-5 constructed by the group of Pieter de Jong. For

features details see  
 http://www.chori.org/bacpac/home.htm  
 VECTOR: PCYPAC2.  
**FEATURES** Location/Qualifiers  
 source  
 1. 131888  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /chromosome="20"  
 /clone="RP5-1057D4"  
 /clone\_lib="RPI-5"  
 313. 930  
 /note="12 repeat: matches 2043. 2749 of consensus"  
 repeat\_region  
 1411. 1543  
 /note="MIR repeat: matches 80. 222 of consensus"  
 repeat\_region  
 1623. 1934  
 /note="AluY repeat: matches 1. 311 of consensus"  
 repeat\_region  
 2162. 2215  
 /note="12 repeat: matches 2696. 2749 of consensus"  
 repeat\_region  
 2444. 2646  
 /note="12 repeat: matches 2353. 2521 of consensus"  
 repeat\_region  
 2929. 3407  
 /note="match: GSS: Em:A0520865"  
 misc\_feature  
 3104. 3214  
 /note="12 repeat: matches 2629. 2746 of consensus"  
 repeat\_region  
 3638. 3839  
 /note="MIR repeat: matches 32. 256 of consensus"  
 repeat\_region  
 3916. 4051  
 /note="AluX repeat: matches 1. 123 of consensus"  
 repeat\_region  
 4052. 4341  
 /note="AluY repeat: matches 1. 295 of consensus"  
 repeat\_region  
 4342. 4477  
 /note="AluX repeat: matches 123. 298 of consensus"  
 repeat\_region  
 5436. 5600  
 /note="AluX repeat: matches 170. 299 of consensus"  
 repeat\_region  
 5601. 5892  
 /note="AluY repeat: matches 1. 291 of consensus"  
 repeat\_region  
 5893. 6050  
 /note="AluX repeat: matches 1. 170 of consensus"  
 repeat\_region  
 6179. 6230  
 /note="MIR repeat: matches 206. 256 of consensus"  
 repeat\_region  
 6186. 6565  
 /note="12 repeat: matches 2292. 2731 of consensus"  
 repeat\_region  
 6567. 6606  
 /note="12 repeat: matches 2148. 2189 of consensus"  
 repeat\_region  
 6607. 6913  
 /note="AluO repeat: matches 1. 307 of consensus"  
 repeat\_region  
 6914. 7005  
 /note="12 repeat: matches 2064. 2148 of consensus"  
 repeat\_region  
 7104. 7559  
 /note="MIR repeat: matches 31. 512 of consensus"  
 repeat\_region  
 8768. 8969  
 /note="MER20 repeat: matches 1. 216 of consensus"  
 repeat\_region  
 9696. 10011  
 /note="12 repeat: matches 2357. 2734 of consensus"  
 repeat\_region  
 11637. 12065  
 /note="MIR repeat: matches 20. 531 of consensus"  
 repeat\_region  
 12302. 12377  
 /note="MIR repeat: matches 115. 190 of consensus"  
 repeat\_region  
 13520. 13783  
 /note="12 repeat: matches 2432. 2749 of consensus"  
 repeat\_region  
 13953. 14155  
 /note="MIR repeat: matches 267. 468 of consensus"  
 repeat\_region  
 14420. 14705  
 /note="AluO repeat: matches 1. 294 of consensus"  
 repeat\_region  
 14545. 15063  
 /note="match: GSS: Em:A0713490"  
 misc\_feature  
 14589. 15060  
 /note="match: GSS: Em:A0760291"  
 misc\_feature  
 14602. 15072  
 /note="match: GSS: Em:A0885065"  
 misc\_feature  
 15070. 15576  
 /note="match: GSS: Em:A0709181"  
 misc\_feature  
 15088. 15403

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/note="match: GSS: Em:AQ198342"
15088. .15583
misc_feature /note="match: GSS: Em:AQ680811"
15094. .15492
misc_feature /note="match: GSS: Em:AQ082327"
15423. .15656
repeat_region /note="L2 repeat: matches 1609. .1854 of consensus"
15716. .15894
repeat_region /note="MER20 repeat: matches 4. .187 of consensus"
15898. .16155
repeat_region /note="L2 repeat: matches 1915. .2159 of consensus"
16156. .16457
repeat_region /note="Alusx repeat: matches 3. .304 of consensus"
16458. .16568
repeat_region /note="L2 repeat: matches 2159. .2263 of consensus"
16569. .16865
repeat_region /note="Alusx repeat: matches 1. .301 of consensus"
16870. .17097
repeat_region /note="L2 repeat: matches 2263. .2531 of consensus"
17103. .17406
repeat_region /note="Alusx repeat: matches 1. .301 of consensus"
18176. .18380
repeat_region /note="MIR repeat: matches 36. .260 of consensus"
19512. .19745
repeat_region /note="MIR repeat: matches 13. .261 of consensus"
/note="match: GSS: Em:AQ383848"
21138. .23316
misc_feature /note="CPG Island"
/evidence="not_experimental"
21792. .22251
repeat_region /note="230 copies 2 mer cc 55% conserved"
21814. .22282
misc_feature /note="single clone region. Assembly confirmed by
restriction digest."
21829. .22122
repeat_region /note="6 copies 49 mer 64% conserved"
21832. .22251
repeat_region /note="12 copies 35 mer 57% conserved"
21934. .22123
repeat_region /note="5 copies 38 mer 67% conserved"
22000. .22257
repeat_region /note="6 copies 43 mer 62% conserved"
23418. .23568
repeat_region /note="MIR repeat: matches 18. .187 of consensus"
23981. .24040
repeat_region /note="MER33 repeat: matches 233. .293 of consensus"
24041. .24328
repeat_region /note="Alub repeat: matches 1. .288 of consensus"
24329. .24543
repeat_region /note="MER33 repeat: matches 23. .233 of consensus"
25195. .25242
repeat_region /note="24 copies 2 mer tg 72% conserved"
27239. .27425
repeat_region /note="MIR repeat: matches 55. .249 of consensus"
27638. .27889
repeat_region /note="LMC4 repeat: matches 7694. .7977 of consensus"
27900. .28343
repeat_region /note="L2 repeat: matches 2292. .2150 of consensus"
28434. .28597
repeat_region /note="MIR repeat: matches 57. .232 of consensus"
29051. .29345
repeat_region /note="Aluio repeat: matches 2. .297 of consensus"
29456. .29717
repeat_region /note="Alusx repeat: matches 1. .254 of consensus"
29873. .30045
repeat_region /note="MLTIC repeat: matches 6. .163 of consensus"
30046. .30348
repeat_region /note="Alusx repeat: matches 1. .306 of consensus"
30349. .30598
repeat_region /note="MLTIC repeat: matches 163. .464 of consensus"
30721. .30798
repeat_region /note="MER5B repeat: matches 44. .117 of consensus"
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repeat_region 30802. .30927
/note="LIMB8 repeat: matches 6040. .6168 of consensus"
30942. .31001
repeat_region /note="MER5B repeat: matches 113. .173 of consensus"
31509. .31809
repeat_region /note="Alusx repeat: matches 1. .304 of consensus"
32898. .33202
repeat_region /note="Alusx repeat: matches 1. .310 of consensus"
33556. .33701
repeat_region /note="MER5A repeat: matches 1. .146 of consensus"

Query Match 1.9%: Score 19; DB 93; Length 131888;
Best Local Similarity 100.0%: Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 215 ctgccgtctgcatccccc 233
|||||
Db 22024 CTGCCGCTGTCGATCCCC 22042

RESULT 39
AC005738/c 134506 bp DNA PRI 20-OCT-1998
LOCUS Homo sapiens chromosome 5, BAC clone 7g12 (LBNL H126), complete
DEFINITION sequence.
ACCESSION AC005738 AC004619 LB1405 LB1406 LB1678 LB1679 LB1680 LB1860 LB1861
LB1862 AC001042 AC001043 AC001520
VERSION AC005738.1 GI:3687213
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 134506)
Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M.,
Kadner,K., Miguel,T., Miller,C., Piltuck,S., Pollard,M.,
Rojeski,H., Subramanian,S. and Martin,C.H.
Submitted (01-OCT-1998) Human Genome Center, DOE Joint Genome
Institute, Lawrence Berkeley National Laboratory, MS 74-157,
Berkeley, CA 94720, U.S.A.
4 (bases 1 to 134506)
Ricke,D.O.
Direct Submission
Submitted (13-OCT-1998) Los Alamos National Laboratory, DOE Joint
Genome Institute, TA43, HRL-1, LS-3, MS M888, Los Alamos, NM 87545,
USA
5 (bases 1 to 134506)
Ricke,D.O.
Direct Submission
Submitted (20-OCT-1998) Los Alamos National Laboratory, DOE Joint
Genome Institute, TA43, HRL-1, LS-3, MS M888, Los Alamos, NM 87545,
USA

COMMENT Sequence submitted by:
FEATURES
source DOE Joint Genome Institute.
location/Qualifiers
1. .134506
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="5p"
/chromosome="5"
join(1. .29755,78169. .82395,123646. .134506)
source
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/map="5p"
/clone="BAC 7612"
/note="LBNL_H126"
complement(748..891)
/note="GRAIL 2 excellent exon, frame 2"
misc_feature
2635..2694
/note="GRAIL 2 excellent exon, frame 2"
repeat_region
complement(2883..2994)
/rpt_family="MLT1"
repeat_region
complement(3940..4205)
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complement(5036..5148)
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9194..9650
/rpt_family="MER42"
9745..10340
/rpt_family="MER42"
10346..10624
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10674..10876
/rpt_family="MER42"
12173..12472
/rpt_family="Alu"
14779..14955
/rpt_family="L1"
15163..15487
/rpt_family="Alu"
complement(19591..19738)
/rpt_family="MIR"
20251..20549
/rpt_family="Alu"
complement(21622..21774)
/note="GRAIL 2 excellent exon, frame 1"
misc_feature
complement(22628..22797)
/rpt_family="MIR"
24507..24641
/rpt_family="Alu"
28893..60995
/rpt_family="MER7"
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/map="5p"
/clone="PI 210h6"
/note="LBNL_H52"
complement(34480..34672)
/rpt_family="MLT1"
complement(34676..34821)
/note="GRAIL 2 excellent exon, frame 0"
repeat_region
complement(34837..35181)
/rpt_family="THE1"
38746..38854
/note="GRAIL 2 excellent exon, frame 1"
repeat_region
39274..39561
/rpt_family="Alu"
39856..40341
/rpt_family="MER1"
complement(40375..40451)
/rpt_family="MLT1"
44067..44382
/rpt_family="Alu"
44592..44900
/rpt_family="Alu"
45213..45338
/rpt_family="L1"
45376..45708
/rpt_family="Alu"
46954..47235
/rpt_family="Alu"

repeat_region
50715..51019
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51522..51600
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complement(58603..58884)
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/db_xref="taxon:9606"
/clone="PI 380h11"
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/map="5p"
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Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      776 atgacaccttgaact 794
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Db      88571 ATGACACCTTCGAACT 88553

RESULT  40
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DEFINITION Mus musculus clone RP23-281H12, *** SEQUENCING IN PROGRESS ***, 68
AC023898
VERSION AC023898.6 GI:11079363
KEYWORDS HTG: HTGS_PHASEL.
SOURCE    house mouse.
ORGANISM  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 141198)
Metzker M.L., Lewis L.R., Hume J., Edwards C., Harris C.,
Dedrich D., Thomas S., Okwuonu G., Carlock C., Garner T.,
Addison S., Pace A., Williams G., Bonnin D., Brooks A., Brown J.,
Bahay C., Bunac C., Burkett C., Chacko J., Chen G., Chen Z.,
Cox C., Davis C., Delgado O., Ding Y., Dugan-Rocha S.,
Fernandez C., Ferraguto D., Forcum-Tansey J., Gill R.,
Gorrell J.H., Gunaratne P., Haller G., Hernandez J., Hoques M.,
Hosak H., Hou X., Huber J., Jackson L., Jia Y., Kelly J., Kelly S.,
Kovar C., Liu D., Liu W., Louised H., Lozado R.J., Martin R.,
Massey E., McLeod M.P., Mel G., Moore S., Morgan M., Morris S.,
Neal D., Nelson A., Nguyen R., Nguyen N., Ogub M., Parish B.,
Perez L., Reiter D., Say J., Shen H., Vasquez L., Wallington S.,
Williamson A., Wrensford G., Zhou X., Bouck J., Hodgson A.,
Muzny D.M., Rives M., Scherer S., Sodergren E., Weinstock G.,
Morley K. and Gibbs R.
Direct Submission
Unpublished
2 (bases 1 to 141198)
Morley K.C.
Submitted (20-FEB-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Nov 3, 2000 this sequence version replaced gi:8248594.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: MABD
Center clone name: RP23-281H12
----- Summary Statistics
Sequencing vector: M13; L08821
Chemistry: Dye-primer Bodipy: 90% of reads
Chemistry: Dye-terminator Big Dye: 10% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 96352 bases at least Q40
Consensus quality: 119814 bases at least Q30
Consensus quality: 130654 bases at least Q20
Estimated insert size: 106211; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 1.5x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
```

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* consists of 68 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 2727 2726: contig of 2726 bp in length
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* 10328 10327: contig of 3420 bp in length
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* 17638 17637: contig of 2987 bp in length
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* 23092 23091: contig of 5354 bp in length
* 23192 23191: gap of unknown length
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* 32009 32108: gap of unknown length
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* 35980 39175: contig of 3196 bp in length
* 39176 39275: gap of unknown length
* 39276 41988: contig of 2714 bp in length
* 41990 42089: contig of 2714 bp in length
* 42090 44449: contig of 2360 bp in length
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* 64983 65082: gap of unknown length
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* 70014 72170: contig of 2157 bp in length
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* 72271 73627: gap of unknown length
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* 139740 139839: gap of unknown length
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 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 941 aggggggtaagcgtggtgt 959  
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 Db 129399 AGGGGGTAAGCCTGTGTGT 129381

RESULT 41  
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 DEFINITION  
 Homo sapiens chromosome 5 clone RP11-148P16 map 5, WORKING DRAFT  
 SEQUENCE, 39 unordered pieces.  
 AC084179  
 VERSION  
 AC084179.2 GI:12229370  
 KEYWORDS  
 HTG: HTGS\_PHASE1; HTGS\_DRAFT.  
 SOURCE  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 147009)  
 Birren,B., Linton,L., Nusbaum,C. and Lander,E.  
 Homo sapiens chromosome 5, clone RP11-148P16  
 Unpublished  
 2 (bases 1 to 147009)  
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,  
 Anderson,S., Barna,N., Bastien,V., Beda,F., Boguslavsky,L.,  
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 Tirrell,A., Traversan,M., Trigglio,J., Vassiliev,H., Viel,R., Vo,A.,  
 Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zahoun,J.,  
 Zimmer,A. and Zody,M.  
 Direct Submission  
 Submitted (14-Oct-2000) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Jan 15, 2001 this sequence version replaced gi:10801407.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

TITLE  
 JOURNAL  
 COMMENT

Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WIBR  
 Web site: http://www-seg.wi.mit.edu  
 Contact: sequence\_submissions@genome.wi.mit.edu  
 Project Information  
 Center project name: L11428  
 Center clone name: 148\_P16  
 Summary Statistics  
 Sequencing vector: plasmid; n/a; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.960731  
 Consensus quality: 132233 bases at least Q40  
 Consensus quality: 139576 bases at least Q30  
 Consensus quality: 142136 bases at least Q20  
 Insert size: 17600; agarose-fp  
 Insert size: 143209; sum-of-ctrls  
 Quality coverage: 3.0 in Q20 bases; agarose-fp  
 Quality coverage: 3.6 in Q20 bases; sum-of-ctrls

\* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 39 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is

\* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

1 1353: contig of 1353 bp in length  
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 1454 2001: contig of 548 bp in length  
 2002 2101: gap of 100 bp  
 2102 3124: contig of 1023 bp in length  
 3125 3224: gap of 100 bp  
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 6016 6115: gap of 100 bp  
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 7300 7399: gap of 100 bp  
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 19862 19961: gap of 100 bp  
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 53728 53827: gap of 100 bp  
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 57632 57731: gap of 100 bp  
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 63869 63968: gap of 100 bp  
 63969 68393: contig of 4425 bp in length  
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 81625 88873: contig of 7249 bp in length  
 88874 88973: gap of 100 bp

\* 88974 96287: contig of 7314 bp in length  
 \* 96288 96387: gap of 100 bp  
 \* 96388 117899: contig of 21512 bp in length  
 \* 117900 117999: gap of 100 bp  
 \* 118000 123663: contig of 5664 bp in length  
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Query Match 1.9%: Score 19; DB 76; Length 147009;  
 Best Local Similarity 100.0%; Pred. No. 33;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 190 agtagcagctataccata 208  
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 DB 10253 AGTAGCAGCTATACCATA 10235

RESULT 42

AC083840  
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DEFINITION Homo sapiens chromosome 8 clone RP11-7319 map 8, WORKING DRAFT  
SEQUENCE, 37 unordered pieces.  
AC083840  
ACCESSION AC083840.2 GI:13184085  
VERSION AC083840.2  
KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 156599)  
Birren, B., Linton, L., Nusbaum, C. and Lander, E.  
Homo sapiens chromosome 8, clone RP11-7319  
Unpublished  
2 (bases 1 to 156599)  
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,  
Anderson, S., Barna, N., Bastien, V., Beda, F., Boguslavsky, L.,  
Bouhagiel, B., Brown, A., Burkett, G., Campopiano, A., Castle, A.,  
Choepe, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,  
Deaellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P.,  
Fitzhugh, M., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M.,  
Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L.,  
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Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lieu, C., Liu, G.,  
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Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T.,  
O'Donnell, P., O'Neill, D., Olivier, T.M., Oliver, J., Peterson, K.,  
Pierre, N., Pisan, C., Pollara, V., Raymond, C., Rieback, M., Riley, R.,  
Rogov, P., Rotman, D., Roy, A., Santos, R., Schauer, S., Severy, P.,  
Sougnie, C., Spencer, B., Stange-Thomann, N., Stojanovic, N.,  
Struss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,  
Tirrell, A., Travers, M., Trigglio, J., Vassiliev, H., Viel, R., Vo, A.,  
Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, C., Zaitoun, J.,  
Zimmer, A. and Zody, M.  
Direct Submission  
Submitted (03-Oct-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Mar 2, 2001 this sequence version replaced gi:105183398.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html  
----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: http://www.seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
----- Project Information  
Center project name: L11308  
Center clone name: 73\_L19  
----- Summary Statistics  
Sequencing vector: Plasmid; n/a; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.960731  
Consensus quality: 141695 bases at least Q40  
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Consensus quality: 151617 bases at least Q20  
Insert size: 152999; sum-of-coverage  
Quality coverage: 4.0 in Q20 bases; sum-of-coverage  
-----  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 37 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
\* 1 816: contig of 816 bp in length  
\* 817 916: gap of 100 bp  
\* 917 2094: contig of 1178 bp in length  
\* 2095 2194: gap of 100 bp

2195 3169: contig of 975 bp in length  
\* 3170 3269: gap of 100 bp  
\* 3270 3766: contig of 497 bp in length  
\* 3767 3866: gap of 100 bp  
\* 3867 5257: contig of 1391 bp in length  
\* 5258 5357: gap of 100 bp  
\* 5358 7176: contig of 1819 bp in length  
\* 7177 7276: gap of 100 bp  
\* 7277 8366: contig of 1090 bp in length  
\* 8367 8466: gap of 100 bp  
\* 8467 9770: contig of 1304 bp in length  
\* 9771 9870: gap of 100 bp  
\* 9871 11023: contig of 1153 bp in length  
\* 11024 11123: gap of 100 bp  
\* 11124 12210: contig of 1087 bp in length  
\* 12211 12310: gap of 100 bp  
\* 12311 13716: contig of 1406 bp in length  
\* 13717 13816: gap of 100 bp  
\* 13817 14696: contig of 880 bp in length  
\* 14697 14796: gap of 100 bp  
\* 14797 16050: contig of 1254 bp in length  
\* 16051 16150: gap of 100 bp  
\* 16151 18691: contig of 2541 bp in length  
\* 18692 18791: gap of 100 bp  
\* 18792 20474: contig of 1683 bp in length  
\* 20475 20574: gap of 100 bp  
\* 20575 22564: contig of 1990 bp in length  
\* 22565 22664: gap of 100 bp  
\* 22665 25349: contig of 2685 bp in length  
\* 25350 25449: gap of 100 bp  
\* 25450 28731: contig of 3282 bp in length  
\* 28732 28831: gap of 100 bp  
\* 28832 41793: contig of 12662 bp in length  
\* 41794 41893: gap of 100 bp  
\* 41894 45562: contig of 3669 bp in length  
\* 45563 45662: gap of 100 bp  
\* 45663 49245: contig of 3583 bp in length  
\* 49246 49345: gap of 100 bp  
\* 49346 52701: contig of 3356 bp in length  
\* 52702 52801: gap of 100 bp  
\* 52802 57587: contig of 4786 bp in length  
\* 57588 57687: gap of 100 bp  
\* 57688 60742: contig of 3055 bp in length  
\* 60743 60842: gap of 100 bp  
\* 60843 64655: contig of 3813 bp in length  
\* 64656 64755: gap of 100 bp  
\* 64756 68878: contig of 4123 bp in length  
\* 68879 68978: gap of 100 bp  
\* 68979 73540: contig of 4562 bp in length  
\* 73541 73640: gap of 100 bp  
\* 73641 79164: contig of 5524 bp in length  
\* 79165 79264: gap of 100 bp  
\* 79265 87667: contig of 8403 bp in length  
\* 87668 87767: gap of 100 bp  
\* 87768 96110: contig of 8343 bp in length  
\* 96111 96210: gap of 100 bp  
\* 96211 104171: contig of 7961 bp in length  
\* 104172 104271: gap of 100 bp  
\* 104272 110622: contig of 6331 bp in length  
\* 110623 110722: gap of 100 bp  
\* 110723 121728: contig of 11006 bp in length  
\* 121729 121828: gap of 100 bp  
\* 121829 129949: contig of 8121 bp in length  
\* 129950 130049: gap of 100 bp  
\* 130050 139747: contig of 9688 bp in length  
\* 139748 139847: gap of 100 bp  
\* 139848 153810: contig of 13863 bp in length  
\* 153811 153910: gap of 100 bp  
\* 153911 156599: contig of 2689 bp in length.  
Location/Qualifiers  
1. 156599  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"

```
/chromosome="8"
/map="8"
/clone_lib="RP11-7319"
/clone_lib="RP11-11 Human Male BAC"
1. .816
/misc_feature /note="assembly_fragment"
vector_side:left"
917. .2094
/misc_feature /note="assembly_fragment"
2195. .3169
/misc_feature /note="assembly_fragment"
3270. .3766
/misc_feature /note="assembly_fragment"
3867. .5257
/misc_feature /note="assembly_fragment"
5358. .7176
/misc_feature /note="assembly_fragment"
7277. .8366
/misc_feature /note="assembly_fragment"
8467. .9770
/misc_feature /note="assembly_fragment"
9871. .11023
/misc_feature /note="assembly_fragment"
11124. .12210
/misc_feature /note="assembly_fragment"
12311. .13716
/misc_feature /note="assembly_fragment"
13817. .14696
/misc_feature /note="assembly_fragment"
14797. .16050
/misc_feature /note="assembly_fragment"
16151. .18691
/misc_feature /note="assembly_fragment"
18792. .20474
/misc_feature /note="assembly_fragment"
20575. .22564
/misc_feature /note="assembly_fragment"
22665. .25349
/misc_feature /note="assembly_fragment"
25450. .28731
/misc_feature /note="assembly_fragment"
28832. .41793
/misc_feature /note="assembly_fragment"
41894. .45562
/misc_feature /note="assembly_fragment"
45663. .49245
/misc_feature /note="assembly_fragment"
49346. .52701
/misc_feature /note="assembly_fragment"
52802. .57587
/misc_feature /note="assembly_fragment"
57688. .60742
/misc_feature /note="assembly_fragment"
60843. .64655

Query Match 1.98; Score 19; DB 76; Length 156599;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 243 cccgttcagccagcc 261
|||||
Db 2492 CCCGTTTCAGCGCCGCC 2510
```

```
RESULT 43
AC034236/c AC034236 160404 bp DNA HTG 18-JUL-2000
LOCUS Homo sapiens chromosome 5 clone CTD-2287016, WORKING DRAFT
DEFINITION
SEQUENCE 16 ordered pieces.
ACCESSION AC034236
VERSION AC034236.2 GI:9256733
KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT.
```

```
SOURCE
ORGANISM human.
REFERENCE
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 5
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 160404)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (05-APR-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jul 18, 2000 this sequence version replaced gi:7417713.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 738109
Center clone name: CITB-RL-2287016
-----
Summary Statistics
Consensus quality: 148274 bases at least Q40
Consensus quality: 155685 bases at least Q30
Consensus quality: 157705 bases at least Q20
Estimated insert size: 145000; pulse field gel estimation
Estimated insert size: 159704; sum-of-contrigs estimation
Quality coverage: 6.47 in Q20 bases; pulse field gel estimation
Quality coverage: 5.87 in Q20 bases; sum-of-contrigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 16 contrigs. Gaps between the contrigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
1 16110: contrig of 16110 bp in length
1 16111 16210: gap of unknown length
1 16211 38617: contrig of 22407 bp in length
1 38618 38717: gap of unknown length
1 38718 71154: contrig of 32437 bp in length
1 71155 71254: gap of unknown length
1 71255 73939: contrig of 2685 bp in length
1 73940 74039: gap of unknown length
1 74040 75830: contrig of 1791 bp in length
1 75831 75930: gap of unknown length
1 75931 79883: contrig of 3953 bp in length
1 79884 79983: gap of unknown length
1 79984 98933: contrig of 18950 bp in length
1 98934 99033: gap of unknown length
1 99034 106554: contrig of 7521 bp in length
1 106555 106654: gap of unknown length
1 106655 112876: contrig of 6222 bp in length
1 112877 112976: gap of unknown length
1 112977 115635: contrig of 2659 bp in length
1 115636 115735: gap of unknown length
1 115736 132099: contrig of 16364 bp in length
1 132100 132199: gap of unknown length
1 132200 138242: contrig of 6043 bp in length
1 138243 138343: gap of unknown length
1 138344 140816: contrig of 2474 bp in length
1 140817 145928: contrig of 5012 bp in length
1 145929 145929: gap of unknown length
1 146029 156365: contrig of 10341 bp in length
1 156370 156469: gap of unknown length
1 156470 160404: contrig of 3935 bp in length.
Location/Qualifiers
1. 160404
```

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/clone="CVD-2287016"
/clone_lib="CalTech human BAC library D"
BASE COUNT      46000 a 28337 c 31268 g 53298 t 1501 others
ORIGIN

```

|                       |                |              |          |               |
|-----------------------|----------------|--------------|----------|---------------|
| Query Match           | 1.9%           | Score 19     | DB 71    | Length 160404 |
| Best Local Similarity | 100.0%         | Pred. No. 33 |          |               |
| Matches 19            | Conservative 0 | Mismatches 0 | Indels 0 | Gaps 0        |

Qy 800 tagagcacagatgtacaga 818  
 |||||  
 Db 141561 TAGAGGCACAGATGACAGA 141543

|            |                                                                     |
|------------|---------------------------------------------------------------------|
| RESULT     | 44                                                                  |
| AC015815/c |                                                                     |
| LOCUS      |                                                                     |
| DEFINITION | AC015815 161549 bp DNA HTG 30-MAR-2000                              |
|            | Homo sapiens clone RP11-21015, WORKING DRAFT SEQUENCE, 21 unordered |

|           |                               |
|-----------|-------------------------------|
| ACCESSION | AC015815                      |
| VERSION   | AC015815.4 GI:7341971         |
| KEYWORDS  | HTG; HTGS_PHASE1; HTGS_DRAFT. |
| SOURCE    | human.                        |
| ORGANISM  | Homo sapiens                  |

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS

Eukaryota; Metazoa; Chordata; Crinacea; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 161549)  
Birten,B., Linton,L., Nusbaum,C. and Lander,E.  
Homo sapiens, clone RP11-21015  
Unpublished  
2 (bases 1 to 161549)  
Birten,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,

**TITLE**  
JOURNAL  
COMMENT

Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Mar 30, 2000 this sequence version replaced g1:6593989.

Direct Submission

Baldwin, J., Barna, N., Beckerly, R., Boguslavsky, L., Boukhalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collmore, A., Cooke, P., Dearellano, K., Dewar, C., Domingo, M., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gaidyna, S., Grant, G., Haas, B., Heiford, A., Horton, L., Howland, J. C., Johnson, R., Jones, C., Kann, L., Karates, A., Klein, J., Lemocky, J., Lieu, C., Locke, C., Macdonald, P., Marquis, N., McMan, P., McGurk, A., McKenna, K., McLaughlin, J., Meldrum, J., Morrow, J., Maylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Sudramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, M. J., Zimmer, A. and zody, M.

```

All repeats were identified using RepeatMasker:
Smitt, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center -----
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIDR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information -----
Center project name: L4073
Center clone name: 21_0_15
----- Summary Statistics -----
Sequencing vector: M13; M77815: 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 151333 bases at least Q40
Consensus quality: 155764 bases at least Q20
Consensus quality: 157650 bases at least Q20
Insert size: 157000; agarose-fp
Insert size: 159549; sum-of-contigs

```

Quality coverage: 4.9 in Q20 bases; agarose-fp  
Quality coverage: 4.8 in Q20 bases; sum-of-contigs

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 21 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

\* I 1138: contig of 1138 bp in length

[illegible]

/note="assembly\_fragment"  
21421..28365  
misc\_feature /note="assembly\_fragment"  
28466..34699  
misc\_feature /note="assembly\_fragment"  
vector\_end:SP6  
clone\_end:SP6  
misc\_feature /note="assembly\_fragment"  
34800..40251  
misc\_feature /note="assembly\_fragment"  
40352..47897  
misc\_feature /note="assembly\_fragment"  
47998..55766  
misc\_feature /note="assembly\_fragment"  
clone\_end:T7  
vector\_side:left"  
misc\_feature 55867..63968  
misc\_feature /note="assembly\_fragment"  
64069..74694  
misc\_feature /note="assembly\_fragment"  
74795..84737  
misc\_feature /note="assembly\_fragment"  
84838..98320  
misc\_feature /note="assembly\_fragment"  
98421..110611  
misc\_feature /note="assembly\_fragment"  
110712..122418  
misc\_feature /note="assembly\_fragment"  
122519..137004  
misc\_feature /note="assembly\_fragment"  
137105..161549  
misc\_feature /note="assembly\_fragment"  
BASE COUNT 41638 a 38819 c 39363 g 39720 t 2009 others  
ORIGIN

Query Match 1.9%; Score 19; DB 64; Length 161549;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 105 cagggaagaacagcgcca 123  
|||||  
Db 28267 CAGGGAAGACAGCGCCA 28249

RESULT 45  
AC009108 AC009108 170431 bp DNA HTG 02-SEP-2000  
LOCUS Homo sapiens chromosome 16 clone RP11-46309, WORKING DRAFT  
DEFINITION  
SEQUENCE, 4 ordered pieces.  
AC009108  
AC009108.8 GI:9964740  
ACCESSION  
VERSION HTG; HTGS\_PHASE2; HTGS\_DRAFT.  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 170431)  
AUTHORS DOE Joint Genome Institute.  
TITLE Unpublished  
JOURNAL  
REFERENCE 2 (bases 1 to 170431)  
AUTHORS DOE Joint Genome Institute.  
TITLE Direct Submission  
JOURNAL  
COMMENT Submitted (03-APR-1999) Production Sequencing Facility, DOE Joint  
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
On Sep 2, 2000 this sequence version replaced gi:8575957.  
-----Genome Center  
Center: Joint Genome Institute  
Center Code: JGI  
Web Site: http://www.jgi.doe.gov  
-----  
Project Information  
Center Project Name: 584502

Center clone name: RPCI-11\_46309

-----  
Summary Statistics  
Consensus quality: 167345 bases at least Q40  
Consensus quality: 169423 bases at least Q30  
Consensus quality: 169900 bases at least Q20  
Estimated insert size: 181440; agarose-fp estimation  
Estimated insert size: 170331; sum-of-contigs estimation  
Quality coverage: 10.63 in Q20 bases; agarose-fp estimation  
Quality coverage: 11.33 in Q20 bases; sum-of-contigs estimation.  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 4 contigs. Gaps between the contigs  
\* are represented as runs of N. The order of the pieces  
\* is believed to be correct as given, however the sizes  
\* of the gaps between them are based on estimates that have  
\* provided by the submittor.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.  
\* 1 24820: contig of 24820 bp in length  
\* 24821 24920: gap of unknown length  
\* 24921 37862: contig of 12942 bp in length  
\* 37863 37962: gap of unknown length  
\* 37963 114671: contig of 76709 bp in length  
\* 114672 114771: gap of unknown length  
\* 114772 170431: contig of 55660 bp in length.  
FEATURES  
Location/Qualifiers  
1..170431  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="16"  
/clone="RP11-46309"  
/clone\_lib="RPCI human BAC library 11"

BASE COUNT 41117 a 43130 c 42591 g 43230 t 303 others  
ORIGIN

Query Match 1.9%; Score 19; DB 61; Length 170431;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 280 gccgcgcgcgcgcgcgcgcgc 298  
|||||  
Db 21976 GCCGCGCGCGCATCGCGTG 21994

RESULT 46  
AC013343 AC013343 175249 bp DNA HTG 30-MAR-2000  
LOCUS Homo sapiens clone RP11-22B10, WORKING DRAFT SEQUENCE, 13 unordered  
DEFINITION  
pieces.  
AC013343  
AC013343.3 GI:7341972  
ACCESSION  
VERSION HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 175249)  
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,  
Baldwin,J., Barne,N., Beckert,J., Boguslavsky,L., Bouckgalter,B.,  
Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,  
Cooke,P., DeRellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,  
Ferreira,P., Fitzhugh,W., Forrest,C., Funke,R., Gage,D., Galagan,J.,  
Galagan,V., Gardyna,S., Grant,G., Hagos,B., Heath,A., Horton,L.,  
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,  
Lehoczky,J., Liu,C., Locke,K., Macdonald,P., Marquis,N.,  
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrum,J.,  
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,





Insert size: 178051; sum-of-contigs  
 Insert size: 150047; 16.7% error; agarose-fp  
 Quality coverage: 5.40x in Q20 bases; sum-of-contigs Quality  
 coverage: 6.47x in Q20 bases; agarose-fp

\* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 8 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

1 2302: contig of 2302 bp in length  
 \* 2303 2402: gap of 100 bp  
 \* 2403 28561: contig of 26159 bp in length  
 \* 28562 28661: gap of 100 bp  
 \* 28662 31199: contig of 2538 bp in length  
 \* 31200 31299: gap of 100 bp  
 \* 31300 33428: contig of 2129 bp in length  
 \* 33429 33528: gap of 100 bp  
 \* 33529 41182: contig of 7654 bp in length  
 \* 41183 41282: gap of 100 bp  
 \* 41283 98057: contig of 56775 bp in length  
 \* 98058 98157: gap of 100 bp  
 \* 98158 104236: contig of 6079 bp in length  
 \* 104237 104336: gap of 100 bp  
 \* 104337 178751: contig of 74415 bp in length.  
 Location/Qualifiers  
 1. 178751  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /chromosome="10"  
 /clone\_id="RP11-47B24"  
 /clone\_id="RP11-11.1"  
 1. 2302  
 /note="assembly\_fragment:02043  
 fragment\_chain:1"  
 2403. 28561  
 /note="assembly\_fragment:00161  
 fragment\_chain:1"  
 28662. 31199  
 /note="assembly\_fragment:02019  
 fragment\_chain:1"  
 31300. 33428  
 /note="assembly\_fragment:01183"  
 33529. 41182  
 /note="assembly\_fragment:01813"  
 41283. 98057  
 /note="assembly\_fragment:01877"  
 98158. 104236  
 /note="assembly\_fragment:02146"  
 104337. 178751  
 /note="assembly\_fragment:02387"  
 700 others

BASE COUNT 53832 a 34081 c 34654 g 55484 t 700 others  
 ORIGIN

Query Match 1.9% Score 19; DB 80; Length 178751;  
 Best Local Similarity 100.0%; Pred. No. 32;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 807 acagatcacagactgcag 825  
 ||||||||||||||||  
 Db 96823 ACAGATCACAGCTGCAG 96841

RESULT 48  
 LOCUS AP002501/c  
 DEFINITION Homo sapiens chromosome 18 clone RP11-680K13 map 18q12, WORKING  
 DRAFT SEQUENCE, 26 unordered pieces.  
 ACCESSION AP002501

VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens

REFERENCE  
 1 (bases 1 to 179844)  
 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,  
 Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.  
 Homo sapiens 179,844 genomic DNA of 18q12  
 Published only in Database (2000) In press

REFERENCE  
 2 (bases 1 to 179844)  
 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,  
 Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.  
 Direct Submission  
 Submitted (09-JUN-2000) Masahira Hattori, The Institute of Physical  
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
 Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,  
 Japan (E-mail:hattori@gsr.riken.go.jp,  
 URL:http://bgp.gsc.riken.go.jp/, Tel:81-42-778-9923,  
 Fax:81-42-778-9924)

TITLE  
 JOURNAL  
 COMMENT

# COMMENT

Center: RIKEN Genomic Sciences Center(GSC)  
 Center code: RIKEN  
 Web site: http://bgp.gsc.riken.go.jp/  
 Contact: hattori@gsr.riken.go.jp  
 Project Information  
 Center project name: HumDraf18  
 Center clone name: RP11-680K13  
 Summary Statistics

Sequencing vector: PCR products; 100% of reads  
 Chemistry: Dye-terminator ET-amersham; 100% of reads  
 Assembly program: Phrap; version 0.990329  
 Consensus quality: 15359 bases at least Q40  
 Consensus quality: 16513 bases at least Q30  
 Consensus quality: 173786 bases at least Q20  
 Insert size: 177344; sum-of-contigs  
 Quality coverage: 4.16x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of  
 26 contigs. The true order of the pieces is not known and their  
 order in this sequence record is arbitrary. Gaps between the  
 contigs are represented as runs N, but the exact sizes of the gaps  
 are unknown. This record will be updated with the finished sequence  
 as soon as it is available and the accession number will be  
 preserved

1 18894 contig of 18894 bp in length  
 19995 39625 contig of 19631 bp in length  
 39726 54530 contig of 14805 bp in length  
 54631 68239 contig of 13609 bp in length  
 68340 78114 contig of 9775 bp in length  
 78215 89873 contig of 11659 bp in length  
 89974 99848 contig of 9875 bp in length  
 99949 109211 contig of 9283 bp in length  
 109312 116907 contig of 7566 bp in length  
 117008 121661 contig of 4654 bp in length  
 121762 128613 contig of 6852 bp in length  
 128714 132862 contig of 4149 bp in length  
 132963 137321 contig of 4359 bp in length  
 137422 142209 contig of 4788 bp in length  
 142310 146753 contig of 4444 bp in length  
 146854 152208 contig of 5355 bp in length  
 152309 158467 contig of 6139 bp in length  
 158568 162342 contig of 3975 bp in length  
 162643 165710 contig of 3068 bp in length  
 165811 168812 contig of 3002 bp in length  
 168913 170572 contig of 1660 bp in length  
 170673 172454 contig of 1782 bp in length  
 172555 175531 contig of 2977 bp in length  
 175632 177476 contig of 1845 bp in length  
 177577 178671 contig of 1095 bp in length  
 178772 179844 contig of 1073 bp in length.

\* NOTE: This is a 'working draft' sequence. It currently

\* consists of 26 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

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1 19894: contig of 19894 bp in length
19895 19994: gap of 100 bp
19995 39625: contig of 19631 bp in length
39626 39725: gap of 100 bp
39726 54530: contig of 14805 bp in length
54531 54630: gap of 100 bp
54631 68239: contig of 13609 bp in length
68240 68339: gap of 100 bp
68340 78114: contig of 9775 bp in length
78115 78214: gap of 100 bp
78215 89873: contig of 11659 bp in length
89874 89973: gap of 100 bp
89974 99848: contig of 9875 bp in length
99849 99948: gap of 100 bp
99949 109211: contig of 9263 bp in length
109212 109311: gap of 100 bp
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121662 121761: gap of 100 bp
121762 128613: contig of 6852 bp in length
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132863 132962: gap of 100 bp
132963 137321: contig of 4359 bp in length
137322 137421: gap of 100 bp
137422 142209: contig of 4788 bp in length
142210 142309: gap of 100 bp
142310 146753: contig of 4444 bp in length
146754 146853: gap of 100 bp
146854 152208: contig of 5355 bp in length
152209 152308: gap of 100 bp
152309 158467: contig of 6159 bp in length
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162543 162642: gap of 100 bp
162643 165710: contig of 3068 bp in length
165711 165810: gap of 100 bp
165811 168812: contig of 3002 bp in length
168813 168912: gap of 100 bp
168913 170572: contig of 1660 bp in length
170573 170672: gap of 100 bp
170673 172454: contig of 1782 bp in length
172455 172554: gap of 100 bp
172555 175531: contig of 2977 bp in length
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177477 177576: gap of 100 bp
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Best Local Similarity 100.0%; Pred. No. 32;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 99697 CCTGTTCAGCCAGCC 99679

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RESULT 49
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DEFINITION Homo sapiens chromosome 17 clone RP11-651B2 map 17, WORKING DRAFT
ACCESSION AC068169
VERSION AC068169.3 GI:1136767
KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 180717)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens chromosome 17, clone RP11-651B2
JOURNAL Unpublished

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REFERENCE  
AUTHORS

2 (bases 1 to 180717)  
 Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavsky, L., Bonkhgalter, B., Brown, A., Burkett, G., Campiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearlano, K., Dewar, K., Diaz, J., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Galan, J., Gardyna, S., Ginde, S., Goeyre, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heatford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karas, A., Klein, J., Laroque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGuck, A., McKernan, K., McPheeters, R., Meldrum, J., Meneus, L., Mihova, T., Miranda, C., Mianga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, T.M., Oliver, T., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Strange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Testave, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission  
 Submitted (29-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Nov 10, 2000 this sequence version replaced gi:8389515.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WtBR  
 Web site: <http://www-seq.wi.mit.edu>  
 Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

Project Information  
 Center project name: L10237  
 Center clone name: 651\_B-2

----- Summary Statistics -----  
 Sequencing vector: M13, M7815; 43% of reads  
 Sequencing vector: Plasmid; n/a; 57% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.960731  
 Consensus quality: 173839 bases at least Q40  
 Consensus quality: 177110 bases at least Q30  
 Consensus quality: 178528 bases at least Q20  
 Insert size: 179000; agarose-fp  
 Insert size: 179317; sum-of-ctnigs  
 Quality coverage: 8.5 in Q20 b.  
 Quality coverage: 8.5 in Q20 b.  
 NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 15 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
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 2309 3715: contig of 1407 bp in length  
 3716 3815: gap of 100 bp  
 3816 5977: contig of 2162 bp in length  
 5978 6077: gap of 100 bp  
 6078 57570: contig of 51493 bp in length  
 57571 57670: gap of 100 bp  
 57671 60754: contig of 3084 bp in length  
 60755 60854: gap of 100 bp  
 60855 65276: contig of 4422 bp in length  
 65277 65376: gap of 100 bp  
 65377 71222: contig of 5846 bp in length  
 71223 71322: gap of 100 bp

71323 81741: contig of 10419 bp in length  
 \* 81742 81841: gap of 100 bp  
 \* 81842 91954: contig of 10113 bp in length  
 \* 91955 92054: gap of 100 bp  
 \* 92055 104839: contig of 12785 bp in length  
 \* 104840 104939: gap of 100 bp  
 \* 104940 125196: contig of 20257 bp in length  
 \* 125197 125296: gap of 100 bp  
 \* 125297 149973: contig of 24677 bp in length  
 \* 149974 150073: gap of 100 bp  
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 Best Local Similarity 100.0%: Pred. No. 32;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 105 cagggaagacagcagca 123  
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 Db 132375 CAGGGAAGACAGCAGCA 132357

RESULT 50  
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 LOCUS Homo sapiens chromosome 1 clone RP11-153J19 map 1, \*\*\* SEQUENCING  
 DEFINITION IN PROGRESS \*\*\*, 55 unordered pieces.

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VERSION AC024507.2 GI:7249351  
KEYWORDS HTG; HTGS\_PHASE1.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 181853)  
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.  
TITLE Homo sapiens chromosome 1, clone RP11-153J19  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 181853)  
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,  
Anderson,S., Baldwin,J., Barna,N., Beda,N., Boguslavsky,L.,  
Bouhagalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,  
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Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Ollivar,T.M.,  
Peterson,K., Pierre,N., Pisanl,C., Pollara,V., Raymond,C.,  
Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S.,  
Severy,P., Spencer,B., Strange-Thomann,N., Stojanovic,N.,  
Subramanian,A., Talamas,J., Testaye,S., Theodore,J., Titrill,A.,  
Travers,M., Triggillo,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B.,  
Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and  
Zody,M.  
Direct Submission  
Submitted (28-FEB-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Mar 16, 2000 this sequence version replaced gi:1108503.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996.1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html  
----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
----- Project Information  
Center project name: L7202  
Center clone name: 153\_J19  
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\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 55 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
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\* 1225: contig of 1225 bp in length  
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\* 3639 3738: gap of 100 bp  
\* 3739 4871: contig of 1133 bp in length  
\* 4872 4971: gap of 100 bp  
\* 4972 6453: contig of 1482 bp in length  
\* 6454 6553: gap of 100 bp  
\* 6554 7651: contig of 1036 bp in length  
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\* 8918 9017: gap of 100 bp  
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\* 17151 17250: gap of 100 bp  
\* 17251 18421: contig of 1171 bp in length  
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\* 18522 20045: contig of 1524 bp in length  
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\* 23170 23269: gap of 100 bp  
\* 23270 24275: contig of 1006 bp in length  
\* 24276 24375: gap of 100 bp  
\* 24376 25509: contig of 1134 bp in length  
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\* 25610 26831: contig of 1222 bp in length  
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\* 30717 32613: contig of 1897 bp in length  
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\* 32714 33958: contig of 1245 bp in length  
\* 33959 34058: gap of 100 bp  
\* 34059 35732: contig of 1674 bp in length  
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\* 60436 64090: contig of 3655 bp in length  
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\* 64191 67400: contig of 3210 bp in length  
\* 67401 67500: gap of 100 bp  
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\* 83837 83936: gap of 100 bp  
\* 83937 89561: contig of 5625 bp in length  
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| * | 113309 | 114008: | gap of    | 100   | bp           |
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| * | 126129 | 132814: | contig of | 6686  | bp in length |
| * | 132815 | 132914: | gap of    | 100   | bp           |
| * | 132915 | 139664: | contig of | 6750  | bp in length |
| * | 139665 | 139764: | gap of    | 100   | bp           |
| * | 139765 | 149445: | contig of | 9731  | bp in length |
| * | 149446 | 149595: | gap of    | 100   | bp           |
| * | 149596 | 157948: | contig of | 8353  | bp in length |
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## FEATURES

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| Best Local Similarity | 100.0%;         | Pred. NO. 32; |           |                |
| Matches 19;           | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0;        |

QY 484 ttggtgcagctaatagtg 502  
|||||  
Db 142035 TTGCTGGCAGCTAATAGTG 142053

Search completed: September 21, 2001, 21:50:28  
Job time: 28248 sec

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**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 21, 2001, 16:24:34 ; Search time 646.95 seconds  
(without alignments)  
947.263 Million cell updates/sec

Title: US-09-138-735-1\_COPY\_1232\_2207

Perfect score: 976  
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Scoring table:  
Gapop 60.0 , Gapext 60.0

Searched: 730101 seqs, 313950809 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

N\_Geneseq\_0601:\*

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22: /cgnl\_9/gcgdata/geneseq/geneseqn/NA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Length | ID    | Description                      |
|------------|-------|--------------|-------|----------------------------------|
| 1          | 976   | 100.0        | 3402  | 20 AAX84092 T. cruzi pTc40 cod   |
| 2          | 874   | 89.5         | 3402  | 17 AAT27310 Trypanosoma cruzi    |
| 3          | 22    | 2.3          | 22    | 17 AAT27313 T. cruzi eplmastiigo |
| 4          | 22    | 2.3          | 22    | 20 AAX84095 PCR primer for T.    |
| 5          | 21    | 2.2          | 21    | 17 AAT27314 T. cruzi eplmastiigo |
| 6          | 21    | 2.2          | 21    | 17 AAT27315 T. cruzi eplmastiigo |
| 7          | 21    | 2.2          | 21    | 20 AAX84096 PCR primer for T.    |
| 8          | 21    | 2.2          | 21    | 20 AAX84097 PCR primer for T.    |
| 9          | 19    | 1.9          | 11878 | 19 AAV30199 Protein kinase cat   |
| 10         | 19    | 1.9          | 11883 | 19 AAV30198 Protein kinase cat   |
| 11         | 18    | 1.8          | 17    | 17 AAT27312 T. cruzi eplmastiigo |

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|----|----|-----|--------|---------------------------------|
| 12 | 18 | 1.8 | 18     | 20 AAX84094                     |
| 13 | 18 | 1.8 | 454    | 21 AAF09309 Fusarium venenatum  |
| 14 | 18 | 1.8 | 479    | 21 AAC04783 Human secreted pro  |
| 15 | 18 | 1.8 | 486    | 21 AAC36458 Arabidopsis thalia  |
| 16 | 18 | 1.8 | 634    | 21 AAC31869 Arabidopsis thalia  |
| 17 | 18 | 1.8 | 866    | 20 AAX39943 Gastric cancer ass  |
| 18 | 18 | 1.8 | 1302   | 21 AAC41168 Arabidopsis thalia  |
| 19 | 18 | 1.8 | 970    | 21 AAC59435 Human secreted pro  |
| 20 | 18 | 1.8 | 2520   | 15 AA077884 Neural thread prot  |
| 21 | 18 | 1.8 | 2520   | 17 AAT27766 AD 16c human neu    |
| 22 | 18 | 1.8 | 68750  | 21 AAZ35887 Sorangium cellulos  |
| 23 | 18 | 1.8 | 71989  | 21 AAA29349 Sorangium cellulos  |
| 24 | 17 | 1.7 | 198    | 20 AAX84320 Stealth virus nucl  |
| 25 | 17 | 1.7 | 334    | 13 AA026088 MFG-2. Mammalian.   |
| 26 | 17 | 1.7 | 353    | 21 AAC09227 Human secreted pro  |
| 27 | 17 | 1.7 | 364    | 21 AAC00184 Human secreted pro  |
| 28 | 17 | 1.7 | 386    | 21 AAC01025 Human secreted pro  |
| 29 | 17 | 1.7 | 513    | 21 AAC38084 Arabidopsis thalia  |
| 30 | 17 | 1.7 | 552    | 21 AAC93440 Human secreted pro  |
| 31 | 17 | 1.7 | 662    | 21 AAF13645 Aspergillus oryzae  |
| 32 | 17 | 1.7 | 673    | 19 AAV16884 Human prostate can  |
| 33 | 17 | 1.7 | 673    | 20 AAX26019 Prostate disease m  |
| 34 | 17 | 1.7 | 673    | 21 AAZ87504 Prostate, breast a  |
| 35 | 17 | 1.7 | 697    | 20 AAZ33534 Human prostate can  |
| 36 | 17 | 1.7 | 763    | 21 AAC39218 Arabidopsis thalia  |
| 37 | 17 | 1.7 | 800    | 21 AAC99839 Human secreted pro  |
| 38 | 17 | 1.7 | 1148   | 21 AAC42507 Arabidopsis thalia  |
| 39 | 17 | 1.7 | 1273   | 21 AAC49884 Arabidopsis thalia  |
| 40 | 17 | 1.7 | 1277   | 21 AAC37359 Arabidopsis thalia  |
| 41 | 17 | 1.7 | 1338   | 19 AAV64526 M. tuberculosis im  |
| 42 | 17 | 1.7 | 1338   | 19 AAV44417 Mycobacterium tube  |
| 43 | 17 | 1.7 | 1338   | 20 AAZ19327 M. tuberculosis an  |
| 44 | 17 | 1.7 | 1338   | 20 AAZ19115 M. tuberculosis re  |
| 45 | 17 | 1.7 | 1470   | 21 AAC78035 Human cancer assoc  |
| 46 | 17 | 1.7 | 1647   | 21 AAC79935 Human secreted pro  |
| 47 | 17 | 1.7 | 1949   | 21 AAA26361 Human secreted pro  |
| 48 | 17 | 1.7 | 2457   | 22 AAA91185 zea mays ZmDIN3-2   |
| 49 | 17 | 1.7 | 2545   | 20 AAX14998 DNA encoding a cyc  |
| 50 | 17 | 1.7 | 2545   | 21 AAX74878 Human chemokine co  |
| 51 | 17 | 1.7 | 3337   | 17 AAT34620 P. vivax ESP-1 blo  |
| 52 | 17 | 1.7 | 3337   | 20 AAX15174 DNA encoding a sec  |
| 53 | 17 | 1.7 | 6171   | 21 AAC74895 Human ORFX ORF450   |
| 54 | 17 | 1.7 | 11212  | 21 AAX58762 DNA encoding a cyc  |
| 55 | 17 | 1.7 | 11672  | 21 AAD01009 Escherichia coli p  |
| 56 | 17 | 1.7 | 15611  | 21 AAD01008 Escherichia coli p  |
| 57 | 17 | 1.7 | 240825 | 12 AAF24497 Human PG-3 gene.    |
| 58 | 16 | 1.6 | 31     | 14 AAO26748 Proctase-A gene pr  |
| 59 | 16 | 1.6 | 41     | 15 AAO36842 Adaptor-primer. S   |
| 60 | 16 | 1.6 | 222    | 14 AAO73710 Retrotransposon pr  |
| 61 | 16 | 1.6 | 334    | 20 AAX25170 HIV-1 group O isol  |
| 62 | 16 | 1.6 | 369    | 21 AAC03019 Human secreted pro  |
| 63 | 16 | 1.6 | 371    | 20 AAX21399 3' Fragment of Abs  |
| 64 | 16 | 1.6 | 398    | 16 AACC01286 Human secreted pro |
| 65 | 16 | 1.6 | 413    | 21 AAX79394 Eucalyptus grandis  |
| 66 | 16 | 1.6 | 549    | 21 AAC01726 Human secreted pro  |
| 67 | 16 | 1.6 | 541    | 19 AAT76907 S. glaucusens Hst   |
| 68 | 16 | 1.6 | 598    | 21 AAA50408 Human increased in  |
| 69 | 16 | 1.6 | 624    | 18 AAT84039 DNA encoding a Sta  |
| 70 | 16 | 1.6 | 651    | 16 AAV15445 Human gene fragmen  |
| 71 | 16 | 1.6 | 717    | 21 AAA61659 cDNA encoding mous  |
| 72 | 16 | 1.6 | 720    | 22 AAF71218 Corynebacterium gl  |
| 73 | 16 | 1.6 | 774    | 19 AAV28667 Ripening banana pu  |
| 74 | 16 | 1.6 | 774    | 20 AA215622 Human gene express  |
| 75 | 16 | 1.6 | 865    | 21 AAZ98109 Human signal pepti  |
| 76 | 16 | 1.6 | 898    | 21 AAC99832 Human secreted pro  |
| 77 | 16 | 1.6 | 928    | 20 AAX61395 DNA encoding a hum  |
| 78 | 16 | 1.6 | 1046   | 21 AAC36246 Arabidopsis thalia  |
| 79 | 16 | 1.6 | 1049   | 21 AAC49065 Arabidopsis thalia  |
| 80 | 16 | 1.6 | 1185   | 19 AAV05039 Alcaligenes eutrop  |
| 81 | 16 | 1.6 | 1185   | 20 AAZ08784 A. eutrophus beta-  |
| 82 | 16 | 1.6 | 1185   | 21 AAA71692 A. eutrophus bktB   |
| 83 | 16 | 1.6 | 1234   | 21 AAC53983 Arabidopsis thalia  |
| 84 | 16 | 1.6 | 1314   | 19 AAV00732 Aspergillus terreu  |

PCR primer for T.  
Fusarium venenatum  
Human secreted pro  
Arabidopsis thalia  
Arabidopsis thalia  
Gastric cancer ass  
Arabidopsis thalia  
Human secreted pro  
Neural thread prot  
AD 16c human neu  
Sorangium cellulos  
Sorangium cellulos  
Stealth virus nucl  
MFG-2. Mammalian.  
Human secreted pro  
Human secreted pro  
Human secreted pro  
Arabidopsis thalia  
Human secreted pro  
Aspergillus oryzae  
Human prostate can  
Prostate disease m  
Prostate, breast a  
Human prostate can  
Arabidopsis thalia  
Human secreted pro  
Arabidopsis thalia  
Arabidopsis thalia  
M. tuberculosis im  
Mycobacterium tube  
M. tuberculosis an  
M. tuberculosis re  
Human cancer assoc  
Human secreted pro  
Human secreted pro  
zea mays ZmDIN3-2  
DNA encoding a cyc  
DNA encoding a mon  
Human chemokine co  
P. vivax ESP-1 blo  
DNA encoding a sec  
Human ORFX ORF450  
DNA encoding a cyc  
Escherichia coli p  
Escherichia coli p  
Human PG-3 gene.  
Proctase-A gene pr  
Adaptor-primer. S  
Retrotransposon pr  
HIV-1 group O isol  
Human secreted pro  
3' Fragment of Abs  
Human secreted pro  
Eucalyptus grandis  
Human secreted pro  
S. glaucusens Hst  
Human increased in  
DNA encoding a Sta  
Human gene fragmen  
cDNA encoding mous  
Corynebacterium gl  
Ripening banana pu  
Human gene express  
Human signal pepti  
Human secreted pro  
DNA encoding a hum  
Arabidopsis thalia  
Arabidopsis thalia  
Alcaligenes eutrop  
A. eutrophus beta-  
A. eutrophus bktB  
Arabidopsis thalia  
Aspergillus terreu

|     |    |     |         |    |           |                    |       |    |     |     |    |          |                    |
|-----|----|-----|---------|----|-----------|--------------------|-------|----|-----|-----|----|----------|--------------------|
| 85  | 16 | 1.6 | 1314    | 19 | AAV09626  | A. terreus FAOD-L  | c 158 | 15 | 1.5 | 44  | 18 | AAV58825 | Glycerol DNP/DNP D |
| 86  | 16 | 1.6 | 1314    | 20 | AAZ07721  | Heat-resistant fru | c 159 | 15 | 1.5 | 81  | 16 | AAV06202 | HIV-1 reverse tran |
| 87  | 16 | 1.6 | 1411    | 14 | AAO41260  | Encodes repressor  | c 160 | 15 | 1.5 | 157 | 18 | AAV84365 | Friedreich's ataxi |
| 88  | 16 | 1.6 | 1411    | 15 | AAO72717  | Dialkylglycine dec | c 161 | 15 | 1.5 | 168 | 21 | AAV44666 | Human secreted exp |
| 89  | 16 | 1.6 | 1464    | 22 | AAV71799  | Corynebacterium g1 | c 162 | 15 | 1.5 | 196 | 21 | AAV41667 | Human secreted exp |
| 90  | 16 | 1.6 | 1580    | 20 | AAV27334  | Human secreted pro | c 163 | 15 | 1.5 | 226 | 19 | AAV15050 | Human secreted exp |
| 91  | 16 | 1.6 | 1589    | 20 | AAV25204  | Maize cinnamate-4- | c 164 | 15 | 1.5 | 295 | 16 | AAV21139 | Human gene signalu |
| 92  | 16 | 1.6 | 1685    | 21 | AAV61660  | CDNA encoding mous | c 165 | 15 | 1.5 | 297 | 21 | AAV77752 | CDNA encoding huma |
| 93  | 16 | 1.6 | 1722    | 16 | AAV00402  | Squalene epoxidase | c 166 | 15 | 1.5 | 300 | 20 | AAV14302 | Human gene express |
| 94  | 16 | 1.6 | 1734    | 17 | AAV5893   | R. capsulatus acet | c 167 | 15 | 1.5 | 300 | 20 | AAV12540 | Human gene express |
| 95  | 16 | 1.6 | 1810    | 22 | AAV54510  | Fructan exohydrola | c 168 | 15 | 1.5 | 300 | 21 | AAV00491 | Human colon cancer |
| 96  | 16 | 1.6 | 1816    | 22 | AAV72758  | Human prostate can | c 169 | 15 | 1.5 | 304 | 21 | AAV28635 | Human secreted pro |
| 97  | 16 | 1.6 | 1864    | 20 | AAZ24942  | Wild type A. eulio | c 170 | 15 | 1.5 | 325 | 20 | AAV86047 | Human secreted pro |
| 98  | 16 | 1.6 | 2040    | 21 | AAZ46364  | Haemorrhagic enter | c 171 | 15 | 1.5 | 325 | 21 | AAV06344 | Exon 1 of the huma |
| 99  | 16 | 1.6 | 2063    | 22 | AAV84244  | Signal transductio | c 172 | 15 | 1.5 | 325 | 21 | AAV06670 | Human neuropeptide |
| 100 | 16 | 1.6 | 2068    | 21 | AAV61661  | CDNA encoding mous | c 173 | 15 | 1.5 | 328 | 21 | AAV12718 | Human secreted pro |
| 101 | 16 | 1.6 | 2070    | 21 | AAV61662  | CDNA encoding mous | c 174 | 15 | 1.5 | 328 | 21 | AAV93718 | CDNA encoding pro  |
| 102 | 16 | 1.6 | 2190    | 14 | AAV37237  | gdhA gene of C.mel | c 175 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 103 | 16 | 1.6 | 2214    | 19 | AAV22682  | New DNA sequence i | c 176 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 104 | 16 | 1.6 | 2274    | 21 | AAV47059  | Zea mays DNA fragm | c 177 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 105 | 16 | 1.6 | 2310    | 20 | AAZ21502  | Saccharopolyspora  | c 178 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 106 | 16 | 1.6 | 2499    | 21 | AAV64076  | Mouse ion channel  | c 179 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 107 | 16 | 1.6 | 2535    | 21 | AAV55201  | C. symbiosum open  | c 180 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 108 | 16 | 1.6 | 2610    | 21 | AAV290578 | Human death induc  | c 181 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 109 | 16 | 1.6 | 2886    | 21 | AAV51244  | Murine TANGO 130 c | c 182 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 110 | 16 | 1.6 | 2891    | 22 | AAV71640  | Corynebacterium g1 | c 183 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 111 | 16 | 1.6 | 3045    | 20 | AAZ12185  | Neisseria meningit | c 184 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 112 | 16 | 1.6 | 3059    | 21 | AAV60191  | Neisseria gonorrh  | c 185 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 113 | 16 | 1.6 | 3059    | 21 | AAV60191  | Hydrophobic domain | c 186 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 114 | 16 | 1.6 | 3148    | 21 | AAV76239  | Human ORFX ORF1794 | c 187 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 115 | 16 | 1.6 | 3153    | 19 | AAV19895  | Glucocorticoid re  | c 188 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 116 | 16 | 1.6 | 3240    | 21 | AAZ98339  | A. thaliana gene 1 | c 189 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 117 | 16 | 1.6 | 3331    | 19 | AAV22683  | New DNA sequence i | c 190 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 118 | 16 | 1.6 | 3331    | 20 | AAZ32021  | Human METL relate  | c 191 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 119 | 16 | 1.6 | 3331    | 22 | AAV090078 | D86074 CDNA clone. | c 192 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 120 | 16 | 1.6 | 4394    | 17 | AAV09898  | Alpha-ketoglutaric | c 193 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 121 | 16 | 1.6 | 4384    | 19 | AAV13157  | B. lactoferrum     | c 194 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 122 | 16 | 1.6 | 4867    | 21 | AAV39170  | hubeP-1 CDNA. Hom  | c 195 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 123 | 16 | 1.6 | 5117    | 16 | AAV06027  | Human CDNA encodi  | c 196 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 124 | 16 | 1.6 | 6242    | 21 | AAV94945  | Maltese binding pr | c 197 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 125 | 16 | 1.6 | 6545    | 17 | AAV27537  | PDZ vector. Synt   | c 198 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 126 | 16 | 1.6 | 7323    | 20 | AAV77723  | N. meningitidis pa | c 199 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 127 | 16 | 1.6 | 9243    | 21 | AAV61534  | CDNA encoding a hu | c 200 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 128 | 16 | 1.6 | 9551    | 20 | AAV22301  | Enterococcus faeca | c 201 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 129 | 16 | 1.6 | 10391   | 20 | AAV13070  | Human low adenosi  | c 202 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 130 | 16 | 1.6 | 16310   | 21 | AAV21086  | Human adenosine re | c 203 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 131 | 16 | 1.6 | 16310   | 21 | AAV34964  | Human low adenosi  | c 204 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 132 | 16 | 1.6 | 17634   | 21 | AAV21087  | Human adenosine re | c 205 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 133 | 16 | 1.6 | 17634   | 21 | AAV34965  | Human adenosine re | c 206 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 134 | 16 | 1.6 | 17920   | 21 | AAV39168  | Erythrina carotova | c 207 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 135 | 16 | 1.6 | 21721   | 20 | AAV83427  | Human lipolysis st | c 208 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 136 | 16 | 1.6 | 22976   | 20 | AAV83426  | Genomic region con | c 209 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 137 | 16 | 1.6 | 23187   | 21 | AAV50273  | Human lipolysis st | c 210 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 138 | 16 | 1.6 | 23187   | 22 | AAV62331  | Human leptin fragm | c 211 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 139 | 16 | 1.6 | 26270   | 21 | AAV46355  | Haemorrhagic enter | c 212 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 140 | 16 | 1.6 | 35133   | 21 | AAV81518  | N. meningitidis pa | c 213 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 141 | 16 | 1.6 | 39796   | 21 | AAV61681  | Nucleotide sequenc | c 214 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 142 | 16 | 1.6 | 42432   | 21 | AAV55187  | Cenarchaeum symbio | c 215 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 143 | 16 | 1.6 | 47475   | 21 | AAV81465  | N. meningitidis pa | c 216 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 144 | 16 | 1.6 | 72928   | 20 | AAV18355  | Human ASH1J 5' ge  | c 217 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 145 | 16 | 1.6 | 72928   | 21 | AAV80253  | Human ASH1J 5' ge  | c 218 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 146 | 16 | 1.6 | 102634  | 21 | AAV81464  | N. meningitidis pa | c 219 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 147 | 16 | 1.6 | 349980  | 21 | AAV21608  | Neisseria meningit | c 220 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 148 | 16 | 1.6 | 349980  | 21 | AAV21609  | Neisseria meningit | c 221 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 149 | 16 | 1.6 | 349980  | 21 | AAV21609  | Neisseria meningit | c 222 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 150 | 16 | 1.6 | 349980  | 21 | AAV21611  | Neisseria meningit | c 223 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 151 | 16 | 1.6 | 349980  | 21 | AAV21612  | Neisseria meningit | c 224 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 152 | 16 | 1.6 | 837096  | 21 | AAV81489  | N. meningitidis pa | c 225 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 153 | 16 | 1.6 | 837096  | 21 | AAV81489  | N. meningitidis pa | c 226 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 154 | 16 | 1.6 | 1437066 | 21 | AAV81490  | N. meningitidis pa | c 227 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 155 | 15 | 1.5 | 40      | 18 | AAV14833  | PCR primer H52.16  | c 228 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 156 | 15 | 1.5 | 40      | 18 | AAV58818  | DNP Du labelled ol | c 229 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |
| 157 | 15 | 1.5 | 44      | 18 | AAV58819  | Glycerol DNP       | c 230 | 15 | 1.5 | 328 | 22 | AAV65140 | Novel human polyu  |



|       |    |     |      |    |           |                    |       |    |     |      |    |           |                     |
|-------|----|-----|------|----|-----------|--------------------|-------|----|-----|------|----|-----------|---------------------|
| 231   | 15 | 1.5 | 1005 | 21 | AA51280   | Arabidopsis thalia | 304   | 15 | 1.5 | 1608 | 14 | AA041461  | Mycobacterium para  |
| 232   | 15 | 1.5 | 1014 | 21 | AA34499   | Arabidopsis thalia | 305   | 15 | 1.5 | 1631 | 21 | AA298141  | Human signal pepti  |
| c 233 | 15 | 1.5 | 1029 | 17 | AA27218   | C protein coupled  | c 306 | 15 | 1.5 | 1632 | 14 | AA02976   | Carnitine 4-O-m     |
| 234   | 15 | 1.5 | 1065 | 21 | AA14557   | Aspergillus oryzae | c 307 | 15 | 1.5 | 1636 | 18 | AA185271  | HMG-CoA reductase   |
| c 235 | 15 | 1.5 | 1068 | 21 | AA48553   | Arabidopsis thalia | c 308 | 15 | 1.5 | 1662 | 19 | AA49559   | Human liver cell c  |
| c 236 | 15 | 1.5 | 1078 | 20 | AA408745  | Nucleotide encodin | c 309 | 15 | 1.5 | 1667 | 21 | AA251207  | Rat lost in leukae  |
| c 237 | 15 | 1.5 | 1102 | 22 | AA22274   | Human prostate can | c 310 | 15 | 1.5 | 1669 | 20 | AA424020  | Human endometrior   |
| c 238 | 15 | 1.5 | 1129 | 21 | AA54524   | Arabidopsis thalia | c 311 | 15 | 1.5 | 1704 | 19 | AA434509  | Human TNF receptor  |
| c 239 | 15 | 1.5 | 1144 | 21 | AA33490   | Arabidopsis thalia | c 312 | 15 | 1.5 | 1704 | 20 | AA483763  | Human tumour necro  |
| c 240 | 15 | 1.5 | 1152 | 21 | AA43754   | Zea mays DNA fragm | c 313 | 15 | 1.5 | 1704 | 21 | AA428135  | Human TR2 receptor  |
| c 241 | 15 | 1.5 | 1159 | 21 | AA47857   | Human cancer assoc | c 314 | 15 | 1.5 | 1707 | 22 | AA472809  | Secreted protein g  |
| c 242 | 15 | 1.5 | 1189 | 21 | AA47514   | Fusarium venenatum | c 315 | 15 | 1.5 | 1715 | 16 | AA404588  | Rat Vh-1 CDNA. R    |
| c 243 | 15 | 1.5 | 1200 | 22 | AA471690  | Corynebacterium g1 | c 316 | 15 | 1.5 | 1738 | 21 | AA251206  | Rat lost in leukae  |
| c 244 | 15 | 1.5 | 1208 | 21 | AA48562   | Arabidopsis thalia | c 317 | 15 | 1.5 | 1739 | 21 | AA453432  | Human endometrior   |
| c 245 | 15 | 1.5 | 1211 | 21 | AA41977   | Arabidopsis thalia | c 318 | 15 | 1.5 | 1765 | 20 | AA206232  | Arabidopsis thalia  |
| c 246 | 15 | 1.5 | 1213 | 21 | AA40267   | Arabidopsis thalia | c 319 | 15 | 1.5 | 1777 | 20 | AA206232  | Human secreted pro  |
| c 247 | 15 | 1.5 | 1221 | 21 | AA497139  | Human gene 75 DNA  | c 320 | 15 | 1.5 | 1777 | 20 | AA493368  | S. lividans protea  |
| c 248 | 15 | 1.5 | 1223 | 21 | AA499054  | Human pancreatic c | c 321 | 15 | 1.5 | 1779 | 21 | AA484067  | Clone PB-2 encodin  |
| c 249 | 15 | 1.5 | 1242 | 21 | AA453434  | Arabidopsis thalia | c 322 | 15 | 1.5 | 1779 | 20 | AA4212073 | Neisseria meningit  |
| c 250 | 15 | 1.5 | 1249 | 19 | AA438987  | CDNA encoding a hu | c 323 | 15 | 1.5 | 1779 | 20 | AA4212074 | Neisseria meningit  |
| c 251 | 15 | 1.5 | 1249 | 19 | AA438987  | CDNA encoding a hu | c 324 | 15 | 1.5 | 1779 | 20 | AA4212075 | Neisseria gonorrh   |
| c 252 | 15 | 1.5 | 1263 | 21 | AA458814  | DNA encoding a hum | c 325 | 15 | 1.5 | 1779 | 20 | AA4212075 | Neisseria gonorrh   |
| c 253 | 15 | 1.5 | 1265 | 21 | AA42091   | Plant retroelement | c 326 | 15 | 1.5 | 1779 | 21 | AA453673  | Neisseria meningit  |
| c 254 | 15 | 1.5 | 1268 | 21 | AA451410  | Arabidopsis thalia | c 327 | 15 | 1.5 | 1779 | 21 | AA453675  | Neisseria meningit  |
| c 255 | 15 | 1.5 | 1275 | 21 | AA460190  | A. thaliana Vb33 c | c 328 | 15 | 1.5 | 1780 | 21 | AA465335  | Human secreted pro  |
| c 256 | 15 | 1.5 | 1275 | 22 | AA47608   | Mevlonate pathway  | c 329 | 15 | 1.5 | 1788 | 22 | AA432651  | Human CDNA encodin  |
| c 257 | 15 | 1.5 | 1278 | 20 | AA490824  | DNA encoding human | c 330 | 15 | 1.5 | 1827 | 21 | AA459692  | Novel human protei  |
| c 258 | 15 | 1.5 | 1281 | 20 | AA415146  | Coding region for  | c 331 | 15 | 1.5 | 1831 | 20 | AA426880  | DNA encoding a pro  |
| c 259 | 15 | 1.5 | 1287 | 22 | AA467832  | Corynebacterium g1 | c 332 | 15 | 1.5 | 1831 | 21 | AA409889  | Human OCTN2 CDNA s  |
| c 260 | 15 | 1.5 | 1290 | 19 | AA459676  | Human secreted pro | c 333 | 15 | 1.5 | 1855 | 22 | AA430190  | Clone 116966905-0-4 |
| c 261 | 15 | 1.5 | 1294 | 20 | AA427438  | Human secreted pro | c 334 | 15 | 1.5 | 1858 | 20 | AA485599  | DNA encoding a hum  |
| c 262 | 15 | 1.5 | 1294 | 21 | AA413611  | Aspergillus oryzae | c 335 | 15 | 1.5 | 1862 | 22 | AA402606  | Human angiotensin   |
| c 263 | 15 | 1.5 | 1313 | 16 | AA091637  | Mouse sonic hedgeh | c 336 | 15 | 1.5 | 1863 | 21 | AA428268  | Yeast essential ge  |
| c 264 | 15 | 1.5 | 1313 | 20 | AA425620  | Mouse sonic hedgeh | c 337 | 15 | 1.5 | 1869 | 20 | AA433970  | Human TIE ligand N  |
| c 265 | 15 | 1.5 | 1313 | 20 | AA425101  | Mouse sonic hedgeh | c 338 | 15 | 1.5 | 1869 | 21 | AA460537  | Human TIE ligand N  |
| c 266 | 15 | 1.5 | 1313 | 20 | AA407274  | Mouse sonic hedgeh | c 339 | 15 | 1.5 | 1869 | 21 | AA4250126 | Maize MLO3 CDNA.    |
| c 267 | 15 | 1.5 | 1313 | 20 | AA416185  | Mouse Shh hedgehog | c 340 | 15 | 1.5 | 1869 | 22 | AA497388  | Human angiogenesis  |
| c 268 | 15 | 1.5 | 1313 | 21 | AA450449  | Mouse sonic hedgeh | c 341 | 15 | 1.5 | 1873 | 22 | AA472220  | Human neovasculari  |
| c 269 | 15 | 1.5 | 1313 | 21 | AA427879  | Mouse sonic hedgeh | c 342 | 15 | 1.5 | 1876 | 12 | AA014498  | Clone 1 for trunca  |
| c 270 | 15 | 1.5 | 1313 | 21 | AA430277  | Partial mouse Shh  | c 343 | 15 | 1.5 | 1876 | 12 | AA014499  | Clone 2 for trunca  |
| c 271 | 15 | 1.5 | 1313 | 21 | AA452260  | Mouse sonic hedgeh | c 344 | 15 | 1.5 | 1876 | 20 | AA415144  | CDNA encoding huma  |
| c 272 | 15 | 1.5 | 1313 | 22 | AA480707  | Nucleotide sequenc | c 345 | 15 | 1.5 | 1879 | 21 | AA4245850 | Human muscle angio  |
| c 273 | 15 | 1.5 | 1313 | 22 | AA427016  | Mouse sonic hedgeh | c 346 | 15 | 1.5 | 1879 | 22 | AA429701  | Human angiotensin   |
| c 274 | 15 | 1.5 | 1314 | 22 | AA437897  | Mouse sonic hedgeh | c 347 | 15 | 1.5 | 1888 | 19 | AA495558  | Human liver cell c  |
| c 275 | 15 | 1.5 | 1330 | 21 | AA454055  | Arabidopsis thalia | c 348 | 15 | 1.5 | 1894 | 20 | AA487858  | Human fibrinogen d  |
| c 276 | 15 | 1.5 | 1340 | 21 | AA426964  | Human coenzyme A-u | c 349 | 15 | 1.5 | 1899 | 21 | AA4259302 | Insulin-like growt  |
| c 277 | 15 | 1.5 | 1359 | 19 | AA441924  | Nucleotide sequenc | c 350 | 15 | 1.5 | 1911 | 21 | AA422396  | Human secreted pro  |
| c 278 | 15 | 1.5 | 1362 | 21 | AA450399  | Human angiotensin  | c 351 | 15 | 1.5 | 1913 | 22 | AA4297138 | Human gene 75 DNA   |
| c 279 | 15 | 1.5 | 1362 | 21 | AA435278  | Soybean retroelme  | c 352 | 15 | 1.5 | 1921 | 22 | AA444835  | RPP5-like protein   |
| c 280 | 15 | 1.5 | 1368 | 21 | AA454153  | Arabidopsis thalia | c 353 | 15 | 1.5 | 1931 | 21 | AA4297093 | Human secreted pro  |
| c 281 | 15 | 1.5 | 1368 | 21 | AA453670  | Neisseria gonorrhe | c 354 | 15 | 1.5 | 1938 | 13 | AA022341  | Sequence encoding   |
| c 282 | 15 | 1.5 | 1368 | 21 | AA453672  | Neisseria meningit | c 355 | 15 | 1.5 | 1938 | 13 | AA022341  | Sequence encoding   |
| c 283 | 15 | 1.5 | 1368 | 22 | AA472256  | Corynebacterium g1 | c 356 | 15 | 1.5 | 1947 | 21 | AA456176  | Human adipophillin- |
| c 284 | 15 | 1.5 | 1368 | 22 | AA472257  | Corynebacterium g1 | c 357 | 15 | 1.5 | 1955 | 21 | AA4295588 | CDNA encoding a hu  |
| c 285 | 15 | 1.5 | 1374 | 21 | AA451258  | Arabidopsis thalia | c 358 | 15 | 1.5 | 1955 | 21 | AA4295588 | DNA encoding a hu   |
| c 286 | 15 | 1.5 | 1376 | 21 | AA433903  | Arabidopsis thalia | c 359 | 15 | 1.5 | 1968 | 21 | AA418104  | Lung cancer associ  |
| c 287 | 15 | 1.5 | 1376 | 22 | AA485554  | CDNA encoding CDIF | c 360 | 15 | 1.5 | 1973 | 21 | AA460998  | Human vesicle asso  |
| c 288 | 15 | 1.5 | 1379 | 21 | AA497132  | Human secreted pro | c 361 | 15 | 1.5 | 1980 | 18 | AA4759454 | H-Delta-1 contig c  |
| c 289 | 15 | 1.5 | 1381 | 20 | AA484482  | Human secreted pro | c 362 | 15 | 1.5 | 2004 | 21 | AA454137  | Arabidopsis thalia  |
| c 290 | 15 | 1.5 | 1390 | 22 | AA460982  | P. putida KT2440-a | c 363 | 15 | 1.5 | 2008 | 20 | AA4241299 | Human normal ovar   |
| c 291 | 15 | 1.5 | 1396 | 21 | AA463740  | Arabidopsis thalia | c 364 | 15 | 1.5 | 2044 | 17 | AA413167  | Rat interleukin-1   |
| c 292 | 15 | 1.5 | 1422 | 22 | AA460986  | P. putida KT2440-a | c 365 | 15 | 1.5 | 2051 | 18 | AA484010  | DNA encoding a sta  |
| c 293 | 15 | 1.5 | 1433 | 17 | AA439049  | CDNA encoding cell | c 366 | 15 | 1.5 | 2051 | 20 | AA484010  | Human secreted pro  |
| c 294 | 15 | 1.5 | 1437 | 20 | AA484973  | Human secreted pro | c 367 | 15 | 1.5 | 2051 | 21 | AA428059  | Heparin sulphate 6  |
| c 295 | 15 | 1.5 | 1448 | 20 | AA424009  | Human endometrium  | c 368 | 15 | 1.5 | 2084 | 21 | AA4254805 | Human HS6571 CDNA.  |
| c 296 | 15 | 1.5 | 1466 | 21 | AA438414  | Arabidopsis thalia | c 369 | 15 | 1.5 | 2093 | 21 | AA423805  | Human secreted pro  |
| c 297 | 15 | 1.5 | 1498 | 21 | AA45265   | Arabidopsis thalia | c 370 | 15 | 1.5 | 2104 | 22 | AA439969  | Human adult brain   |
| c 298 | 15 | 1.5 | 1504 | 17 | AA436177  | Murine int6 gene a | c 371 | 15 | 1.5 | 2104 | 22 | AA439969  | Nucleotide sequenc  |
| c 299 | 15 | 1.5 | 1512 | 21 | AA464513  | Nucleotide sequenc | c 372 | 15 | 1.5 | 2160 | 20 | AA486635  | Human PRO861 CDNA.  |
| c 300 | 15 | 1.5 | 1572 | 20 | AA402671  | T. versicolor lacc | c 373 | 15 | 1.5 | 2185 | 22 | AA402671  | Human PRO861 CDNA.  |
| c 301 | 15 | 1.5 | 1572 | 20 | AA402672  | DNA encoding prote | c 374 | 15 | 1.5 | 2185 | 22 | AA402671  | Human PRO861 CDNA.  |
| c 302 | 15 | 1.5 | 1591 | 16 | AA4097586 | Human ORF2605      | c 375 | 15 | 1.5 | 2187 | 21 | AA4229701 | Wild-type human c-  |
| c 303 | 15 | 1.5 | 1592 | 21 | AA4097586 | Human ORF2605      | c 376 | 15 | 1.5 | 2187 | 21 | AA4229701 | Wild-type human c-  |

|       |    |     |      |    |           |                       |       |    |     |        |    |           |                     |
|-------|----|-----|------|----|-----------|-----------------------|-------|----|-----|--------|----|-----------|---------------------|
| C 377 | 15 | 1.5 | 2200 | 22 | AAF27713  | Human transport pr    | C 450 | 15 | 1.5 | 3867   | 21 | AA293224  | Fatty acid desatur  |
| C 378 | 15 | 1.5 | 2221 | 20 | AAZ00370  | Partial nucleotide    | 451   | 15 | 1.5 | 3981   | 19 | AAV40381  | Strawberry structu  |
| C 379 | 15 | 1.5 | 2249 | 21 | AA377055  | Human PRO1374 (UNQ    | 452   | 15 | 1.5 | 4030   | 20 | AA231717  | Human patched-2 co  |
| C 380 | 15 | 1.5 | 2249 | 22 | AAF54285  | DNA encoding prote    | 453   | 15 | 1.5 | 4066   | 19 | AAV69921  | Expression vector   |
| C 381 | 15 | 1.5 | 2263 | 20 | AAV80628  | Kidney injury asso    | 454   | 15 | 1.5 | 4201   | 21 | AACT8084  | Human cancer assoc  |
| C 382 | 15 | 1.5 | 2271 | 11 | AAQ06844  | Amylase gene from     | 455   | 15 | 1.5 | 4263   | 20 | AAV72672  | Hamster 3' DNA seq  |
| C 383 | 15 | 1.5 | 2276 | 18 | AAI86161  | PHA depolymerase g    | 456   | 15 | 1.5 | 4263   | 21 | AAAI3431  | cDNA encoding mur   |
| C 384 | 15 | 1.5 | 2288 | 21 | AAZ97061  | Human secreted pro    | 457   | 15 | 1.5 | 4263   | 21 | AAAI3379  | Mouse MT5-MMP mat   |
| C 385 | 15 | 1.5 | 2291 | 9  | AAAB0309  | Entire amyLase gen    | 458   | 15 | 1.5 | 4296   | 20 | AAZ23436  | Rat TMO2 kinase en  |
| C 386 | 15 | 1.5 | 2311 | 9  | AAFI8225  | Lung cancer associ    | 459   | 15 | 1.5 | 4751   | 20 | AAZ09496  | Human heart tissue  |
| C 387 | 15 | 1.5 | 2315 | 21 | AAC90027  | Clone HPRCD20 codi    | 460   | 15 | 1.5 | 4879   | 18 | AAV74400  | Staphylococcus aur  |
| C 388 | 15 | 1.5 | 2324 | 21 | AAAI5288  | cDNA encoding prot    | 461   | 15 | 1.5 | 4880   | 14 | AAQ36660  | Sequence of the po  |
| C 389 | 15 | 1.5 | 2332 | 21 | AAV72398  | Human nucleic acid    | 462   | 15 | 1.5 | 4984   | 19 | AAV18986  | Polyhydroxyalkanoa  |
| C 390 | 15 | 1.5 | 2339 | 22 | AAE92112  | Human PRO1753 cDNA    | 463   | 15 | 1.5 | 5162   | 19 | AAV69919  | Expression vector   |
| C 391 | 15 | 1.5 | 2420 | 21 | AAZ46489  | PKA substrate, Csk    | 464   | 15 | 1.5 | 5162   | 19 | AAV69922  | Mutagenic plasmid   |
| C 392 | 15 | 1.5 | 2501 | 21 | AAAS2499  | 2.5 kb human MN ge    | 465   | 15 | 1.5 | 5262   | 19 | AAV69927  | Promoter probe vec  |
| C 393 | 15 | 1.5 | 2501 | 21 | AAAI6580  | MN genomic region     | 466   | 15 | 1.5 | 5342   | 21 | AAAD0374  | Rat smooth muscle-  |
| C 394 | 15 | 1.5 | 2507 | 21 | AAZ52365  | NSBQ gene-17 assoc    | 467   | 15 | 1.5 | 5375   | 22 | AAAC62160 | Nucleotide sequenc  |
| C 395 | 15 | 1.5 | 2510 | 20 | AAZ41256  | Human normal ovari    | 468   | 15 | 1.5 | 5531   | 20 | AAQ96274  | Human tumour supp   |
| C 396 | 15 | 1.5 | 2517 | 20 | AAZ33560  | Human breast tumou    | 469   | 15 | 1.5 | 5531   | 20 | AACT7588  | Human ORFX ORF143   |
| C 397 | 15 | 1.5 | 2524 | 21 | AACT7206  | Human ORFX ORF2761    | 470   | 15 | 1.5 | 6570   | 20 | AAZ20540  | Poly nucleotide seq |
| C 398 | 15 | 1.5 | 2526 | 20 | AAQ06819  | Chlamydia pneumoni    | 471   | 15 | 1.5 | 6850   | 19 | AAV69920  | Expression vector   |
| C 399 | 15 | 1.5 | 2526 | 21 | AAAS28691 | C. pneumoniae CPN1    | 472   | 15 | 1.5 | 7989   | 21 | AAV98968  | Hepatitis C virus   |
| C 400 | 15 | 1.5 | 2538 | 21 | AAAS5217  | C. symbiosum open     | 473   | 15 | 1.5 | 8001   | 21 | AAV98967  | Hepatitis C virus   |
| C 401 | 15 | 1.5 | 2551 | 9  | AAAB1251  | Bio F, Bio C and B    | 474   | 15 | 1.5 | 8528   | 14 | AAQ46249  | Construct ECL2 (Co  |
| C 402 | 15 | 1.5 | 2623 | 21 | AACT7596  | Human ORFX ORF151     | 475   | 15 | 1.5 | 8637   | 21 | AAV98966  | Hepatitis C virus   |
| C 403 | 15 | 1.5 | 2635 | 20 | AAV84521  | Human secreted pro    | 476   | 15 | 1.5 | 8649   | 21 | AAV98969  | Hepatitis C virus   |
| C 404 | 15 | 1.5 | 2646 | 16 | AAAT02405 | Rice mature pullul    | 477   | 15 | 1.5 | 8906   | 16 | AAAT85392 | Human TRIO phospho  |
| C 405 | 15 | 1.5 | 2649 | 20 | AAV37749  | Rat HNK-1 cDNA. R     | 478   | 15 | 1.5 | 9558   | 18 | AAO88328  | Valencia orange ri  |
| C 406 | 15 | 1.5 | 2653 | 18 | AAAT70174 | Proliferation and     | 479   | 15 | 1.5 | 9706   | 21 | AAV65342  | NDO related comple  |
| C 407 | 15 | 1.5 | 2663 | 20 | AAAI6300  | Human delta-1 prot    | 480   | 15 | 1.5 | 9840   | 21 | AAV65340  | NDO related comple  |
| C 408 | 15 | 1.5 | 2663 | 20 | AAAI6817  | Human delta-1 gene    | 481   | 15 | 1.5 | 9994   | 22 | AAAC85191 | S. avermitilis 10   |
| C 409 | 15 | 1.5 | 2750 | 9  | AAAB28690 | C. pneumoniae CPN1    | 482   | 15 | 1.5 | 10427  | 21 | AAZ36325  | Mechanical stress   |
| C 410 | 15 | 1.5 | 2762 | 21 | AAAB0976  | Sequence of 2 cont    | 483   | 15 | 1.5 | 10897  | 17 | AAZ09187  | Mut putative onco   |
| C 411 | 15 | 1.5 | 2764 | 18 | AAAT84358 | STR7. I gene associ   | 484   | 15 | 1.5 | 10898  | 21 | AAAS2462  | Human MN complete   |
| C 412 | 15 | 1.5 | 2768 | 12 | AAAT01502 | Polyhydroxybutyrat    | 485   | 15 | 1.5 | 10898  | 21 | AAAI6543  | Hepatitis C virus   |
| C 413 | 15 | 1.5 | 2824 | 21 | AAAC5843  | Human secreted pro    | 486   | 15 | 1.5 | 11076  | 21 | AAV98965  | Hepatitis C virus   |
| C 414 | 15 | 1.5 | 2883 | 18 | AAV58898  | C-Delta-1 gene (al    | 487   | 15 | 1.5 | 11279  | 21 | AAV98389  | Pseudomonas sp. WF  |
| C 415 | 15 | 1.5 | 2933 | 21 | AAAS54105 | PRO172 cDNA. Homo     | 488   | 15 | 1.5 | 11871  | 20 | AAAI3108  | Enterococcus faeca  |
| C 416 | 15 | 1.5 | 2933 | 21 | AAAC58587 | Human PRO172 prote    | 489   | 15 | 1.5 | 12019  | 20 | AAAI8867  | Alcaligenes sp. Po  |
| C 417 | 15 | 1.5 | 2933 | 21 | AAAT77512 | Human PRO172 cDNA     | 490   | 15 | 1.5 | 12286  | 21 | AAZ35261  | Plant generic retr  |
| C 418 | 15 | 1.5 | 2933 | 21 | AAAC93703 | PRO172 DNA35916-11    | 491   | 15 | 1.5 | 12571  | 21 | AAZ35272  | Soybean retroelme   |
| C 419 | 15 | 1.5 | 2933 | 22 | AAAC97368 | Human angiogenesis    | 492   | 15 | 1.5 | 12808  | 21 | AAV65347  | NDO related comple  |
| C 420 | 15 | 1.5 | 2982 | 16 | AAAT02400 | Pullulanase expres    | 493   | 15 | 1.5 | 12886  | 21 | AAV65347  | Human patched-like  |
| C 421 | 15 | 1.5 | 2988 | 16 | AAAT02399 | Rice mature pullul    | 494   | 15 | 1.5 | 13518  | 20 | AAV20563  | Polynucleotide seq  |
| C 422 | 15 | 1.5 | 2999 | 21 | AACT78119 | Human cancer assoc    | 495   | 15 | 1.5 | 13574  | 21 | AAAB1529  | N. meningitidis pa  |
| C 423 | 15 | 1.5 | 3035 | 21 | AAAF63462 | Streptomyces globi    | 496   | 15 | 1.5 | 16020  | 21 | AAV39283  | Streptomyces nega   |
| C 424 | 15 | 1.5 | 3046 | 22 | AAAF5137  | Murine semaphorin     | 497   | 15 | 1.5 | 18436  | 19 | AAV52220  | Streptococcus pneu  |
| C 425 | 15 | 1.5 | 3046 | 22 | AAAF5140  | Murine DNA: SEQ ID    | 498   | 15 | 1.5 | 24417  | 18 | AAAT97221 | Pseudomonas aerugi  |
| C 426 | 15 | 1.5 | 3103 | 21 | AAZ50708  | Nucleotide sequenc    | 499   | 15 | 1.5 | 25871  | 21 | AAV09888  | Human genomic OCTN  |
| C 427 | 15 | 1.5 | 3105 | 18 | AAV74840  | Staphylococcus aur    | 500   | 15 | 1.5 | 26281  | 21 | AAZ60929  | Nucleotide sequenc  |
| C 428 | 15 | 1.5 | 3105 | 18 | AAV94468  | Human FcHd540 gene    | 501   | 15 | 1.5 | 26778  | 21 | AAAB1477  | N. meningitidis pa  |
| C 429 | 15 | 1.5 | 3111 | 22 | AAZ66660  | Human Smd7 nucleo     | 502   | 15 | 1.5 | 32998  | 21 | AAAS5186  | Cenarchaesus symbi  |
| C 430 | 15 | 1.5 | 3141 | 14 | AAQ49903  | Nicotiana tabacum     | 503   | 15 | 1.5 | 36519  | 19 | AAV22141  | Chimpanzee adenovi  |
| C 431 | 15 | 1.5 | 3153 | 19 | AAV18895  | Glucocorticoid gene   | 504   | 15 | 1.5 | 37544  | 21 | AAV50029  | Cosmid cHR15 enco   |
| C 432 | 15 | 1.5 | 3162 | 21 | AAZ98679  | Human delta protei    | 505   | 15 | 1.5 | 42000  | 21 | AAV65349  | Streptomyces globi  |
| C 433 | 15 | 1.5 | 3218 | 22 | AAAF63440 | Human ADAMTS-7 CDN    | 506   | 15 | 1.5 | 44576  | 21 | AAZ62572  | L5 mycobacterioph   |
| C 434 | 15 | 1.5 | 3284 | 20 | AAV02677  | T. versicolor lacc    | 507   | 15 | 1.5 | 50341  | 19 | AAV22674  | Nucleotide sequenc  |
| C 435 | 15 | 1.5 | 3300 | 18 | AAAT62589 | Thermotoga neopoli    | 508   | 15 | 1.5 | 50341  | 21 | AAZ39519  | Streptomyces globi  |
| C 436 | 15 | 1.5 | 3309 | 21 | AAAF21886 | Human breast and o    | 509   | 15 | 1.5 | 50937  | 21 | AAV09469  | WFS1 variant genom  |
| C 437 | 15 | 1.5 | 3337 | 10 | AAAN91089 | Fragment of Pseudo    | 510   | 15 | 1.5 | 52297  | 16 | AAAT51411 | N. meningitidis pa  |
| C 438 | 15 | 1.5 | 3435 | 8  | AAAT70434 | Sequence of S.11v1    | 511   | 15 | 1.5 | 52298  | 14 | AAQ47357  | Genomic fragment #  |
| C 439 | 15 | 1.5 | 3435 | 14 | AAQ48429  | Streptomyces lividi   | 512   | 15 | 1.5 | 58857  | 21 | AAV58471  | BAC containing rep  |
| C 440 | 15 | 1.5 | 3517 | 17 | AAAT31287 | S. lividans gal op    | 513   | 15 | 1.5 | 63164  | 21 | AAAF63348 | Neisseria meningit  |
| C 441 | 15 | 1.5 | 3517 | 17 | AAAT31287 | Rabbit poly-immuno    | 514   | 15 | 1.5 | 67212  | 21 | AAV08954  | Hereditary haemoch  |
| C 442 | 15 | 1.5 | 3532 | 21 | AAAS2530  | Human MN 5' UTR fr    | 515   | 15 | 1.5 | 78845  | 21 | AAV08954  | Hereditary haemoch  |
| C 443 | 15 | 1.5 | 3532 | 21 | AAAI6611  | Human hippocampal     | 516   | 15 | 1.5 | 98629  | 22 | AAV28550  | Neisseria meningit  |
| C 444 | 15 | 1.5 | 3550 | 20 | AAV99701  | Human promoter region | 517   | 15 | 1.5 | 109973 | 21 | AAV22298  | Neisseria meningit  |
| C 445 | 15 | 1.5 | 3550 | 20 | AAV24125  | Human hippocampal     | 518   | 15 | 1.5 | 172325 | 21 | AAV21613  | Neisseria meningit  |
| C 446 | 15 | 1.5 | 3571 | 22 | AAV99702  | Human mammary sel-    | 519   | 15 | 1.5 | 235033 | 19 | AAV57926  | Hereditary haemoch  |
| C 447 | 15 | 1.5 | 3571 | 22 | AAV24126  | Human mammary sel-    | 520   | 15 | 1.5 | 237326 | 19 | AAV57903  | Hereditary haemoch  |
| C 448 | 15 | 1.5 | 3821 | 15 | AAO56609  | Human PGE-2/NF-3 5    | 521   | 15 | 1.5 | 349980 | 21 | AAV21608  | Neisseria meningit  |
| C 449 | 15 | 1.5 | 3821 | 20 | AAV34365  | Human nerve growth    | 522   | 15 | 1.5 | 349980 | 21 | AAV21612  | Neisseria meningit  |

|     |    |     |         |     |           |                     |     |    |     |     |    |           |                    |
|-----|----|-----|---------|-----|-----------|---------------------|-----|----|-----|-----|----|-----------|--------------------|
| 523 | 15 | 1.5 | 1082138 | 21  | AAF22305  | Arabidopsis thalia  | 596 | 14 | 1.4 | 246 | 21 | AAC09887  | Human secreted pro |
| 524 | 15 | 1.5 | 1230025 | 20  | AA9X1990  | Nucleotide sequenc  | 597 | 14 | 1.4 | 251 | 19 | AA312270  | Human biallelic po |
| 525 | 14 | 1.4 |         | 15  | AA259280  | Human NR8 gene pro  | 598 | 14 | 1.4 | 255 | 11 | AA003507  | Sequence encoding  |
| 526 | 14 | 1.4 |         | 15  | AA477941  | IGFBP3 oligonucleo  | 599 | 14 | 1.4 | 255 | 18 | AA188164  | Nucleotide sequenc |
| 527 | 14 | 1.4 |         | 15  | AA477942  | IGFBP3 oligonucleo  | 600 | 14 | 1.4 | 255 | 18 | AA188164  | Polynucleotide seq |
| 528 | 14 | 1.4 |         | 18  | AA232752  | Human protease-act  | 601 | 14 | 1.4 | 255 | 21 | AA450098  | Arabidopsis herbic |
| 529 | 14 | 1.4 |         | 20  | AA062027  | Mutant Ki-ras 5'-U  | 602 | 14 | 1.4 | 255 | 21 | AAC18419  | Human secreted pro |
| 530 | 14 | 1.4 |         | 20  | AA079846  | Ki-ras modulating s | 603 | 14 | 1.4 | 263 | 21 | AAC15554  | Human secreted pro |
| 531 | 14 | 1.4 |         | 20  | AA096704  | PCR primer used to  | 604 | 14 | 1.4 | 265 | 21 | AA475473  | Partial cDNA seque |
| 532 | 14 | 1.4 |         | 20  | AA056986  | Ras gene modulator  | 605 | 14 | 1.4 | 265 | 21 | AAC31308  | Human secreted pro |
| 533 | 14 | 1.4 |         | 20  | AA021622  | Human Ki-ras speci  | 606 | 14 | 1.4 | 268 | 21 | AAC02717  | Human secreted pro |
| 534 | 14 | 1.4 |         | 20  | AA084026  | Antisense oligonuc  | 607 | 14 | 1.4 | 269 | 21 | AAC17678  | Human secreted pro |
| 535 | 14 | 1.4 |         | 20  | AA058606  | Human Ki-ras antis  | 608 | 14 | 1.4 | 270 | 18 | AA678889  | Human secreted pro |
| 536 | 14 | 1.4 |         | 21  | AA090193  | Human biallelic po  | 609 | 14 | 1.4 | 270 | 18 | AAC74427  | H. pylori cytoplas |
| 537 | 14 | 1.4 |         | 21  | AA064537  | PCR primer G7 used  | 610 | 14 | 1.4 | 276 | 19 | AAV20119  | Human secreted pro |
| 538 | 14 | 1.4 |         | 29  | AA019247  | Integrin alpha 6 s  | 611 | 14 | 1.4 | 282 | 11 | AA003335  | Probe (20) for mic |
| 539 | 14 | 1.4 |         | 29  | AA019772  | Integrin alpha 6 s  | 612 | 14 | 1.4 | 282 | 14 | AA042653  | Fragment of post-l |
| 540 | 14 | 1.4 |         | 30  | AA087738  | Human cytochrome P  | 613 | 14 | 1.4 | 291 | 21 | AAC00592  | PT-NAB virus lamb  |
| 541 | 14 | 1.4 |         | 30  | AA048336  | Human cytochrome P  | 614 | 14 | 1.4 | 293 | 20 | AA051660  | Human secreted pro |
| 542 | 14 | 1.4 |         | 30  | AA026928  | Primer for 0.6 kb   | 615 | 14 | 1.4 | 293 | 20 | AAV87616  | Human secreted pro |
| 543 | 14 | 1.4 |         | 31  | AA017403  | Human cytochrome P  | 616 | 14 | 1.4 | 294 | 21 | AAC05481  | EST clone BC259.   |
| 544 | 14 | 1.4 |         | 31  | AA067562  | Human derived cyto  | 617 | 14 | 1.4 | 295 | 21 | AA073711  | Human secreted pro |
| 545 | 14 | 1.4 |         | 32  | AA059008  | Nucleotide fragmen  | 618 | 14 | 1.4 | 295 | 15 | AA073711  | Retrolansposon pro |
| 546 | 14 | 1.4 |         | 37  | AA033355  | Mouse epididymis-s  | 619 | 14 | 1.4 | 295 | 21 | AAC06337  | Human secreted pro |
| 547 | 14 | 1.4 |         | 37  | AA033355  | Anti-IL-8 Mab 5.12  | 620 | 14 | 1.4 | 297 | 17 | AA092005  | Virulence factor s |
| 548 | 14 | 1.4 |         | 37  | AA033355  | Anti IL-8 antibody  | 621 | 14 | 1.4 | 298 | 17 | AA092007  | Human gene express |
| 549 | 14 | 1.4 |         | 37  | AA093560  | Murine Mab (5.12.1  | 622 | 14 | 1.4 | 300 | 20 | AA212673  | Human gene express |
| 550 | 14 | 1.4 |         | 37  | AA078555  | Monoclonal antibod  | 623 | 14 | 1.4 | 300 | 20 | AA212605  | Human gene express |
| 551 | 14 | 1.4 |         | 37  | AA055083  | Murine anti-IL-8 M  | 624 | 14 | 1.4 | 300 | 21 | AA001198  | Human colon cancer |
| 552 | 14 | 1.4 |         | 37  | AA010277  | Murine monoclonal   | 625 | 14 | 1.4 | 300 | 21 | AA001198  | Human colon cancer |
| 553 | 14 | 1.4 |         | 37  | AA060432  | Murine Mab (5.12.1  | 626 | 14 | 1.4 | 300 | 21 | AA001144  | Human colon cancer |
| 554 | 14 | 1.4 |         | 37  | AA090552  | Murine 5.12.14 ant  | 627 | 14 | 1.4 | 303 | 21 | AA011374  | Human colon cancer |
| 555 | 14 | 1.4 |         | 37  | AA065479  | Murine anti-IL-8 a  | 628 | 14 | 1.4 | 304 | 21 | AA018914  | Human colon cancer |
| 556 | 14 | 1.4 |         | 40  | AA0287940 | Murine anti-IL-8 a  | 629 | 14 | 1.4 | 304 | 21 | AA030331  | DNA encoding spide |
| 557 | 14 | 1.4 |         | 42  | AA005507  | Probe to N-termina  | 630 | 14 | 1.4 | 304 | 21 | AA024295  | Human secreted pro |
| 558 | 14 | 1.4 |         | 42  | AA015219  | Human fibronectin   | 631 | 14 | 1.4 | 305 | 18 | AA012653  | Human 5' EST Isola |
| 559 | 14 | 1.4 |         | 47  | AA028991  | Sequence of PCR pr  | 632 | 14 | 1.4 | 305 | 19 | AA066013  | Human XAG growth f |
| 560 | 14 | 1.4 |         | 48  | AA019184  | Human growth facto  | 633 | 14 | 1.4 | 312 | 16 | AA024501  | Human gene signatu |
| 561 | 14 | 1.4 |         | 48  | AA063329  | PCR primer specifi  | 634 | 14 | 1.4 | 312 | 16 | AA064583  | Nucleotide sequenc |
| 562 | 14 | 1.4 |         | 54  | AA026611  | Polyketide synthas  | 635 | 14 | 1.4 | 313 | 16 | AA019149  | Human gene signatu |
| 563 | 14 | 1.4 |         | 90  | AA017330  | Primer CME00972 us  | 636 | 14 | 1.4 | 314 | 21 | AAC23276  | Human secreted pro |
| 564 | 14 | 1.4 |         | 97  | AA012931  | Human secreted pro  | 637 | 14 | 1.4 | 316 | 21 | AAC00622  | Human secreted pro |
| 565 | 14 | 1.4 |         | 101 | AA002808  | Human RRAM genom    | 638 | 14 | 1.4 | 320 | 21 | AA042333  | Human 5' EST Isola |
| 566 | 14 | 1.4 |         | 108 | AA090209  | Recombinant DNA fo  | 639 | 14 | 1.4 | 322 | 21 | AAC01859  | Human secreted pro |
| 567 | 14 | 1.4 |         | 110 | AA029865  | Human secreted pro  | 640 | 14 | 1.4 | 324 | 21 | AA071620  | Human ORFX ORF51   |
| 568 | 14 | 1.4 |         | 115 | AA021334  | Human secreted pro  | 641 | 14 | 1.4 | 324 | 21 | AA071620  | N. meningitidis BA |
| 569 | 14 | 1.4 |         | 117 | AA026958  | Guinea pig PAF rec  | 642 | 14 | 1.4 | 324 | 21 | AA053434  | Neisseria meningit |
| 570 | 14 | 1.4 |         | 124 | AA021511  | Human gene signatu  | 643 | 14 | 1.4 | 326 | 22 | AA053435  | Neisseria meningit |
| 571 | 14 | 1.4 |         | 132 | AA010479  | Human biallelic po  | 644 | 14 | 1.4 | 326 | 22 | AA053435  | Human XAG growth f |
| 572 | 14 | 1.4 |         | 138 | AA032093  | Human secreted pro  | 645 | 14 | 1.4 | 328 | 21 | AA063340  | HuXAG-2 related cd |
| 573 | 14 | 1.4 |         | 153 | AA073766  | Brevibacterium fla  | 646 | 14 | 1.4 | 328 | 21 | AAC22609  | Human secreted pro |
| 574 | 14 | 1.4 |         | 153 | AA086761  | Seq ID No: 1 of JP  | 647 | 14 | 1.4 | 330 | 20 | AA089310  | EST clone CM423.   |
| 575 | 14 | 1.4 |         | 166 | AA037721  | Human PRO266 clone  | 648 | 14 | 1.4 | 331 | 20 | AA0219430 | M. tuberculosis an |
| 576 | 14 | 1.4 |         | 171 | AA042248  | Human secreted exp  | 649 | 14 | 1.4 | 332 | 21 | AA0219218 | M. tuberculosis re |
| 577 | 14 | 1.4 |         | 172 | AA031926  | Human secreted pro  | 650 | 14 | 1.4 | 332 | 21 | AA08918   | Fusarium venenatum |
| 578 | 14 | 1.4 |         | 177 | AA090208  | Staphylococcus pro  | 651 | 14 | 1.4 | 335 | 21 | AAC70608  | Single nucleotide  |
| 579 | 14 | 1.4 |         | 177 | AA011649  | FB fragment of pro  | 652 | 14 | 1.4 | 338 | 21 | AAC14174  | Human secreted pro |
| 580 | 14 | 1.4 |         | 192 | AA001767  | Binding region for  | 653 | 14 | 1.4 | 341 | 21 | AA011086  | Fusarium venenatu  |
| 581 | 14 | 1.4 |         | 202 | AA042960  | Human secreted exp  | 654 | 14 | 1.4 | 343 | 20 | AA028036  | Partial sequence o |
| 582 | 14 | 1.4 |         | 209 | AA051708  | Human colon cancer  | 655 | 14 | 1.4 | 346 | 21 | AAC15981  | Human secreted pro |
| 583 | 14 | 1.4 |         | 213 | AA051795  | Human secreted pro  | 656 | 14 | 1.4 | 348 | 13 | AA028981  | Sequence encoding  |
| 584 | 14 | 1.4 |         | 215 | AA010349  | Encodes Immunoglob  | 657 | 14 | 1.4 | 353 | 20 | AA066600  | EST clone BE101.   |
| 585 | 14 | 1.4 |         | 216 | AA051573  | Human secreted pro  | 658 | 14 | 1.4 | 353 | 22 | AAC75340  | Human ORFX ORF95   |
| 586 | 14 | 1.4 |         | 218 | AA076820  | Human genome fragm  | 659 | 14 | 1.4 | 354 | 22 | AA066171  | Novel human polyu  |
| 587 | 14 | 1.4 |         | 218 | AA067074  | Eucalyptus grandis  | 660 | 14 | 1.4 | 357 | 13 | AA028982  | Sequence encoding  |
| 588 | 14 | 1.4 |         | 220 | AA041733  | Human secreted exp  | 661 | 14 | 1.4 | 357 | 21 | AAC06032  | Human secreted pro |
| 589 | 14 | 1.4 |         | 227 | AA090320  | Human secreted exp  | 662 | 14 | 1.4 | 357 | 21 | AAC09562  | Human secreted pro |
| 590 | 14 | 1.4 |         | 227 | AA090320  | EST clone DK230.    | 663 | 14 | 1.4 | 360 | 18 | AAV17306  | Humanised antibody |
| 591 | 14 | 1.4 |         | 228 | AA015874  | DNA encoding VEGF-  | 664 | 14 | 1.4 | 360 | 18 | AAV17307  | Humanised antibody |
| 592 | 14 | 1.4 |         | 231 | AA008265  | Human secreted pro  | 665 | 14 | 1.4 | 360 | 18 | AAV17308  | Humanised antibody |
| 593 | 14 | 1.4 |         | 240 | AA032414  | Human secreted pro  | 666 | 14 | 1.4 | 360 | 18 | AAV17309  | Humanised antibody |
| 594 | 14 | 1.4 |         | 242 | AA053346  | Myrtaceae microsat  | 667 | 14 | 1.4 | 360 | 18 | AAV17310  | Humanised antibody |
| 595 | 14 | 1.4 |         | 242 | AA088009  | Human T gene DNA f  | 668 | 14 | 1.4 | 360 | 18 | AAV17311  | Humanised antibody |
|     |    |     |         | 242 | AAC08117  | Human secreted pro  |     |    |     |     |    | AAV17271  | Anti-CEA antibody  |

|       |    |     |     |    |           |                    |       |    |     |     |    |           |                     |
|-------|----|-----|-----|----|-----------|--------------------|-------|----|-----|-----|----|-----------|---------------------|
| 669   | 14 | 1.4 | 363 | 21 | AAZ54189  | Neisseria meningit | c 742 | 14 | 1.4 | 446 | 21 | AAC20933  | Human secreted pro  |
| 670   | 14 | 1.4 | 363 | 21 | AAZ54190  | Neisseria meningit | 743   | 14 | 1.4 | 448 | 18 | AAZ58802  | Human telomerase R  |
| c 671 | 14 | 1.4 | 363 | 22 | AAC91755  | Human 10 kd Clara  | 744   | 14 | 1.4 | 448 | 21 | AAZ4869   | Human ORFX ORF424   |
| c 672 | 14 | 1.4 | 363 | 22 | AAC91756  | Human 10 kd Clara  | 745   | 14 | 1.4 | 448 | 21 | AAC57415  | Archidonic acid m   |
| c 673 | 14 | 1.4 | 363 | 22 | AAC91759  | Human 10 kd Clara  | c 746 | 14 | 1.4 | 448 | 21 | AAC57415  | Archidonic acid m   |
| c 674 | 14 | 1.4 | 363 | 22 | AAC91760  | Human 10 kd Clara  | c 747 | 14 | 1.4 | 448 | 21 | AAC57417  | Archidonic acid m   |
| c 675 | 14 | 1.4 | 363 | 22 | AAC91763  | Human 10 kd Clara  | c 748 | 14 | 1.4 | 448 | 21 | AAC57937  | Archidonic acid m   |
| c 676 | 14 | 1.4 | 363 | 22 | AAC91764  | Human 10 kd Clara  | c 749 | 14 | 1.4 | 449 | 20 | AAZ89588  | Archidonic acid m   |
| c 677 | 14 | 1.4 | 366 | 21 | AAC09579  | Human secreted pro | 750   | 14 | 1.4 | 451 | 19 | AAV41195  | EST clone CT729.    |
| c 678 | 14 | 1.4 | 367 | 22 | AAC91750  | Human Clara cell p | 751   | 14 | 1.4 | 452 | 21 | AAC00293  | RNA component of h  |
| c 679 | 14 | 1.4 | 369 | 13 | AAQ28983  | Sequence encoding  | 752   | 14 | 1.4 | 454 | 14 | AAQ61409  | Human secreted pro  |
| c 680 | 14 | 1.4 | 374 | 21 | AAC04098  | Human secreted pro | 753   | 14 | 1.4 | 456 | 22 | AAZ71010  | Human brain Expres  |
| c 681 | 14 | 1.4 | 375 | 21 | AAC41703  | Human secreted pro | 754   | 14 | 1.4 | 458 | 22 | AAZ71010  | C. glutamicum SRT   |
| c 682 | 14 | 1.4 | 377 | 22 | AAC91753  | Arabidopsis thalia | c 755 | 14 | 1.4 | 461 | 21 | AAC06277  | Human secreted pro  |
| c 683 | 14 | 1.4 | 377 | 22 | AAC91757  | Human 10 kd Clara  | c 756 | 14 | 1.4 | 464 | 21 | AAZ67550  | Human secreted pro  |
| c 684 | 14 | 1.4 | 377 | 22 | AAC91761  | Human 10 kd Clara  | c 757 | 14 | 1.4 | 466 | 21 | AAZ53503  | Plus radiata sur    |
| c 685 | 14 | 1.4 | 378 | 22 | AAZ4420   | Human 10 kd Clara  | c 758 | 14 | 1.4 | 466 | 22 | AAZ65887  | Zea mays DNA fragm  |
| c 686 | 14 | 1.4 | 378 | 22 | AAC91754  | Human 10 kd Clara  | c 759 | 14 | 1.4 | 468 | 21 | AAC41757  | Novel human polynu  |
| c 687 | 14 | 1.4 | 378 | 22 | AAC91758  | Human 10 kd Clara  | c 760 | 14 | 1.4 | 472 | 21 | AAC27906  | Arabidopsis thalia  |
| c 688 | 14 | 1.4 | 378 | 22 | AAC91762  | Human 10 kd Clara  | 761   | 14 | 1.4 | 473 | 21 | AAC09986  | Human secreted pro  |
| c 689 | 14 | 1.4 | 381 | 14 | AAQ60707  | Human brain Expres | c 762 | 14 | 1.4 | 475 | 21 | AAC35799  | Human secreted pro  |
| c 690 | 14 | 1.4 | 381 | 19 | AAV03584  | Neisseria meningit | c 763 | 14 | 1.4 | 475 | 21 | AAC21638  | Zea mays DNA fragm  |
| c 691 | 14 | 1.4 | 381 | 21 | AAC03400  | Human secreted pro | c 764 | 14 | 1.4 | 477 | 21 | AAC76187  | Human secreted pro  |
| c 692 | 14 | 1.4 | 384 | 22 | AAZ64565  | Novel human polynu | c 765 | 14 | 1.4 | 478 | 21 | AAC06307  | Human ORFX ORF1742  |
| c 693 | 14 | 1.4 | 385 | 18 | AAV17295  | Humanised anti-CEA | c 766 | 14 | 1.4 | 481 | 13 | AAC268307 | Human secreted pro  |
| c 694 | 14 | 1.4 | 386 | 9  | AAZ80184  | DNA encoding modif | 767   | 14 | 1.4 | 481 | 18 | AAZ75041  | Phetomone receptor  |
| c 695 | 14 | 1.4 | 386 | 9  | AAZ80184  | DNA encoding modif | c 768 | 14 | 1.4 | 483 | 19 | AAZ75041  | Staphylococcus aur  |
| c 696 | 14 | 1.4 | 387 | 9  | AAZ80192  | Human secreted pro | c 769 | 14 | 1.4 | 485 | 20 | AAZ51803  | Nucleic acid E69r   |
| c 697 | 14 | 1.4 | 391 | 22 | AAZ64566  | DNA encoding biosy | c 770 | 14 | 1.4 | 487 | 21 | AAZ45506  | Human secreted pro  |
| c 698 | 14 | 1.4 | 394 | 22 | AAZ65032  | Novel human polynu | c 771 | 14 | 1.4 | 488 | 21 | AAC39752  | Zea mays DNA fragm  |
| c 699 | 14 | 1.4 | 395 | 21 | AAC23566  | Human secreted pro | 772   | 14 | 1.4 | 489 | 20 | AAZ91716  | Potphorymonas gling |
| c 700 | 14 | 1.4 | 395 | 22 | AAC91765  | Human 10 kd Clara  | 773   | 14 | 1.4 | 490 | 21 | AAZ88251  | Human telomerase R  |
| c 701 | 14 | 1.4 | 396 | 21 | AAZ59695  | DNA encoding light | 774   | 14 | 1.4 | 491 | 14 | AAQ39688  | Expressed Sequence  |
| c 702 | 14 | 1.4 | 396 | 21 | AAC02889  | Human secreted pro | 775   | 14 | 1.4 | 491 | 14 | AAQ59100  | Human brain Expres  |
| c 703 | 14 | 1.4 | 396 | 22 | AAZ94867  | Human ovarian can  | 776   | 14 | 1.4 | 492 | 21 | AAC76066  | Human ORFX ORF1621  |
| c 704 | 14 | 1.4 | 397 | 20 | AAZ87051  | EST clone B197. H  | c 777 | 14 | 1.4 | 492 | 21 | AAZ81919  | N. meningitidis pa  |
| c 705 | 14 | 1.4 | 398 | 14 | AAQ61228  | Human brain Expres | c 778 | 14 | 1.4 | 492 | 22 | AAZ54745  | Nucleotide sequenc  |
| c 706 | 14 | 1.4 | 399 | 17 | AAZ44532  | Partial sequence o | c 779 | 14 | 1.4 | 500 | 21 | AAC40965  | Zea mays DNA fragm  |
| c 707 | 14 | 1.4 | 399 | 17 | AAZ44536  | Partial sequence o | c 780 | 14 | 1.4 | 501 | 17 | AAZ07039  | Immunogen DNA fragm |
| c 708 | 14 | 1.4 | 399 | 17 | AAZ44537  | Partial sequence o | 781   | 14 | 1.4 | 505 | 19 | AAZ19167  | Human XAS growth f  |
| c 709 | 14 | 1.4 | 399 | 17 | AAZ44539  | Partial sequence o | 782   | 14 | 1.4 | 505 | 20 | AAZ25692  | Human CAGS47 deriv  |
| c 710 | 14 | 1.4 | 400 | 10 | AAZ81652  | Fc binding region  | 783   | 14 | 1.4 | 505 | 22 | AAZ63342  | HuXAG-2 related cd  |
| c 711 | 14 | 1.4 | 400 | 18 | AAZ78295  | Staphylococcus aur | 784   | 14 | 1.4 | 507 | 20 | AAZ34575  | Corn CDC-16 cDNA c  |
| c 712 | 14 | 1.4 | 402 | 21 | AAC75003  | Human ORFX ORF558  | c 785 | 14 | 1.4 | 507 | 21 | AAC51616  | Arabidopsis thalia  |
| c 713 | 14 | 1.4 | 403 | 18 | AAZ75454  | Staphylococcus aur | c 786 | 14 | 1.4 | 508 | 21 | AAC53128  | Arabidopsis thalia  |
| c 714 | 14 | 1.4 | 403 | 22 | AAZ64800  | Novel human polynu | c 787 | 14 | 1.4 | 510 | 20 | AAZ91589  | Porphyromonas gling |
| c 715 | 14 | 1.4 | 404 | 21 | AAZ64510  | Nucleotide sequenc | c 788 | 14 | 1.4 | 510 | 21 | AAZ63736  | DNA encoding a pol  |
| c 716 | 14 | 1.4 | 405 | 20 | AAZ01709  | Human anti-angioge | 789   | 14 | 1.4 | 512 | 21 | AAZ52491  | Human MN gene intr  |
| c 717 | 14 | 1.4 | 406 | 21 | AAC04333  | Human secreted pro | 790   | 14 | 1.4 | 512 | 21 | AAZ16572  | Human MN intron 7   |
| c 718 | 14 | 1.4 | 407 | 14 | AAZ059351 | Human brain Expres | 791   | 14 | 1.4 | 513 | 17 | AAZ42239  | HIV-1 group O stra  |
| c 719 | 14 | 1.4 | 408 | 20 | AAZ90910  | Nucleotide sequenc | 792   | 14 | 1.4 | 513 | 21 | AAZ07693  | Fusarium venenatum  |
| c 720 | 14 | 1.4 | 408 | 20 | AAZ90625  | Nucleotide sequenc | c 793 | 14 | 1.4 | 513 | 21 | AAZ40819  | Clone HP01766 enco  |
| c 721 | 14 | 1.4 | 409 | 21 | AAC74651  | Human ORFX ORF206  | 794   | 14 | 1.4 | 516 | 20 | AAZ28678  | Arabidopsis thalia  |
| c 722 | 14 | 1.4 | 409 | 22 | AAZ67423  | Novel human polynu | 795   | 14 | 1.4 | 516 | 22 | AAZ45139  | Murine TANGO 273 O  |
| c 723 | 14 | 1.4 | 412 | 19 | AAZ28851  | Targeting vector T | c 796 | 14 | 1.4 | 518 | 21 | AAZ14892  | Trichoderma reesei  |
| c 724 | 14 | 1.4 | 412 | 21 | AAZ09592  | Fusarium venenatum | c 797 | 14 | 1.4 | 520 | 22 | AAZ91014  | Human secreted pro  |
| c 725 | 14 | 1.4 | 418 | 18 | AAZ84976  | Mouse GDNFR alpha  | c 798 | 14 | 1.4 | 522 | 20 | AAZ26098  | S. aureus phosphor  |
| c 726 | 14 | 1.4 | 418 | 21 | AAZ45297  | Human secreted exp | c 799 | 14 | 1.4 | 522 | 21 | AAZ50476  | L. esculentum MAP   |
| c 727 | 14 | 1.4 | 420 | 21 | AAZ26848  | Human secreted pro | c 800 | 14 | 1.4 | 522 | 22 | AAZ85479  | Korean mistletoe 1  |
| c 728 | 14 | 1.4 | 421 | 14 | AAZ38597  | Human glucose regu | 801   | 14 | 1.4 | 523 | 21 | AAZ34976  | Mouse F1222 (inhib  |
| c 729 | 14 | 1.4 | 421 | 20 | AAZ83882  | EST clone DD285.   | c 802 | 14 | 1.4 | 524 | 21 | AAZ15310  | Trichoderma reesei  |
| c 730 | 14 | 1.4 | 421 | 21 | AAC76624  | Human ORFX ORF2179 | c 803 | 14 | 1.4 | 525 | 20 | AAZ26097  | S. aureus phosphor  |
| c 731 | 14 | 1.4 | 427 | 22 | AAZ68261  | Human lung tumour  | c 804 | 14 | 1.4 | 525 | 21 | AAZ11017  | Fusarium venenatum  |
| c 732 | 14 | 1.4 | 433 | 21 | AAZ18019  | Lung cancer associ | c 805 | 14 | 1.4 | 526 | 22 | AAZ85555  | CDNA encoding CD1E  |
| c 733 | 14 | 1.4 | 433 | 21 | AAZ65825  | E. coli prolifera  | c 806 | 14 | 1.4 | 527 | 22 | AAZ44783  | Testis Enhanced Ge  |
| c 734 | 14 | 1.4 | 435 | 11 | AAZ05642  | Clone hp33 encodin | c 807 | 14 | 1.4 | 528 | 21 | AAZ50579  | Human epidermal pr  |
| c 735 | 14 | 1.4 | 436 | 20 | AAZ9723   | EST clone CT738.   | c 808 | 14 | 1.4 | 528 | 21 | AAZ45623  | DNA encoding a mar  |
| c 736 | 14 | 1.4 | 438 | 21 | AAZ48195  | Arabidopsis thalia | 809   | 14 | 1.4 | 534 | 14 | AAZ45088  | Human glucokinase   |
| c 737 | 14 | 1.4 | 438 | 21 | AAZ66074  | E. coli prolifera  | c 810 | 14 | 1.4 | 534 | 21 | AAZ41505  | Arabidopsis thalia  |
| c 738 | 14 | 1.4 | 441 | 21 | AAZ67106  | Eucalyptus grandis | c 811 | 14 | 1.4 | 535 | 19 | AAZ22070  | DNA encoding a Krl  |
| c 739 | 14 | 1.4 | 441 | 21 | AAZ04165  | Human secreted pro | c 812 | 14 | 1.4 | 535 | 21 | AAZ90474  | White shrimp multi  |
| c 740 | 14 | 1.4 | 443 | 21 | AAC56803  | Eucalyptus grandis | c 813 | 14 | 1.4 | 536 | 19 | AAZ22071  | DNA encoding a Krl  |
| c 741 | 14 | 1.4 | 444 | 21 | AAZ08190  | Human telomerase R | 814   | 14 | 1.4 | 536 | 21 | AAZ56058  | Eucalyptus grandis  |

|       |    |     |    |           |                      |       |    |     |     |    |           |                      |
|-------|----|-----|----|-----------|----------------------|-------|----|-----|-----|----|-----------|----------------------|
| C 815 | 14 | 536 | 21 | AAA90471  | White shrimp multi   | 888   | 14 | 1.4 | 665 | 21 | AAC03822  | Human secreted pro   |
| C 816 | 14 | 538 | 19 | AAV13839  | Homo sapiens telom   | C 889 | 14 | 1.4 | 670 | 22 | AAFC3410  | Human SDC1 DNA seq   |
| C 817 | 14 | 538 | 19 | AAV16093  | Human telomerase p   | C 890 | 14 | 1.4 | 672 | 21 | AAC34816  | Arabidopsis thaliana |
| C 818 | 14 | 540 | 19 | AAV13833  | Homo sapiens telom   | C 891 | 14 | 1.4 | 673 | 21 | AAA02035  | Human colon cancer   |
| C 819 | 14 | 540 | 19 | AAV13838  | Homo sapiens telom   | C 892 | 14 | 1.4 | 674 | 21 | AAAF12652 | Aspergillus oryzae   |
| C 820 | 14 | 540 | 19 | AAV13837  | Homo sapiens telom   | C 893 | 14 | 1.4 | 676 | 21 | AAAF12612 | Aspergillus oryzae   |
| C 821 | 14 | 540 | 19 | AAV05373  | Human telomerase p   | C 894 | 14 | 1.4 | 680 | 18 | AAAF58803 | Aspergillus oryzae   |
| C 822 | 14 | 540 | 19 | AAV05374  | Human telomerase p   | C 895 | 14 | 1.4 | 683 | 21 | AAAF31147 | Human telomerase e   |
| C 823 | 14 | 540 | 19 | AAV16092  | Human telomerase p   | C 896 | 14 | 1.4 | 689 | 21 | AAAF13926 | Aspergillus oryzae   |
| C 824 | 14 | 545 | 21 | AAAF09347 | Fusarium venenatum   | C 897 | 14 | 1.4 | 689 | 20 | AAAX56152 | Human alpha-7 nicot  |
| C 825 | 14 | 549 | 16 | AAO84578  | Pseudomonas aerugi   | C 898 | 14 | 1.4 | 689 | 20 | AAAX22265 | Human secreted pro   |
| C 826 | 14 | 549 | 21 | AAA45041  | Mouse secreted exp   | C 899 | 14 | 1.4 | 695 | 21 | AAAC81731 | Human secreted pro   |
| C 827 | 14 | 550 | 21 | AAAC93988 | Cat flea hindgut a   | C 900 | 14 | 1.4 | 700 | 20 | AAAZ42018 | Human endometrium    |
| C 828 | 14 | 552 | 21 | AAAF14939 | trichoderma reesei   | C 901 | 14 | 1.4 | 703 | 20 | AAAV84514 | Human secreted pro   |
| C 829 | 14 | 556 | 21 | AAAA1937  | Human secreted exp   | C 902 | 14 | 1.4 | 705 | 21 | AAAC51968 | Arabidopsis thaliana |
| C 830 | 14 | 559 | 17 | AAAT10282 | RNA component of h   | C 903 | 14 | 1.4 | 705 | 21 | AAAF10094 | Yeast codon-biased   |
| C 831 | 14 | 559 | 17 | AAAT11031 | Human telomerase R   | C 904 | 14 | 1.4 | 705 | 22 | AAAF59010 | Mouse epididymis-5   |
| C 832 | 14 | 566 | 21 | AAAO8340  | Human cancer assoc   | C 905 | 14 | 1.4 | 710 | 21 | AAAC44000 | Arabidopsis thaliana |
| C 833 | 14 | 567 | 20 | AAAX89539 | Human Dnp composi    | C 906 | 14 | 1.4 | 714 | 16 | AAAO76262 | PNA lectin, Arabid   |
| C 834 | 14 | 568 | 21 | AAAF16436 | Human prostate can   | C 907 | 14 | 1.4 | 718 | 21 | AAAF14570 | Aspergillus oryzae   |
| C 835 | 14 | 572 | 21 | AAAF08337 | Fusarium venenatum   | C 908 | 14 | 1.4 | 719 | 20 | AAAX39664 | Renal cancer assoc   |
| C 836 | 14 | 573 | 21 | AAAF08372 | Fusarium venenatum   | C 909 | 14 | 1.4 | 722 | 22 | AAAF26777 | Human gastric can    |
| C 837 | 14 | 574 | 20 | AAV90119  | EST clone DG82. H    | C 910 | 14 | 1.4 | 723 | 21 | AAZ97462  | Human prostate can   |
| C 838 | 14 | 575 | 21 | AAAC78221 | Human cancer assoc   | C 911 | 14 | 1.4 | 727 | 19 | AAVA42211 | Nucleotide sequen    |
| C 839 | 14 | 579 | 20 | AAAX01708 | Human anti-angioge   | C 912 | 14 | 1.4 | 735 | 21 | AAAO02383 | Human colon cancer   |
| C 840 | 14 | 591 | 20 | AAZ12127  | Neisseria gonorrhoe  | C 913 | 14 | 1.4 | 735 | 21 | AAAO02383 | Human colon cancer   |
| C 841 | 14 | 591 | 21 | AAZ54405  | Neisseria gonorrhoe  | C 914 | 14 | 1.4 | 738 | 21 | AAAF26406 | Pseudomonas sp hea   |
| C 842 | 14 | 593 | 21 | AAAF09085 | Fusarium venenatum   | C 915 | 14 | 1.4 | 743 | 21 | AAAC56031 | Eucaalyptus grandis  |
| C 843 | 14 | 597 | 21 | AAAF16408 | Fusarium venenatum   | C 916 | 14 | 1.4 | 743 | 21 | AAAC38823 | Arabidopsis thaliana |
| C 844 | 14 | 597 | 21 | AAAC77643 | Human prostate can   | C 917 | 14 | 1.4 | 744 | 21 | AAAZ97461 | Human prostate can   |
| C 845 | 14 | 597 | 21 | AAA30451  | Human cancer assoc   | C 918 | 14 | 1.4 | 746 | 21 | AAAC43849 | Arabidopsis thaliana |
| C 846 | 14 | 597 | 21 | AAA15654  | Human brain cDNA c   | C 919 | 14 | 1.4 | 750 | 21 | AAZ55507  | Canine mature Flt    |
| C 847 | 14 | 599 | 17 | AAAT08608 | HIV p24 G1 fragme    | C 919 | 14 | 1.4 | 750 | 21 | AAZ55508  | Canine mature Flt    |
| C 848 | 14 | 599 | 19 | AAV23065  | Protoplasmic membr   | C 920 | 14 | 1.4 | 755 | 21 | AAAC43985 | Canine mature Flt    |
| C 849 | 14 | 599 | 21 | AAA90470  | DNA encoding a kri   | C 921 | 14 | 1.4 | 755 | 21 | AAAC3985  | Arabidopsis thaliana |
| C 850 | 14 | 600 | 21 | AAAC46771 | White shrimp multi   | C 922 | 14 | 1.4 | 756 | 19 | AAV35555  | Human tumour anti    |
| C 851 | 14 | 600 | 18 | AAAC30888 | Streptococcus thalia | C 923 | 14 | 1.4 | 757 | 21 | AAAC43961 | Arabidopsis thaliana |
| C 852 | 14 | 608 | 21 | AAAC49033 | Streptococcus pneu   | C 924 | 14 | 1.4 | 759 | 20 | AAAX96929 | Human validated ce   |
| C 853 | 14 | 611 | 21 | AAAF07754 | Arabidopsis thalia   | C 925 | 14 | 1.4 | 762 | 22 | AAAC85472 | A-chain gene isofo   |
| C 854 | 14 | 611 | 21 | AAAC35687 | Fusarium venenatum   | C 926 | 14 | 1.4 | 762 | 22 | AAAC85473 | A-chain gene isofo   |
| C 855 | 14 | 616 | 21 | AAAF09569 | Arabidopsis thalia   | C 927 | 14 | 1.4 | 765 | 18 | AAAV17299 | Humanised antibod    |
| C 856 | 14 | 619 | 21 | AAZ80495  | Fusarium venenatum   | C 928 | 14 | 1.4 | 776 | 19 | AAV23103  | CDNA encoding a h    |
| C 857 | 14 | 620 | 18 | AAAT79540 | Human colon cancer   | C 929 | 14 | 1.4 | 776 | 20 | AAAB89573 | Human apoptotis-r    |
| C 858 | 14 | 623 | 21 | AAAB87734 | Upstream DNA seque   | C 930 | 14 | 1.4 | 777 | 21 | AAAF5468  | CDNA encoding a r    |
| C 859 | 14 | 623 | 21 | AAAC33194 | Human secreted pro   | C 931 | 14 | 1.4 | 777 | 21 | AAAO08846 | Human DKK-2 DNA o    |
| C 860 | 14 | 623 | 22 | AAAF64016 | Arabidopsis thalia   | C 932 | 14 | 1.4 | 779 | 21 | AAAC99883 | Human secreted pro   |
| C 861 | 14 | 624 | 8  | AAAT71272 | CDNA encoding huma   | C 933 | 14 | 1.4 | 780 | 18 | AAV17313  | Humanised heavy ch   |
| C 862 | 14 | 624 | 21 | AAAC57319 | Sequence of adult    | C 934 | 14 | 1.4 | 780 | 22 | AAAF22462 | Human breast cance   |
| C 863 | 14 | 626 | 21 | AAAC41611 | Pinus radiata tran   | C 935 | 14 | 1.4 | 785 | 21 | AAAF15932 | Human breast cance   |
| C 864 | 14 | 629 | 21 | AAAF1568  | Arabidopsis thalia   | C 936 | 14 | 1.4 | 785 | 22 | AAAF72778 | Human prostate ca    |
| C 865 | 14 | 631 | 21 | AAAC3898  | Aspergillus oryzae   | C 937 | 14 | 1.4 | 793 | 21 | AAZ55517  | Human prostate ca    |
| C 866 | 14 | 633 | 19 | AAV23068  | Arabidopsis thalia   | C 938 | 14 | 1.4 | 794 | 21 | AAAC42255 | Arabidopsis thaliana |
| C 867 | 14 | 633 | 21 | AAA90472  | DNA encoding a kri   | C 939 | 14 | 1.4 | 795 | 21 | AAZ55522  | Arabidopsis thaliana |
| C 868 | 14 | 634 | 21 | AAAC48206 | White shrimp multi   | C 940 | 14 | 1.4 | 795 | 21 | AAZ55523  | Arabidopsis thaliana |
| C 869 | 14 | 636 | 21 | AAAF09598 | Arabidopsis thalia   | C 941 | 14 | 1.4 | 798 | 21 | AAAF15953 | Human prostate ca    |
| C 870 | 14 | 636 | 21 | AAAF65944 | Fusarium venenatum   | C 942 | 14 | 1.4 | 804 | 21 | AAA01865  | Human colon cance    |
| C 871 | 14 | 637 | 21 | AAAF12391 | E. coli proliferat   | C 943 | 14 | 1.4 | 804 | 21 | AAZ55501  | Canine mature Flt    |
| C 872 | 14 | 637 | 21 | AAAF13850 | Aspergillus oryzae   | C 944 | 14 | 1.4 | 804 | 21 | AAZ55502  | Canine mature Flt    |
| C 873 | 14 | 637 | 21 | AAAC03783 | Aspergillus oryzae   | C 945 | 14 | 1.4 | 806 | 21 | AAZ98177  | Canine mature Flt    |
| C 874 | 14 | 638 | 21 | AAAC60989 | Human secreted pro   | C 946 | 14 | 1.4 | 810 | 21 | AAAC79876 | Canine mature Flt    |
| C 875 | 14 | 640 | 22 | AAAF93990 | Human vesicle asso   | C 947 | 14 | 1.4 | 811 | 8  | AAAT70093 | Human secreted pro   |
| C 876 | 14 | 641 | 21 | AAAF15013 | Primer specific fo   | C 948 | 14 | 1.4 | 813 | 21 | AAAZ17326 | Sequence of the np   |
| C 877 | 14 | 642 | 18 | AAAT7786  | trichoderma reesei   | C 949 | 14 | 1.4 | 817 | 21 | AAZ34967  | Human gene express   |
| C 878 | 14 | 643 | 21 | AAAF14799 | CDNA encoding huma   | C 950 | 14 | 1.4 | 822 | 21 | AAZ97326  | Corn beta-carotene   |
| C 879 | 14 | 643 | 21 | AAAF0844  | Aspergillus oryzae   | C 951 | 14 | 1.4 | 825 | 21 | AAA69536  | Eucaalyptus grandis  |
| C 880 | 14 | 643 | 21 | AAAC47491 | Fusarium venenatum   | C 952 | 14 | 1.4 | 828 | 21 | AAZ55506  | Canine Flt-3 ligand  |
| C 881 | 14 | 646 | 21 | AAAC34315 | Arabidopsis thalia   | C 953 | 14 | 1.4 | 828 | 21 | AAZ55506  | Canine Flt-3 ligand  |
| C 882 | 14 | 649 | 19 | AAV12744  | REB1 transcription   | C 954 | 14 | 1.4 | 830 | 21 | AAAC76325 | Human ORFX ORF188    |
| C 883 | 14 | 655 | 21 | AAAC34197 | Arabidopsis thalia   | C 955 | 14 | 1.4 | 841 | 18 | AAAT49161 | Partial DNA clone    |
| C 884 | 14 | 655 | 21 | AAAC40068 | Arabidopsis thalia   | C 956 | 14 | 1.4 | 842 | 22 | AAAF59007 | Mouse epididymis-5   |
| C 885 | 14 | 661 | 20 | AAV88531  | EST clone H0141.     | C 957 | 14 | 1.4 | 846 | 21 | AAZ36892  | CDNA encoding an a   |
| C 886 | 14 | 661 | 21 | AAAT79401 | Eucaalyptus grandis  | C 958 | 14 | 1.4 | 849 | 21 | AAAB62041 | Hydrophobic domain   |
| C 887 | 14 | 665 | 21 | AAAT79943 | Human secreted pro   | C 959 | 14 | 1.4 | 858 | 21 | AAAC52817 | Arabidopsis thaliana |
| C 888 | 14 | 665 | 21 | AAAT79943 | Human secreted pro   | C 960 | 14 | 1.4 | 861 | 10 | AAAN91840 | Sequence encoding    |

|        |    |     |     |    |          |                      |
|--------|----|-----|-----|----|----------|----------------------|
| 961    | 1  | 1.4 | 861 | 10 | AA095097 | Gene encoding cons   |
| 962    | 1  | 1.4 | 867 | 9  | AA080177 | Encodes murine ant   |
| C 963  | 14 | 1.4 | 872 | 7  | AA060469 | OmPa-tc-met-secret   |
| C 964  | 14 | 1.4 | 873 | 21 | AA255550 | Feline Flt-3 ligand  |
| C 965  | 14 | 1.4 | 873 | 21 | AA255521 | Feline Flt-3 ligand  |
| C 966  | 14 | 1.4 | 877 | 21 | AA015250 | Trichoderma reesei   |
| C 967  | 14 | 1.4 | 882 | 21 | AA255489 | Canine Flt-3 ligand  |
| C 968  | 14 | 1.4 | 882 | 21 | AA255480 | Canine Flt-3 ligand  |
| C 969  | 14 | 1.4 | 883 | 21 | AA255442 | Pinus radiata tricin |
| C 970  | 14 | 1.4 | 886 | 22 | AAE59416 | Actinobacillus acti  |
| C 971  | 14 | 1.4 | 888 | 21 | AA070534 | Fusarium venenatum   |
| C 972  | 14 | 1.4 | 891 | 19 | AA052483 | Streptococcus pneu   |
| C 973  | 14 | 1.4 | 902 | 21 | AA043788 | Zea mays DNA fragm   |
| C 974  | 14 | 1.4 | 904 | 21 | AA097662 | Human PRO1376 CDNA   |
| C 975  | 14 | 1.4 | 912 | 22 | AA092513 | Human T2R13 nucleo   |
| C 976  | 14 | 1.4 | 918 | 18 | AA017312 | Humanised antibody   |
| C 977  | 14 | 1.4 | 918 | 21 | AA048470 | Arabidopsis thalia   |
| C 978  | 14 | 1.4 | 920 | 7  | AA060468 | OmPa-secretory, leu  |
| C 979  | 14 | 1.4 | 923 | 21 | AA038659 | Arabidopsis thalia   |
| C 980  | 14 | 1.4 | 926 | 21 | AA053418 | DNA encoding a rep   |
| C 981  | 14 | 1.4 | 927 | 18 | AA094570 | Polynucleotide seq   |
| C 982  | 14 | 1.4 | 928 | 18 | AA063666 | Braesia hsp80 gene   |
| C 983  | 14 | 1.4 | 931 | 21 | AA059123 | Human secreted pro   |
| C 984  | 14 | 1.4 | 937 | 19 | AA028651 | Human native hepat   |
| C 985  | 14 | 1.4 | 939 | 13 | AA028984 | Sequence encoding    |
| C 986  | 14 | 1.4 | 939 | 17 | AA030695 | Kaposi's sarcoma a   |
| C 987  | 14 | 1.4 | 939 | 17 | AA016811 | Kaposi's sarcoma a   |
| C 988  | 14 | 1.4 | 941 | 21 | AA261804 | CDNA encoding murti  |
| C 989  | 14 | 1.4 | 941 | 22 | AA039757 | Skin cell CDNA, SE   |
| C 990  | 14 | 1.4 | 942 | 11 | AA004736 | Multifunctional pr   |
| C 991  | 14 | 1.4 | 942 | 21 | AA065941 | Human secreted pro   |
| C 992  | 14 | 1.4 | 942 | 21 | AA255518 | Feline Flt-3 ligand  |
| C 993  | 14 | 1.4 | 942 | 21 | AA255519 | Feline Flt-3 ligand  |
| C 994  | 14 | 1.4 | 942 | 22 | AA053832 | Human secreted pro   |
| C 995  | 14 | 1.4 | 943 | 19 | AA022064 | DNA encoding a kri   |
| C 996  | 14 | 1.4 | 943 | 21 | AA022066 | DNA encoding a kri   |
| C 997  | 14 | 1.4 | 943 | 21 | AA090469 | White shrimp mult    |
| C 998  | 14 | 1.4 | 945 | 21 | AA050548 | Arabidopsis thalia   |
| C 999  | 14 | 1.4 | 946 | 20 | AA050503 | Human secreted pro   |
| C 1000 | 14 | 1.4 | 951 | 18 | AA068792 | Melanocortin-1 rec   |

## ALIGNMENTS

|          |                      |                                                              |
|----------|----------------------|--------------------------------------------------------------|
|          | RESULT               | 1                                                            |
| AAx84092 | ID                   | AAx84092 standard; cDNA; 3402 BP.                            |
| XX       | AC                   |                                                              |
| XX       | AAx84092;            |                                                              |
| XX       | 27-AUG-1999          | (first entry)                                                |
| DT       | T. cruzi             | PtC40 coding sequence.                                       |
| XX       | DE                   |                                                              |
| XX       | PtC40; Tc40;         | Infection; diagnosis; immune complex; antigenic determinant; |
| KM       | therapy; antibody;   | ds.                                                          |
| XX       | OS                   | Trypanosoma cruzi.                                           |
| XX       | MO9292867-Al.        |                                                              |
| PN       |                      |                                                              |
| XX       | 17-JUN-1999.         |                                                              |
| PD       |                      |                                                              |
| XX       | 10-DEC-1998;         | 98WO-IB01987.                                                |
| PF       |                      |                                                              |
| XX       | 10-DEC-1997;         | 97US-0988242.                                                |
| PR       |                      |                                                              |
| XX       | (INMR )              | BIO MERIEUX.                                                 |
| PA       | Jullivet M,          | Lesenechal M, Mandrand B, Paranhos-Baccala G;                |
| PI       |                      |                                                              |
| XX       | WPI; 1999-394978/33. |                                                              |
| XX       | DR                   |                                                              |

|    |                                                                           |
|----|---------------------------------------------------------------------------|
| DR | P-PSDB; AAY22124.                                                         |
| XX |                                                                           |
| PT | New Trypanosoma cruzi antigen                                             |
| XX |                                                                           |
| PS | Claim 1; Page 52-56; 65pp; English.                                       |
| XX |                                                                           |
| CC | This sequence encodes the Trypanosoma cruzi pTc40 protein of the          |
| CC | invention, and is designated Tc40. The pTc40 antigenic determinant is     |
| CC | useful as a reagent for detection and/or monitoring of Trypanosoma cruzi  |
| CC | infection from samples including blood serum or plasma, saliva, or        |
| CC | tears, by contacting with the sample and detecting an immune complex. The |
| CC | pTc40 antigenic determinant, the vector, expression cassette, cell or     |
| CC | antibody are useful for treatment or prevention (vaccine) of a            |
| CC | Trypanosoma cruzi infection in a man or animal. Current Trypanosoma cruzi |
| CC | antigens are obtained from protein fractions of the noninfectious stage   |
| CC | of the parasite, and these do not allow sufficient production of antigens |
| CC | for use in reliable serological diagnostic tests. The strain to strain    |
| CC | polymorphism reduces reliability of the tests.                            |
| XX |                                                                           |
| XQ | Sequence 3402 BP; 888 A; 821 C; 956 G; 737 T; 0 other;                    |

|                           |        |              |        |                   |
|---------------------------|--------|--------------|--------|-------------------|
| Query Match               | 100.0% | Score 976;   | DB 20; | Length 3402;      |
| Best Local Similarity     | 100.0% | Pred. No. 0; |        |                   |
| Matches 976; Conservative | 0;     | Mismatches   | 0;     | Indels 0; Gaps 0; |

[illegible]



DB 2132 ctgttctcattgcgagcttcctctctcgaacatcaagaagggtggaagcgtgtgtg 2191  
 QY 961 aacgagccattatgt 976  
 |||||||  
 DB 2192 aacgagccattatgt 2207

## RESULT 3

AAAT27313  
 ID AAT27313 standard; cDNA; 22 BP.

XX  
 AC AAT27313;

DT 26-NOV-1996 (first entry)

DE T.cruzi epimastigotic Prc100t antigen primer corresp. to bases 1266-87.

KW Antigen; Trypanosoma cruzi; epimastigote; serum; Chagas disease; probe;  
 primer; PCR; polymerase chain reaction; amplification; antibody; ss.

XX Synthetic.

OS  
 PN FR2723589-A1.

XX  
 PD 16-FEB-1996.

XX 12-AUG-1994; 94FR-0010132.

XX 12-AUG-1994; 94FR-0010132.

XX (INMR ) BIO MERIEUX.

XX Jolivet M, Lesenechal M, Paranhos-Baccala G;

XX WPI; 1996-190287/20.

XX PT New nucleic acid encoding Trypanosoma cruzi epimastigotic antigen -  
 useful for diagnosis, monitoring and therapy of Chagas disease

XX  
 XX Claim 29; Page 37; 55pp; French.

XX The primers AAT27311-5 were used to PCR amplify the sequence encoding a  
 CC novel isolated antigenic protein from Trypanosoma cruzi epimastigotes,  
 CC designated Prc100t (AAT27310). The primers, derived from the sequences  
 CC of a 594 and 1041 bp fragment of Prc100t, amplified the gene as 3  
 CC fragments. This primer corresponds to nucleotides 1266-87 of the Prc100t  
 CC sequence, derived from the 594 bp fragment. The 594 bp fragment was  
 CC isolated from a T.cruzi genomic expression library in lambda gtl1, using  
 CC a mixture of sera from patients with Chagas disease. It corresponds to  
 CC nucleotides 1232-1825 of Prc100t. The 1041 bp fragment was isolated from  
 CC a lambda gtl10 library using the 594 bp fragment as a probe. The protein,  
 CC or antibodies raised against it, can be used in the detection and  
 CC monitoring of T.cruzi infection i.e. Chagas disease.

XX  
 XX Sequence 22 BP; 3 A; 8 C; 7 G; 4 T; 0 other;

Query Match 2.3%; Score 22; DB 17; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 0.2;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 cagccgaggtagctgcgtct 56  
 |||||||

DB 1 cagccgaggtagctgcgtct 22

## RESULT 4

AAAX84095  
 ID AAX84095 standard; DNA; 22 BP.

XX  
 AC AAX84095;

XX  
 DT 27-AUG-1999 (first entry)

XX PCR primer for T. cruzi Prc40 coding sequence.  
 DE  
 XX Prc40; Tc40; infection; diagnosis; immune complex; antigenic determinant;  
 KW therapy; antibody; PCR primer; ss.

XX Synthetic.

OS Trypanosoma cruzi.

PN WO9229867-A1.

XX  
 PD 17-JUN-1999.

XX 10-DEC-1998; 98WO-IB01987.

XX 10-DEC-1997; 97US-0988242.

XX (INMR ) BIO MERIEUX.

XX Jolivet M, Lesenechal M, Mandrand B, Paranhos-Baccala G;

XX WPI; 1999-394978/33.

XX New Trypanosoma cruzi antigen

XX Disclosure; Page 21; 65pp; English.

XX This sequence is a PCR primer for DNA encoding the Trypanosoma cruzi  
 CC Prc40 protein of the invention. The Prc40 antigenic determinant is  
 CC useful as a reagent for detection and/or monitoring of Trypanosoma cruzi  
 CC infection from samples including blood serum or plasma, urine, saliva, or  
 CC tears, by contacting with the sample and detecting an immune complex. The  
 CC Prc40 antigenic determinant, the vector, expression cassette, cell or  
 CC antibody are useful for treatment or prevention (vaccine) of a  
 CC Trypanosoma cruzi infection in a man or animal. Current Trypanosoma cruzi  
 CC antigens are obtained from protein fractions of the noninfectious stage  
 CC of the parasite, and these do not allow sufficient production of antigens  
 CC for use in reliable serological diagnostic tests. The strain to strain  
 CC polymorphism reduces reliability of the tests.

XX  
 XX Sequence 22 BP; 3 A; 8 C; 7 G; 4 T; 0 other;

Query Match 2.3%; Score 22; DB 20; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 0.2;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 cagccgaggtagctgcgtct 56  
 |||||||

DB 1 cagccgaggtagctgcgtct 22

## RESULT 5

AAAT27314/C  
 ID AAT27314 standard; cDNA; 21 BP.

XX  
 AC AAT27314;

DT 26-NOV-1996 (first entry)

DE T.cruzi epimastigotic Prc100t antigen primer corresp. to bases 2187-2207.

KW Antigen; Trypanosoma cruzi; epimastigote; serum; Chagas disease; probe;  
 primer; PCR; polymerase chain reaction; amplification; antibody; ss.

XX Synthetic.

OS  
 PN FR2723589-A1.

XX  
 PD 16-FEB-1996.

XX 12-AUG-1994; 94FR-0010132.



```
PR 12-AUG-1994; 94FR-0010132.
XX
XX (INMR ) BIO MERIEUX.
XX
XX Jolivet M, Lesenechal M, Paranhos-Baccala G;
XX
XX WPI; 1996-190287/20.
XX
XX New nucleic acid encoding Trypanosoma cruzi epimastigotic antigen -
PT useful for diagnosis, monitoring and therapy of Chagas disease
XX
XX Claim 29; Page 38; 55pp; French.
XX
XX The primers AAT27311-5 were used to PCR amplify the sequence encoding a
CC novel isolated antigenic protein from Trypanosoma cruzi epimastigotes,
CC designated Prc100t (AAT27310). The primers, derived from the sequences
CC of a 594 and 1041 bp fragment of Prc100t, amplified the gene as 3
CC fragments. This primer corresponds to nucleotides 2187-2207 of the P1100t
CC sequence, derived from the 1041 bp fragment. The 594 bp fragment was
CC isolated from a T. cruzi genomic expression library in lambda gt11, using
CC a mixture of sera from patients with Chagas disease. It corresponds to
CC nucleotides 1232-1825 of Prc100t. The 1041 bp fragment was isolated from
CC a lambda gt10 library using the 594 bp fragment as a probe. The protein,
CC or antibodies raised against it, can be used in the detection and
CC monitoring of T. cruzi infection i.e. Chagas disease.
XX
XX Sequence 21 BP; 6 A; 7 C; 3 G; 5 T; 0 other;

Query Match 2.28; Score 21; DB 17; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 956 gctgtgaacgagccatcatgt 976
   |||||||
DB 21 GTGTGAACGAGCCATCATGT 1

RESULT 6
AAT27315
ID AAT27315 standard; cDNA; 21 BP.
XX
XX AAT27315;
XX
XX 26-NOV-1996 (first entry)
XX
XX T. cruzi epimastigotic Prc100t antigen primer corresp. to bases 1997-2017.
XX
XX Antigen; Trypanosoma cruzi; epimastigote; serum; Chagas disease; probe;
XX
XX Primer; PCR; polymerase chain reaction; amplification; antibody; ss.
XX
XX Synthetic.
XX
XX FR2723589-A1.
XX
XX 16-FEB-1996.
XX
XX 12-AUG-1994; 94FR-0010132.
XX
XX 12-AUG-1994; 94FR-0010132.
XX
XX (INMR ) BIO MERIEUX.
XX
XX Jolivet M, Lesenechal M, Paranhos-Baccala G;
XX
XX WPI; 1996-190287/20.
XX
XX New nucleic acid encoding Trypanosoma cruzi epimastigotic antigen -
PT useful for diagnosis, monitoring and therapy of Chagas disease
XX
XX Claim 29; Page 40; 55pp; French.
XX
XX The primers AAT27311-5 were used to PCR amplify the sequence encoding a
```

```
CC novel isolated antigenic protein from Trypanosoma cruzi epimastigotes,
CC designated Prc100t (AAT27310). The primers, derived from the sequences
CC of a 594 and 1041 bp fragment of Prc100t, amplified the gene as 3
CC fragments. This primer corresponds to nucleotides 1997-2017 of the P1100t
CC sequence, derived from the 1041 bp fragment. The 594 bp fragment was
CC isolated from a T. cruzi genomic expression library in lambda gt11, using
CC a mixture of sera from patients with Chagas disease. It corresponds to
CC nucleotides 1232-1825 of Prc100t. The 1041 bp fragment was isolated from
CC a lambda gt10 library using the 594 bp fragment as a probe. The protein,
CC or antibodies raised against it, can be used in the detection and
CC monitoring of T. cruzi infection i.e. Chagas disease.
XX
XX Sequence 21 BP; 9 A; 5 C; 4 G; 3 T; 0 other;

Query Match 2.28; Score 21; DB 17; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 766 cgaagagaccatgaacaact 786
   |||||||
DB 1 cgaagagaccatgaacaact 21

RESULT 7
AAx84096/C
ID AAx84096 standard; DNA; 21 BP.
XX
XX AAx84096;
XX
XX 27-AUG-1999 (first entry)
XX
XX PCR primer for T. cruzi Prc40 coding sequence.
XX
XX Prc40; Tc40; infection; diagnosis; immune complex; antigenic determinant;
XX
XX therapy; antibody; PCR primer; ss.
XX
XX Synthetic.
XX
XX Trypanosoma cruzi.
XX
XX WO9929867-A1.
XX
XX 17-JUN-1999.
XX
XX 10-DEC-1998; 98WO-IB01987.
XX
XX 10-DEC-1998; 98WO-IB01987.
XX
XX 10-DEC-1997; 97US-0988242.
XX
XX (INMR ) BIO MERIEUX.
XX
XX Jolivet M, Lesenechal M, Mandrand B, Paranhos-Baccala G;
XX
XX WPI; 1999-394978/33.
XX
XX New Trypanosoma cruzi antigen
XX
XX Disclosure; Page 21; 65pp; English.
XX
XX This sequence is a PCR primer for DNA encoding the Trypanosoma cruzi
XX Prc40 protein of the invention. The Prc40 antigenic determinant is
XX useful as a reagent for detection and/or monitoring of Trypanosoma cruzi
XX infection from samples including blood serum or plasma, urine, saliva, or
XX tears, by contacting with the sample and detecting an immune complex. The
XX Prc40 antigenic determinant, the vector, expression cassette, cell or
XX antibody are useful for treatment or prevention (vaccine) of a
XX Trypanosoma cruzi infection in a man or animal. Current Trypanosoma cruzi
XX antigens are obtained from protein fractions of the noninfectious stage
XX of the parasite, and these do not allow sufficient production of antigens
XX for use in reliable serological diagnostic tests. The strain to strain
XX polymorphism reduces reliability of the tests.
XX
XX Sequence 21 BP; 6 A; 7 C; 3 G; 5 T; 0 other;
```

Query Match 2.2%; Score 21; DB 20; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 0.64;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 956 gctgtgaacgagccattatgt 976  
 ||||||||||||||||||  
 DB 21 GTCGTGAACGAGCCATTATGCT 1

## RESULT 3

AAV30199  
 ID AAV30199 standard; DNA; 21 BP.

AC AAV30199;

DT 27-AUG-1999 (first entry)

DE PCR primer for T. cruzi PTC40 coding sequence.

XX PTC40; Tc40; infection; diagnosis; immune complex; antigenic determinant;  
 KW therapy; antibody; PCR primer; ss.

XX Synthetic.

OS Trypanosoma cruzi.

PN WO9229867-A1.

PD 17-JUN-1999.

PF 10-DEC-1998; 98WO-IB01987.

PR 10-DEC-1997; 97US-0988242.

PA (INMR ) BIO MERIEUX.

PI Jolivet M, Lesenechal M, Mandrand B, Paranhos-Baccala G;

DR WPI; 1999-394978/33.

PT New Trypanosoma cruzi antigen

PS Disclosure; Page 22; 65pp; English.

XX This sequence is a PCR primer for DNA encoding the Trypanosoma cruzi  
 CC PTC40 protein of the invention. The PTC40 antigenic determinant is  
 CC useful as a reagent for detection and/or monitoring of Trypanosoma cruzi  
 CC infection from samples including blood serum or plasma, urine, saliva, or  
 CC tears, by contacting with the sample and detecting an immune complex. The  
 CC PTC40 antigenic determinant, the vector, expression cassette, cell or  
 CC antibody are useful for treatment or prevention (vaccine) of a  
 CC Trypanosoma cruzi infection in a man or animal. Current Trypanosoma cruzi  
 CC antigens are obtained from protein fractions of the noninfectious stage  
 CC of the parasite, and these do not allow sufficient production of antigens  
 CC for use in reliable serological diagnostic tests. The strain to strain  
 CC polymorphism reduces reliability of the tests.

XX Sequence 21 BP; 9 A; 5 C; 4 G; 3 T; 0 other;

Query Match 2.2%; Score 21; DB 20; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 0.64;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 766 cgaagagacatgaacactt 786  
 ||||||||||||||||||  
 DB 1 cgaagagacatgaacactt 21

RESULT 9  
 ID AAV30199/c  
 XX AAV30199 standard; DNA; 11878 BP.

AC AAV30199;  
 XX 14-SEP-1998 (first entry)

DE Protein kinase catalytic subunit gene.

XX Severe combined immunodeficiency disease; SCID; horse; diagnosis;  
 KW DNA-dependent protein kinase; ds.

XX Equus caballus.

OS WO9821367-A1.

PN 22-MAY-1998.

PF 14-NOV-1997; 97WO-US21066.

PR 15-NOV-1996; 96US-0031261.

PA (TEXA ) UNIV TEXAS SYSTEM.

PI Weeks K;

DR WPI; 1998-297967/26.

XX DNA-dependent protein kinase catalytic subunit - useful for  
 PT determining equine severe combined immunodeficiency alleles

PS Disclosure; Page 70-78; 98pp; English.

XX This isolated DNA molecule encodes an equine DNA-dependent protein  
 CC kinase catalytic subunit (DNA-PKcs). A claimed method of  
 CC identifying an Arabian horse that is a carrier of equine severe  
 CC combined immunodeficiency (SCID) comprises determining whether the  
 CC horse has a mutation in a SCID determinant region of the DNA-PKcs  
 CC gene (see also AAV30196 and AAV30197). Sequence analysis of DNA-PKcs  
 CC genes from normal and SCID equine fibroblasts shows that a 5 bp  
 CC deletion is present in SCID foals at a site that corresponds to  
 CC nucleotide 9454 of the 12,381 nucleotide coding sequence of the  
 CC human transcript. This results in premature termination of the  
 CC DNA-PKcs at amino acid 3160 (see AAV56642). Oligonucleotide probes  
 CC (see AAV30194 and AAV30195) are provided that precisely span the SCID  
 CC determinant region of the DNA-PKcs gene, and which are diagnostic  
 CC for the normal and SCID alleles, respectively. Methods are also  
 CC provided for identifying for differentiating SCID homozygotes,  
 CC heterozygotes and normal horses.

XX Sequence 11878 BP; 3586 A; 2323 C; 2668 G; 3301 T; 0 other;

Query Match 1.9%; Score 19; DB 19; Length 11878;  
 Best Local Similarity 100.0%; Pred. No. 5.7;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 211 actctgcgcgcgcgcgcgc 229  
 ||||||||||||||||||  
 DB 6446 ACTTCGCGCGCTGTCGAT 6428

RESULT 10  
 ID AAV30198/c  
 XX AAV30198 standard; DNA; 11863 BP.

AC AAV30198;  
 DT 14-SEP-1998 (first entry)

XX Protein kinase catalytic subunit gene.  
 DE Severe combined immunodeficiency disease; SCID; horse; diagnosis;  
 KW DNA-dependent protein kinase; ds.  
 XX Equus caballus.

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XX      WO9821367-A1.
PN      22-MAY-1998.
XX      14-NOV-1997; 97WO-US21066.
XX      15-NOV-1996; 96US-0031261.
XX      (TEXA ) UNIV TEXAS SYSTEM.
XX      Meeks K;
XX      WPI: 1998-297967/26.
DR      P-PSDB: AAW56642.
XX      DNA-dependent protein kinase catalytic subunit - useful for
PT      determining equine severe combined immunodeficiency alleles
XX      Claim 1; Page 39-44; 98pp; English.
XX      This isolated DNA molecule encodes a DNA-dependent protein kinase
CC      catalytic subunit (DNA-PKcs, see AAW56642) found in Arabian horses.
CC      A claimed method of identifying an Arabian horse that is a carrier
CC      of equine severe combined immunodeficiency (SCID) comprises
CC      determining whether the horse has a mutation in a SCID determinant
CC      region of the DNA-PKcs gene (see also AAV30196 and AAV30197). Sequence
CC      analysis of DNA-PKcs genes from normal and SCID equine fibroblasts
CC      shows that a 5 bp deletion is present in SCID foals at a site that
CC      corresponds to nucleotide 9454 of the 12,381 nucleotide coding
CC      sequence of the human transcript. This results in premature
CC      termination of the DNA-PKsc at amino acid 3160. Oligonucleotide
CC      probes (see AAV30194 and AAV30195) are provided that precisely span the
CC      SCID determinant region of the DNA-PKcs gene, and which are
CC      diagnostic for the normal and SCID alleles, respectively. Methods
CC      are also provided for identifying for differentiating SCID
CC      homozygotes, heterozygotes and normal horses. A claimed plasmid
CC      contains the DNA-PKcs DNA and regulatory elements necessary for
CC      expression of the DNA in a recombinant cell.
XX      Sequence 11883 BP; 3588 A; 2324 C; 2669 G; 3302 T; 0 other;
SQ
Query Match      1.9%; Score 19; DB 19; Length 11883;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      211 actctgcgcgtcgtcat 229
        |||||
        6449 ACTTCTGCCGCTGCTGCAT 6431
Db
RESULT 11
AAT27312/C
ID      AAT27312 standard; cDNA: 18 BP.
XX      AAT27312;
XX      AC
XX      AT
XX      26-NOV-1996 (first entry)
XX      T.cruzi epimastigotic PTC100t antigen primer corresp. to bases 1442-59.
XX      Antigen: Trypanosoma cruzi; epimastigote; serum; Chagas disease; probe;
KW      Primer; PCR; polymerase chain reaction; amplification; antibody; ss.
XX      Synthetic.
XX      OS
XX      FR2723589-A1.
XX      PN
XX      16-FEB-1996.
XX      PD
XX      12-AUG-1994; 94FR-0010132.
XX      CC

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FR      12-AUG-1994; 94FR-0010132.
XX      PA
XX      (IMMR ) BIO MERIEUX.
XX      Jolivet M, Lesenechal M, Paranhos-Bacala G;
XX      WPI: 1996-190287/20.
XX      New nucleic acid encoding Trypanosoma cruzi epimastigotic antigen -
PT      useful for diagnosis, monitoring and therapy of Chagas disease
XX      Claim 29; Page 36; 55pp; French.
XX      The primers AAT27311-5 were used to PCR amplify the sequence encoding a
CC      novel isolated antigenic protein from Trypanosoma cruzi epimastigotes,
CC      designated PTC100t (AAT27310). The primers, derived from the sequences
CC      of a 594 and 1041 bp fragment of PTC100t, amplified the gene as 3
CC      fragments. This primer corresponds to nucleotides 1442-59 of the PTC100t
CC      sequence, derived from the 594 bp fragment. The 594 bp fragment was
CC      isolated from a T.cruzi genomic expression library in lambda gt11, using
CC      a mixture of sera from patients with Chagas disease. It corresponds to
CC      nucleotides 1232-1825 of PTC100t. The 1041 bp fragment was isolated from
CC      a lambda gt10 library using the 594 bp fragment as a probe. The protein,
CC      or antibodies raised against it, can be used in the detection and
CC      monitoring of T.cruzi infection i.e. Chagas disease.
XX      Sequence 18 BP; 5 A; 4 C; 7 G; 2 T; 0 other;
SQ
Query Match      1.8%; Score 18; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      211 actctgcgcgtcgtcga 228
        |||||
        18 ACTTCTGCCGCTGCTGCA 1
Db
RESULT 12
AAx84094/C
ID      AAx84094 standard; DNA: 18 BP.
XX      AAx84094;
XX      AC
XX      27-AUG-1999 (first entry)
XX      PCR primer for T. cruzi PTC40 coding sequence.
XX      DE
XX      PTC40; Tc40; infection; diagnosis; immune complex; antigenic determinant;
KW      therapy; antibody; PCR primer; ss.
XX      KW
XX      Synthetic.
XX      OS
XX      Trypanosoma cruzi.
XX      PN
XX      WO9929867-A1.
XX      PD
XX      17-JUN-1999.
XX      PF
XX      10-DEC-1998; 98WO-IB01987.
XX      PR
XX      10-DEC-1997; 97US-0988242.
XX      (IMMR ) BIO MERIEUX.
XX      PA
XX      Jolivet M, Lesenechal M, Mandrand B, Paranhos-Bacala G;
XX      WPI: 1999-394978/33.
XX      DR
XX      New Trypanosoma cruzi antigen
PT      Disclosure; Page 21; 65pp; English.
XX      PS
XX      This sequence is a PCR primer for DNA encoding the Trypanosoma cruzi
CC

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CC Prt40 protein of the invention. The Prt40 antigenic determinant is  
 CC useful as a reagent for detection and/or monitoring of *Trypanosoma cruzi*  
 CC infection from samples including blood serum or plasma, urine, saliva, or  
 CC tears, by contacting with the sample and detecting an immune complex. The  
 CC Prt40 antigenic determinant, the vector, expression cassette, cell or  
 CC antibody are useful for treatment or prevention (vaccine) of a  
 CC *Trypanosoma cruzi* infection in a man or animal. Current *Trypanosoma cruzi*  
 CC antigens are obtained from protein fractions of the noninfectious stage  
 CC of the parasite, and these do not allow sufficient production of antigens  
 CC for use in reliable serological diagnostic tests. The strain to strain  
 CC polymorphism reduces reliability of the tests.

XX Sequence 18 BP: 5 A; 4 C; 7 G; 2 T; 0 other;

Query Match 1.8%; Score 18; DB 20; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 22;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 211 actctcgcgcgtcgtcga 228  
 |||  
 Db 18 ACTTCTGCCGCTCTGCA 1

RESULT 13

AAFO9309 standard; cDNA; 454 BP.

AAFO9309;

13-MAR-2001 (first entry)

Fusarium venenatum EST SEQ ID NO:1832.

Multiple gene expression; filamentous fungal cell; EST;

expressed sequence tag; *Fusarium venenatum*; *Aspergillus niger*;

*Aspergillus oryzae*; *Trichoderma reesei*; identification; recombination;

culture condition; environmental stress; spore morphogenesis;

metabolic pathway engineering; catabolic pathway engineering; ss.

*Fusarium venenatum*.

WO200056762-A2.

28-SEP-2000.

22-MAR-2000; 2000WO-US07781.

22-MAR-1999; 99US-0273623.

(NOVO ) NOVO NORDISK BIOTECH INC.

(NOVO ) NOVO NORDISK AS.

Berta RM, Rey MM, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;

WPI: 2000-594572/56.

Monitoring differential expression of genes in filamentous fungal cells.

substrate of expressed sequence tags -

Claim 86; Page 1068; 3161pp; English.

XX The present invention describes a method for monitoring differential  
 CC expression of genes in a first filamentous fungal (FF) cell relative to  
 CC expression of the same genes in one or more second filamentous fungal  
 CC cells. The method uses fluorescence-labeled nucleic acids isolated from  
 CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs  
 CC are used in the methods for monitoring differential expression of genes  
 CC in a first filamentous fungal (FF) cell relative to expression of the  
 CC same genes in one or more second filamentous fungal cells. Monitoring  
 CC the global expression of genes from FF cells allows the production  
 CC potential of the microorganisms to be improved. New genes may be

CC discovered, possible functions of unknown open reading frames can be  
 CC identified and gene copy number variation and stability can be  
 CC monitored. The expression of genes can be used to study how FF cells  
 CC adapt to changes in culture conditions, environmental stress, spore  
 CC morphogenesis, recombination, metabolic or catabolic pathway  
 CC engineering. Using ESTs provides several advantages over genomic or  
 CC random cDNA clones including elimination of redundancy as one spot on an  
 CC array equals one gene or open reading frame, and organization of the  
 CC microarrays based on function of the gene products to facilitate  
 CC analysis of the results. AAF07478 to AAF11247 represents ESTs from  
 CC *Fusarium venenatum*; AAF11248 to AAF11853 represents ESTs from *Aspergillus*  
 CC *niger*; AAF11854 to AAF14878 represents ESTs from *Aspergillus oryzae*; and  
 CC AAF14879 to AAF1537 represents ESTs from *Trichoderma reesei*, which are  
 CC all specifically claimed in the present invention.

XX Sequence 454 BP: 141 A; 116 C; 89 G; 108 T; 0 other;

Query Match 1.8%; Score 18; DB 21; Length 454;  
 Best Local Similarity 100.0%; Pred. No. 20;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 gctgcgcacatccctcga 237  
 |||  
 Db 205 gctgcgcacatccctcga 222

RESULT 14

AAFO4783 standard; cDNA; 479 BP.

AAFO4783;

06-OCT-2000 (first entry)

Human secreted protein 5' EST, SEQ ID NO: 8858.

Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;

gene therapy; chromosome mapping; ss.

*Homo sapiens*.

EP1033401-A2.

06-SEP-2000.

21-FEB-2000; 2000EP-0200610.

26-FEB-1999; 99US-0122487.

(GEST ) GENSET.

Dumas Milne Edwards J, Duclert A, Giordano J;

WPI: 2000-500381/45.

New nucleic acid that is a 5' expressed sequence tag (5' EST) for

obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for

diagnostic, forensic, gene therapy and chromosome mapping procedures -

Claim 1; SEQ ID 8858; 71pp + CD-ROM; English.

XX The present sequence is one of a large number of 5' ESTs derived from  
 CC mRNAs encoding secreted proteins. No ORF has yet been conclusively  
 CC identified within the present sequence. The 5' ESTs were prepared from  
 CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST  
 CC sequences usually correspond mainly to the 3' untranslated region (UTR)  
 CC of the mRNA because they are often obtained from oligo-dT primed cDNA  
 CC libraries. Such ESTs are not well suited for isolating cDNA sequences  
 CC derived from the 5' ends of mRNAs and even in those cases where longer  
 CC cDNA sequences have been obtained, the full 5' UTR is rarely included.  
 CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be  
 CC used to obtain full length cDNAs with genomic DNAs. 5' ESTs are also used

CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.  
CC They are used to obtain upstream regulatory sequences and to design  
CC expression and secretion vectors.  
XX  
SQ Sequence 479 BP; 109 A; 109 C; 99 G; 160 T; 2 other;

Query Match 1.8%; Score 18; DB 21; Length 479;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 492 agcataagtggtgccag 509  
Db 64 agcataagtggtgccag 81

RESULT 15  
AAC36458/c  
ID AAC36458 standard; DNA; 486 BP.  
XX  
AC AAC36458;  
XX  
DE 17-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 13881.  
XX  
KW Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway;  
KW metabolic pathway; promoter; termination sequence; ss.  
XX  
OS Arabidopsis thaliana.  
XX  
PN EP1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-0301439.  
XX  
PR 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130510.  
PR 23-APR-1999; 99US-0130891.  
PR 28-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
PR 30-APR-1999; 99US-0132407.  
PR 04-MAY-1999; 99US-0132484.  
PR 05-MAY-1999; 99US-0132485.  
PR 06-MAY-1999; 99US-0132486.  
PR 07-MAY-1999; 99US-0132487.  
PR 07-MAY-1999; 99US-0132863.  
PR 11-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134218.  
PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.

PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 14-JUN-1999; 99US-0138847.  
PR 16-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 17-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139492.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0138763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 28-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144884.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145085.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.  
PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 02-AUG-1999; 99US-0146389.  
PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147302.

PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.  
PR 09-AUG-1999; 99US-0147935.  
PR 10-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148319.  
PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148684.  
PR 16-AUG-1999; 99US-0149368.  
PR 17-AUG-1999; 99US-0149175.  
PR 18-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149722.  
PR 20-AUG-1999; 99US-0149723.  
PR 20-AUG-1999; 99US-0149929.  
PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149930.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151066.  
PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 13-SEP-1999; 99US-0154018.  
PR 16-SEP-1999; 99US-0154039.  
PR 20-SEP-1999; 99US-0154779.  
PR 22-SEP-1999; 99US-0155139.  
PR 23-SEP-1999; 99US-0155486.  
PR 24-SEP-1999; 99US-0155659.  
PR 28-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156599.  
PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157753.  
PR 06-OCT-1999; 99US-0157865.  
PR 07-OCT-1999; 99US-0158029.  
PR 08-OCT-1999; 99US-0158232.  
PR 12-OCT-1999; 99US-0158369.  
PR 13-OCT-1999; 99US-0159293.  
PR 13-OCT-1999; 99US-0159294.  
PR 13-OCT-1999; 99US-0159295.  
PR 14-OCT-1999; 99US-0159329.  
PR 14-OCT-1999; 99US-0159330.  
PR 14-OCT-1999; 99US-0159331.  
PR 14-OCT-1999; 99US-0159637.  
PR 14-OCT-1999; 99US-0159638.  
PR 18-OCT-1999; 99US-0159584.  
PR 21-OCT-1999; 99US-0160741.  
PR 21-OCT-1999; 99US-0160767.  
PR 21-OCT-1999; 99US-0160768.  
PR 21-OCT-1999; 99US-0160770.  
PR 21-OCT-1999; 99US-0160814.  
PR 21-OCT-1999; 99US-0160815.  
PR 22-OCT-1999; 99US-0160980.  
PR 22-OCT-1999; 99US-0160981.  
PR 22-OCT-1999; 99US-0160989.  
PR 25-OCT-1999; 99US-0161404.  
PR 25-OCT-1999; 99US-0161405.  
PR 25-OCT-1999; 99US-0161406.  
PR 26-OCT-1999; 99US-0161359.  
PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.

Query Match 1.8%; Score 18; DB 21; Length 486;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 930 caacatcaggaagggt 947  
Db 164 CAACATCAGGAGGGGT 147  
RESULT 16  
AAC51869/c  
ID AAC51869 standard; DNA: 634 BP.  
XX  
AC AAC51869;  
XX  
DT 18-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 69916.  
XX  
XX Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway;  
KW metabolic pathway; promoter; termination sequence; ss.  
XX  
OS Arabidopsis thaliana.  
XX  
XX EP1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-0301439.  
XX  
XX 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130449.  
PR 23-APR-1999; 99US-0130510.  
PR 23-APR-1999; 99US-0130891.  
PR 28-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
PR 30-APR-1999; 99US-0132407.  
PR 04-MAY-1999; 99US-0132484.  
PR 05-MAY-1999; 99US-0132485.  
PR 06-MAY-1999; 99US-0132486.  
PR 07-MAY-1999; 99US-0132487.  
PR 11-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134218.  
PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135533.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.

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PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139753.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
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PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140823.
PR 28-JUN-1999; 99US-0140833.
PR 29-JUN-1999; 99US-0140981.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
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PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.

PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
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PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
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PR 25-OCT-1999; 99US-0161404.
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PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 1.8%; Score 18; DB 21; Length 634;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 930 caacatcagaaggggt 947
DB 165 CAACATCAGAAAGGGGT 148
```

RESULT 17  
 ID AAX39943 standard; DNA; 866 BP.  
 AC AAX39943;  
 XX  
 DT 02-JUL-1999 (first entry)  
 DE Gastric cancer associated gene.  
 KW Cancer associated antigen; diagnosis; research; treatment; human;  
 KW breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;  
 KW prostate cancer; ss.  
 OS Homo sapiens.  
 PN WO9904265-A2.  
 PD 28-JAN-1999.  
 XX  
 PF 15-JUL-1998; 98WO-US14679.  
 XX  
 PR 22-JUN-1998; 98US-0102322.  
 PR 17-JUL-1997; 97US-0896164.  
 PR 10-OCT-1997; 97US-0061599.  
 PR 10-OCT-1997; 97US-0061765.  
 PR 10-OCT-1997; 97US-0948705.  
 PR 11-OCT-1997; 97GB-0021697.  
 XX  
 PA (LUDM-) LUDMIG INST CANCER RES.  
 PI Chen Y, Gout I, Gure A, O'Hare M, Obata Y, Old LJ;  
 PI Pfrendschuh M, Sahin U, Scanlan MJ, Stockert E;  
 PI Tureci O;  
 XX  
 DR WPI; 1999-132448/11.  
 XX  
 PR New isolated cancer associated nucleic acids and polypeptides -  
 PR isolated using sera from cancer patients, used to develop products  
 PR for the diagnosis, monitoring or treatment of cancers  
 XX  
 PS Claim 67; Page 607; 787pp; English.  
 XX  
 CC The invention relates to a method for diagnosing a disorder characterised  
 CC by expression of a human cancer associated antigen precursor coded for by  
 CC a nucleic acid molecule (NAM). The method comprises: (a) contacting a  
 CC biological sample isolated from a subject with an agent that specifically  
 CC binds to the NAM, an expression product or a fragment of an expression  
 CC product complexed with an HLA molecule; and (b) determining the  
 CC interaction between the agent and the NAM or the expression product as a  
 CC determination of the disorder. The products and methods can be used in  
 CC the diagnosis, monitoring, research, or treatment of conditions  
 CC characterised by the expression of various cancer associated antigens.  
 CC The invention provides nucleic acid sequences and encoded polypeptides  
 CC which are cancer associated antigen precursors expressed in human breast  
 CC cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and  
 CC lung cancer.  
 XX  
 SO Sequence 866 BP; 222 A; 235 C; 197 G; 206 T; 6 other;

Query Match 1.8%; Score 18; DB 20; Length 866;  
 Best Local Similarity 100.0%; Pred. No. 20;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 230 cccctgcacacccctg 247  
 ||||||||||||||||  
 Db 37 cccctgcacacccctg 54

RESULT 18

AAC41168/c  
 ID AAC41168 standard; DNA; 970 BP.  
 AC AAC41168;  
 XX  
 DT 17-OCT-2000 (first entry)  
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 30900.  
 XX  
 KW Hybridisation assay; genetic mapping; gene expression control;  
 KW protein identification; signal transduction pathway;  
 KW metabolic pathway; promoter; termination sequence; ss.  
 OS Arabidopsis thaliana.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 XX  
 PF 25-FEB-2000; 2000EP-0301439.  
 XX  
 PR 25-FEB-1999; 99US-0121825.  
 PR 05-MAR-1999; 99US-0123180.  
 PR 09-MAR-1999; 99US-0123548.  
 PR 23-MAR-1999; 99US-0125788.  
 PR 25-MAR-1999; 99US-0126264.  
 PR 29-MAR-1999; 99US-0126785.  
 PR 01-APR-1999; 99US-0127462.  
 PR 06-APR-1999; 99US-0128234.  
 PR 08-APR-1999; 99US-0128714.  
 PR 16-APR-1999; 99US-0129845.  
 PR 19-APR-1999; 99US-0130077.  
 PR 21-APR-1999; 99US-0130449.  
 PR 23-APR-1999; 99US-0130510.  
 PR 28-APR-1999; 99US-0130891.  
 PR 30-APR-1999; 99US-0131449.  
 PR 30-APR-1999; 99US-0132048.  
 PR 30-APR-1999; 99US-0132407.  
 PR 04-MAY-1999; 99US-0132484.  
 PR 05-MAY-1999; 99US-0132485.  
 PR 06-MAY-1999; 99US-0132486.  
 PR 06-MAY-1999; 99US-0132487.  
 PR 07-MAY-1999; 99US-0132863.  
 PR 11-MAY-1999; 99US-0134256.  
 PR 14-MAY-1999; 99US-0134218.  
 PR 14-MAY-1999; 99US-0134219.  
 PR 14-MAY-1999; 99US-0134221.  
 PR 14-MAY-1999; 99US-0134370.  
 PR 18-MAY-1999; 99US-0134768.  
 PR 19-MAY-1999; 99US-0134941.  
 PR 20-MAY-1999; 99US-0135124.  
 PR 21-MAY-1999; 99US-0135353.  
 PR 24-MAY-1999; 99US-0135629.  
 PR 25-MAY-1999; 99US-0136021.  
 PR 27-MAY-1999; 99US-0136392.  
 PR 28-MAY-1999; 99US-0136782.  
 PR 01-JUN-1999; 99US-0137222.  
 PR 03-JUN-1999; 99US-0137528.  
 PR 04-JUN-1999; 99US-0137502.  
 PR 07-JUN-1999; 99US-0137724.  
 PR 08-JUN-1999; 99US-0138094.  
 PR 10-JUN-1999; 99US-0138540.  
 PR 10-JUN-1999; 99US-0138847.  
 PR 14-JUN-1999; 99US-0139119.  
 PR 16-JUN-1999; 99US-0139452.  
 PR 16-JUN-1999; 99US-0139453.  
 PR 17-JUN-1999; 99US-0139492.  
 PR 18-JUN-1999; 99US-0139454.  
 PR 18-JUN-1999; 99US-0139455.  
 PR 18-JUN-1999; 99US-0139456.  
 PR 18-JUN-1999; 99US-0139457.  
 PR 18-JUN-1999; 99US-0139458.  
 PR 18-JUN-1999; 99US-0139459.





DE Human secreted protein CDNA #44.  
 XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;  
 KM antiallergic; hepatotropic; antidiabetic; antiinflammatory; anticancer;  
 KM vulnerability; anticonvulsant; antibacterial; antifungal; antiparasitic;  
 KM cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;  
 KM neurological disease; infection; human; secreted protein; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO200056765-A1.  
 XX  
 PD 28-SEP-2000.  
 XX  
 PF 16-MAR-2000; 2000MO-US06823.  
 XX  
 PR 19-MAR-1999; 99US-0125364.  
 XX 08-DEC-1999; 99US-0169623.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PI Rosen CA, Ruben SM, Komatsoulis G;  
 XX  
 DR WPI: 2000-602215/57.  
 DR P-PSDB; AAB34002.  
 XX  
 PT Nucleic acid molecules encoding human secreted proteins, used in  
 PT preventing, treating or ameliorating a disorder, e.g. Alzheimer's and  
 PT Parkinson's diseases and cancers -  
 XX  
 PS Claim 1: Page 355; 410pp; English.  
 XX  
 CC The invention relates to the isolation of genes AAC59392-C59439 encoding  
 CC 48 human secreted proteins AAB3963-B34006. The genes can be used to  
 CC generate fusion proteins by linking to the gene for the human  
 CC immunoglobulin G Fc portion (SEQID) for increasing the stability of  
 CC the fusion protein as compared to the human protein only. The genes and  
 CC proteins are useful for preventing, ameliorating or treating medical  
 CC conditions, e.g. by protein or gene therapy. The genes are isolated  
 CC from a range of human tissues disclosed in the specification. The  
 CC nucleic acids, proteins, antibodies and (ant)agonists are useful in  
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast  
 CC and ovarian cancer, and other cancers of the adrenal gland, bone, bone  
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;  
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune  
 CC hemolytic anemia, autoimmune thyroiditis, diabetes mellitus, Crohn's  
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative  
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d)  
 CC wound healing; (e) neurological diseases e.g. cerebral anoxia and  
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal  
 CC and parasitic infections.  
 CC  
 SQ Sequence 1302 BP; 249 A; 470 C; 338 G; 230 T; 15 other:

Query Match 1.8%; Score 18; DB 21; Length 1302;  
 Best Local Similarity 100.0%; Pred. No. 20;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 44 gtatgctgctctgctgctg 61  
 ||||||||||||||||  
 Db 669 gtagctgctgctgctg 652

RESULT 20  
 ID AA077884  
 AC AA077884 standard; CDNA: 2520 BP.  
 XX  
 AC AA077884;  
 XX  
 DT 06-JUL-1995 (first entry)  
 XX  
 PI Neural thread protein AD16c CDNA.

XX  
 KM Neural thread protein AD16c; Alzheimer's; neuroectodermal tumours;  
 KM malignant astrocytomas; glioblastomas; ss.  
 XX  
 OS Rattus rattus.  
 XX  
 PN W09423756-A.  
 XX  
 PD 27-OCT-1994.  
 XX  
 PF 20-APR-1994; 94MO-US04321.  
 XX  
 PR 20-APR-1993; 93US-0050559.  
 XX  
 PA (GEHO ) GEN HOSPITAL CORP.  
 XX  
 PI De la Monte SM, Wands JR;  
 XX  
 DR WPI: 1994-341497/42.  
 XX  
 PT Detection of neural thread proteins - to detect sporadic and  
 PT familial Alzheimer's disease, neuroectodermal tumours, malignant  
 PT astrocytomas and glioblastomas (Eng).  
 XX  
 PS Example 4; Fig 165; 158pp; English.  
 XX  
 CC AA077884 is the AD16c neural thread protein (NTP) CDNA. This  
 CC sequence was used in the development of an antibody dependent  
 CC method, for the detection of NTPs. This new method could be  
 CC used to diagnose Alzheimer's disease (differentiating between  
 CC sporadic and familial), neuroectodermal tumours, malignant  
 CC astrocytomas and glioblastomas.  
 CC  
 SQ Sequence 2520 BP; 661 A; 577 C; 581 G; 701 T; 0 other:

Query Match 1.8%; Score 18; DB 15; Length 2520;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 230 cccctgcatcaccctg 247  
 ||||||||||||||||  
 Db 298 cccctgcatcaccctg 315

RESULT 21  
 ID AAT27766  
 AC AAT27766 standard; CDNA: 2520 BP.  
 XX  
 AC AAT27766;  
 XX  
 DT 14-NOV-1996 (first entry)  
 XX  
 DE AD 16c human neural thread protein clone (partial sequence).  
 XX  
 KM Neural thread protein; NTP; diagnosis; detection;  
 KM Alzheimer's disease; neuroectodermal tumour; malignant astrocytoma;  
 KM monoclonal antibody; binding fragment; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W09615272-A1.  
 XX  
 PD 23-MAY-1996.  
 XX  
 PF 14-NOV-1995; 95MO-US17111.  
 XX  
 PR 14-NOV-1994; 94US-0340426.  
 XX  
 PA (GEHO ) GEN HOSPITAL CORP.  
 XX  
 PI De la Monte S, Wands JR;  
 XX

DR WPI: 1996-259865/26.  
XX  
PT Detection of neural thread protein in diagnosis of Alzheimer's  
PT disease - also NTP DNA and protein sequences used in gene and  
PT anti:sense therapy  
PS Example 4c: Figure 16S; 238pp; English.  
XX  
CC A method for detecting the presence of neural thread protein (NTP)  
CC having a molecular weight of 8, 14, 17, 21, 26 or 42 kD in a human  
CC subject comprises (a) contacting a sample from a human subject that  
CC is suspected of containing the NTP with at least one molecule  
CC capable of binding to the protein; and (b) detecting any of the  
CC molecule bound to the protein. The binding molecule is selected  
CC from an antibody free of natural impurities, a monoclonal antibody  
CC or a binding fragment of either of these. The method may be used for  
CC diagnosing the presence of Alzheimer's disease, neuroectodermal  
CC tumours and a malignant astrocytoma in a human. A number of clones  
CC of neural thread protein were isolated from healthy 17-18 week old  
CC foetal human brain (HB) 2 year old temporal lobe neocortex and end  
CC stage Alzheimer's disease (AD) cerebral cortex. See AAT7753-75.  
XX  
SQ Sequence 2520 BP; 661 A; 577 C; 581 G; 701 T; 0 other;  
  
Query Match 1.8%; Score 18; DB 17; Length 2520;  
Best Local Similarity 100.0%; Pred. NO. 19;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 230 cccctgcacacccctg 247  
|||||  
Db 298 cccctgcacacccctg 315  
  
RESULT 22  
AAZ55887/C  
ID AAZ55887 standard; DNA; 68750 BP.  
XX  
AC AAZ55887;  
XX  
DT 10-APR-2000 (first entry)  
XX  
DE Sorangium cellulosum 68.75 kb contig.  
XX  
KM Epothilone biosynthesis; type I polyketide synthase; taxol substitute;  
XX anticancer; ds.  
XX  
OS Sorangium cellulosum.  
XX  
FH Key  
FT CDS  
FT  
FT location/Qualifiers  
FT 1..1826  
FT /\*tag= a  
FT /partial  
FT /product= "Partial Orf 1 protein (AAZ55880)"  
FT /note= "No initiation codon given in the specification"  
FT complement (1900..3171)  
FT /\*tag= b  
FT /product= "Orf 2 protein (AAZ55881)"  
FT 3415..5556  
FT /\*tag= c  
FT /product= "Orf 3 protein (AAZ55882)"  
FT complement (5612..5992)  
FT /\*tag= d  
FT /product= "Orf 4 protein (AAZ55883)"  
FT 6226..6675  
FT /\*tag= e  
FT /product= "Orf 5 protein (AAZ55884)"  
FT 7610..11875  
FT /\*tag= f  
FT /product= "Type I polyketide synthase, EPOS A  
FT (AAZ55873)" CDS  
FT 11872..116104  
FT /\*tag= g  
FT /product= "Non-ribosomal peptide synthetase, EPOS P

FT CDS  
FT 16251..21749  
FT /\*tag= h  
FT /product= "Type I polyketide synthase, EPOS B  
FT 21746..43519  
FT (AAZ58575)" CDS  
FT /\*tag= i  
FT /product= "Type I polyketide synthase, EPOS C  
FT 43524..54920  
FT (AAZ58576)" CDS  
FT /\*tag= j  
FT /product= "Type I polyketide synthase, EPOS D  
FT 54935..62254  
FT (AAZ58577)" CDS  
FT /\*tag= k  
FT /product= "Type I polyketide synthase, EPOS E  
FT 62369..63628  
FT (AAZ58578)" CDS  
FT /\*tag= l  
FT /product= "Cytochrome P450 oxygenase homologue, EPOS F  
FT (AAZ58579)"  
FT 63779..64333  
FT /\*tag= m  
FT /product= "Orf 6 protein (AAZ58585)"  
FT complement (63853..64290)  
FT (AAZ58577)" CDS  
FT /\*tag= n  
FT /product= "Orf 7 protein (AAZ58586)"  
FT 64363..64920  
FT /\*tag= o  
FT /product= "Orf 8 protein (AAZ58587)"  
FT complement (64287..64727)  
FT (AAZ58578)" CDS  
FT /\*tag= p  
FT /product= "Orf 9 protein (AAZ58588)"  
FT 65063..65767  
FT /\*tag= q  
FT /product= "Orf 10 protein"  
FT complement (65008..65874)  
FT (AAZ58577)" CDS  
FT /\*tag= r  
FT /product= "Orf 11 protein (AAZ58590)"  
FT complement (65871..66338)  
FT (AAZ58577)" CDS  
FT /\*tag= s  
FT /product= "Orf 12 protein (AAZ58591)"  
FT 66667..67137  
FT /\*tag= t  
FT /product= "Orf 13 protein (AAZ58592)"  
FT 67334..68251  
FT /\*tag= u  
FT /product= "Orf 14 protein (AAZ58593)"  
FT 68346..68750  
FT (AAZ58594)" CDS  
FT /\*tag= v  
FT /product= "Partial Orf 15 protein (AAZ58594)"  
FT /note= "No termination codon given in the specification"  
  
W09966028-A2.  
XX  
XX 23-DEC-1999.  
XX  
XX 16-JUN-1999; 99WO-EP04171.  
XX  
XX 18-JUN-1998; 98US-0099504.  
XX 24-SEP-1998; 98US-0101631.  
XX 05-FEB-1999; 99US-0118906.  
XX  
XX (NOVS ) NOVARTIS AG.  
XX (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
XX  
XX Schupp T, Ligon JM, Molnar I, Zirkle R, Goerlach J, Cyr D;  
XX WPI: 2000-097741/08.  
XX P-PSDB; AAZ58573, AAZ58574, AAZ58575, AAZ58576, AAZ58577, AAZ58578,  
XX AAZ58579, AAZ58580, AAZ58581, AAZ58582, AAZ58583, AAZ58584,  
XX AAZ58585, AAZ58586, AAZ58587, AAZ58588, AAZ58590, AAZ58591,  
XX AAZ58592, AAZ58593, AAZ58594.  
XX  
XX New isolated epothilone synthase genes, used for the recombinant  
XX production of epothilone for use in cancer therapy -

XX Claim 14; Page 87-104; 174pp; English.  
PS  
XX This sequence represents a 68.75 kb contig from *Sorangium cellulosum*  
CC comprising 22 open reading frames (ORFs) and includes genes encoding  
CC proteins involved in the biosynthesis of epothilones. Epothilones A and  
CC B are 16-membered macrocyclic polyketides with an acylcysteine-derived  
CC starter unit; polyketides being synthesised from two-carbon building  
CC blocks, the beta-carbon of which always carries a keto group. Each round  
CC of two-carbon addition is carried out by a complex of enzymes known as  
CC the polyketide synthase in a manner similar to fatty acid biosynthesis.  
CC EPOS A (AA158513) and EPOS P (AA158574) are involved in formation of  
CC the thiazole ring formation of epothilones, and EPOS B, EPOS C, EPOS D  
CC and EPOS E (AA158575-Y58578) are involved in polyketide backbone  
CC formation. EPO F (AA158579) is an epothilone macrolactone oxidase, and  
CC the proteins Orf 3 (AA158582) and Orf14 (AA158593) are thought to be  
CC involved in transport. Epothilones mimic the biological activity of  
CC taxol, and may be substituted for taxol in cancer chemotherapeutic  
CC compositions. Epothilones exhibit a much lower drop in potency against a  
CC multiply drug-resistant cell line compared with taxol, and are  
CC considerably less efficiently exported from such cells by the multidrug  
CC resistance protein (MDR, or P-glycoprotein). Despite the potential of  
CC epothilones as anticancer agents, they are problematical to produce on a  
CC large scale. Epothilones are too complex for industrial scale chemical  
CC synthesis, and *Sorangium cellulosum* is difficult to ferment, producing  
CC poor yields of epothilones. The nucleic acids of the invention may be  
CC used for the recombinant production of epothilones in a heterologous host  
CC that is more amenable to fermentation.  
XX  
SQ Sequence 66750 BP; 9596 A; 22458 C; 25537 G; 11159 T; 0 other;

Query Match 1.8%; Score 18; DB 21; Length 68750;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 517 tcgtctccacagcgcg 534  
IIIIIIIIIIIIIIIIII  
DB 19020 TCCTCTCCACACGCGC 19003

RESULT 23  
AA129349/c ID AAA29349 standard; DNA; 71989 BP.  
XX  
AC AAA29349;  
XX  
DT 12-SEP-2000 (first entry)  
XX  
DE *Sorangium cellulosum* epothilone polyketide synthase operon genomic DNA.  
XX  
XX Epothilone; polyketide synthase; epOA; epOB; epOC; epOD; epOE; epOF;  
KW epOL; epOK; P450 epoxidase; ORFA; ORFB; promoter; enhancer; anti-fungal;  
KM tubulin polymerization assay; anti-tumour; cytostatic; ds.  
XX  
XX *Sorangium cellulosum*.  
OS  
XX  
FH Key Location/Qualifiers  
FT CDS 3..992  
FT /tag= a  
FT /label= ORF A  
FT /product= transposase  
FT /note= "not part of the PKS"  
FT 989..1501  
FT /tag= b  
FT /label= ORF B  
FT /product= transposase  
FT /note= "not part of the PKS"  
FT CDS 1998..6263  
FT /tag= c  
FT /label= epOA\_gene  
FT /note= "encodes the loading domain"  
FT misc\_RNA 2031..3548

FT /tag= d  
FT /note= "encodes ketide synthase (KS-Y) of the loading  
FT domain"  
FT misc\_RNA 3621..4661  
FT /tag= e  
FT /note= "encodes acyl transferase (AT) of the loading  
FT domain"  
FT misc\_RNA 4917..5810  
FT /tag= f  
FT /note= "encodes enoyl reductase (ER) of the loading  
FT domain, potentially involved in formation of the  
FT thiazole moiety"  
FT misc\_RNA 5856..6135  
FT /tag= g  
FT /note= "encodes acyl carrier protein (ACP) of the loading  
FT domain"  
FT CDS 6260..10493  
FT /tag= h  
FT /label= epOB\_gene  
FT /note= "encodes module 1, the NRPS module"  
FT misc\_RNA 2031..3548  
FT /tag= i  
FT /note= "encodes condensation domain C2 of the NRPS  
FT module"  
FT misc\_RNA 2031..3548  
FT /tag= j  
FT /note= "encodes condensation domain C2 of the NRPS  
FT module"  
FT misc\_RNA 6861..6887  
FT /tag= k  
FT /note= "encodes heterocyclization signature sequence"  
FT misc\_RNA 6861..6887  
FT /tag= l  
FT /note= "encodes condensation domain C4 of the NRPS  
FT module"  
FT misc\_RNA 7358..7366  
FT /tag= m  
FT /note= "encodes condensation domain C7 (partial) of the  
FT NRPS module"  
FT misc\_RNA 7898..7921  
FT /tag= n  
FT /note= "encodes adenylation domain A1 of the NRPS module"  
FT misc\_RNA 7898..7921  
FT /tag= o  
FT /note= "encodes adenylation domain A1 of the NRPS module"  
FT misc\_RNA 8261..8308  
FT /tag= p  
FT /note= "encodes adenylation domain A3 of the NRPS module"  
FT misc\_RNA 8411..8422  
FT /tag= q  
FT /note= "encodes adenylation domain A4 of the NRPS module"  
FT misc\_RNA 8861..8905  
FT /tag= r  
FT /note= "encodes adenylation domain A6 of the NRPS module"  
FT misc\_RNA 8966..8983  
FT /tag= s  
FT /note= "encodes adenylation domain A7 of the NRPS module"  
FT misc\_RNA 9090..9179  
FT /tag= t  
FT /note= "encodes adenylation domain A8 of the NRPS module"  
FT misc\_RNA 9183..9992  
FT /tag= u  
FT /note= "encodes oxidation region for forming thiazole"  
FT misc\_RNA 10121..10138  
FT /tag= v  
FT /note= "encodes adenylation domain A10 of the NRPS  
FT module"  
FT misc\_RNA 10261..10306  
FT /tag= w  
FT /note= "encodes thiolation domain (PCP) of the NRPS  
FT module"  
FT CDS 10639..16137  
FT /tag= x

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FT /label= epoc_gene
FT /note= "encodes module 2"
FT 10654..12033
FT /*tag= y
FT /note= "encodes KS2, the KS domain of module 2"
FT 12250..13287
FT /*tag= z
FT /note= "encodes AT2, the AT domain of module 2"
FT 13327..13899
FT /*tag= aa
FT /note= "encodes dehydratase (DH) 2, the DH domain of
FT module 2"
FT 14962..15756
FT /*tag= ab
FT /note= "encodes ketoreductase (KR) 2, the KR domain of
FT module 2"
FT 15763..16008
FT /*tag= ac
FT /note= "encodes ACP2, the ACP domain of module 2"
FT 16134..37907
FT /*tag= ad
FT /label= epod_gene
FT /note= "encodes modules 3-6"
FT 16425..17606
FT /*tag= ae
FT /note= "encodes KS3"
FT 17817..18857
FT /*tag= af
FT /note= "encodes AT3"
FT 19581..20396
FT /*tag= ag
FT /note= "encodes KR3"
FT 20424..20642
FT /*tag= ah
FT /note= "encodes ACP3"
FT 20706..22082
FT /*tag= ai
FT /note= "encodes KS4"
FT 22296..23336
FT /*tag= aj
FT /note= "encodes AT4"
FT 24069..24647
FT /*tag= ak
FT /note= "encodes KR4"
FT 24867..25151
FT /*tag= al
FT /note= "encodes ACP4"
FT 25203..26576
FT /*tag= am
FT /note= "encodes KS5"
FT 26793..27883
FT /*tag= an
FT /note= "encodes AT5"
FT 27966..28574
FT /*tag= ao
FT /note= "encodes DH5"
FT 29433..30287
FT /*tag= ap
FT /note= "encodes ER5"
FT 30321..30869
FT /*tag= aq
FT /note= "encodes KR5"
FT 31077..31373
FT /*tag= ar
FT /note= "encodes ACP5"
FT 31440..32807
FT /*tag= as
FT /note= "encodes KS6"
FT 33018..34067
FT /*tag= at
FT /note= "encodes AT6"
FT 34107..34676
FT /*tag= au

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FT /note= "encodes DH6"
FT 35760..36641
FT /*tag= av
FT /note= "encodes ER6"
FT 36705..37256
FT /*tag= aw
FT /note= "encodes KR6"
FT 37470..37769
FT /*tag= ax
FT /note= "encodes ACP6"
FT 37912..49308
FT /*tag= ay
FT /label= epoe_gene
FT /note= "encodes modules 7 and 8"
FT 38014..39375
FT /*tag= az
FT /note= "encodes KS7"
FT 39589..40626
FT /*tag= ba
FT /note= "encodes AT7"
FT 41341..41922
FT /*tag= bb
FT /note= "encodes KR7"
FT 42181..42423
FT misc_RNA

Query Match 1.88; Score 18; DB 21; Length 71989;
Best Local Similarity 100.08; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 517 tgcgtctccacagccgcg 534
Db 13408 TCGTCTCCACAGCCGCG 13391

RESULT 24
AAx84320
ID AAx84320 standard; DNA; 198 BP.
XX
AC AAx84320;
XX
DT 08-SEP-1999 (first entry)
XX
DE Stealth virus nucleic acid clone, SPQ ID NO: 12.
XX
KW Stealth virus; detection; diagnosis; infection; ss.
XX
OS Stealth virus.
XX
PN W09934019-A1.
XX
PD 08-JUL-1999.
XX
PE 30-DEC-1998; 98WO-US27744.
XX
PR 30-DEC-1997; 97US-0001184.
XX
PA (MART/) MARTIN W J.
XX
PI Martin WJ;
XX
DR WPI: 1999-405521/34.
XX
PT Novel strains of stealth virus
XX
PS Claim 19; Page 44; 95bp; English.
XX

This sequence represents a stealth virus nucleic acid clone. The
invention relates to a method of detecting and characterising a stealth
virus by reacting a sample suspected of containing a stealth virus with a
probe from a known stealth virus and sequencing the resultant isolated
nucleotide. The method comprises the steps of: (a) isolating DNA or RNA
from a sample suspected of containing a stealth virus, e.g. a culture of
cells showing a viral cytopathic effect; (b) testing the reactivity of

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AAC00184/C  
 ID AAC00184 standard; cDNA: 364 BP.  
 XX  
 AC AAC00184;  
 XX  
 DT 06-OCT-2000 (first entry)  
 XX  
 DE Human secreted protein 5' EST, SEQ ID NO: 182.  
 XX  
 KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
 KW gene therapy; chromosome mapping; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EPI033401-A2.  
 XX  
 PD 06-SEP-2000.  
 XX  
 PF 21-FEB-2000; 2000EP-0200610.  
 XX  
 PR 26-FEB-1999; 99US-0122487.  
 XX  
 PA (GEST ) GENSET.  
 PI Dumas Milne Edwards J, Duclert A, Giordano J;  
 XX  
 DR WPI: 2000-500381/45.  
 DR P-PSDB; AAG00178.  
 XX  
 PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for  
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -  
 XX  
 PS Claim 1; SEQ ID 182; 71pp + CD-ROM; English.  
 XX  
 CC The present sequence is one of a large number of 5' ESTs derived from  
 CC mRNAs encoding secreted proteins. An ORF has been identified within the  
 CC sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs  
 CC derived from 30 different tissues. EST sequences usually correspond  
 CC mainly to the 3' untranslated region (UTR) of the mRNA because they are  
 CC often obtained from oligo-dT primed cDNA libraries. Such ESTs are not  
 CC well suited for isolating cDNA sequences derived from the 5' ends of  
 CC mRNAs and even in those cases where longer cDNA sequences have been  
 CC obtained, the full 5' UTR is rarely included. 5' ESTs are derived from  
 CC cDNAs with intact 5' ends and can therefore be used to obtain full length  
 CC cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,  
 CC gene therapy and chromosome mapping procedures. They are used to obtain  
 CC upstream regulatory sequences and to design expression and secretion  
 CC vectors.  
 CC  
 XX  
 XX Sequence 364 BP; 125 A; 78 C; 74 G; 83 T; 4 other;

Query Match 1.7%; Score 17; DB 21; Length 364;  
 Best Local Similarity 100.0%; Pred. No. 66;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 787 ctgaactggttaga 803  
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 DB 300 CTGAATCTGGGTTTGA 284

RESULT 28  
 AAC01025  
 ID AAC01025 standard; cDNA: 386 BP.  
 XX  
 AC AAC01025;  
 XX  
 DT 06-OCT-2000 (first entry)  
 XX  
 DE Human secreted protein 5' EST, SEQ ID NO: 1023.  
 XX  
 KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;

KW gene therapy; chromosome mapping; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EPI033401-A2.  
 XX  
 PD 06-SEP-2000.  
 XX  
 PF 21-FEB-2000; 2000EP-0200610.  
 XX  
 PR 26-FEB-1999; 99US-0122487.  
 XX  
 PA (GEST ) GENSET.  
 PI Dumas Milne Edwards J, Duclert A, Giordano J;  
 XX  
 DR WPI: 2000-500381/45.  
 DR P-PSDB; AAG01019.  
 XX  
 PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for  
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -  
 XX  
 PS Claim 1; SEQ ID 1023; 71pp + CD-ROM; English.  
 XX  
 CC The present sequence is one of a large number of 5' ESTs derived from  
 CC mRNAs encoding secreted proteins. An ORF has been identified within the  
 CC sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs  
 CC derived from 30 different tissues. EST sequences usually correspond  
 CC mainly to the 3' untranslated region (UTR) of the mRNA because they are  
 CC often obtained from oligo-dT primed cDNA libraries. Such ESTs are not  
 CC well suited for isolating cDNA sequences derived from the 5' ends of  
 CC mRNAs and even in those cases where longer cDNA sequences have been  
 CC obtained, the full 5' UTR is rarely included. 5' ESTs are derived from  
 CC mRNAs with intact 5' ends and can therefore be used to obtain full length  
 CC cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,  
 CC gene therapy and chromosome mapping procedures. They are used to obtain  
 CC upstream regulatory sequences and to design expression and secretion  
 CC vectors.  
 CC  
 XX  
 XX Sequence 386 BP; 125 A; 88 C; 102 G; 70 T; 1 other;

Query Match 1.7%; Score 17; DB 21; Length 386;  
 Best Local Similarity 100.0%; Pred. No. 66;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 aacagcagcgagccaa 129  
 ||R|||||||||||  
 DB 92 aacgagcgagcgagccaa 108

RESULT 29  
 AAC38084  
 ID AAC38084 standard; DNA: 513 BP.  
 XX  
 AC AAC38084;  
 XX  
 DT 17-OCT-2000 (first entry)  
 XX  
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 19733.  
 XX  
 KW Hybridisation assay; genetic mapping; gene expression control;  
 KW protein identification; signal transduction pathway;  
 KW metabolic pathway; promoter; termination sequence; ss.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 PN EPI033405-A2.  
 XX  
 PD 06-SEP-2000.  
 XX  
 PF 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 990S-0121825.  
PR 05-MAR-1999; 990S-0123180.  
PR 09-MAR-1999; 990S-0123548.  
PR 23-MAR-1999; 990S-0125788.  
PR 25-MAR-1999; 990S-0126264.  
PR 29-MAR-1999; 990S-0126785.  
PR 01-APR-1999; 990S-0127462.  
PR 06-APR-1999; 990S-0128234.  
PR 08-APR-1999; 990S-0128714.  
PR 16-APR-1999; 990S-0129845.  
PR 19-APR-1999; 990S-0130077.  
PR 21-APR-1999; 990S-0130449.  
PR 23-APR-1999; 990S-0130510.  
PR 28-APR-1999; 990S-0130891.  
PR 30-APR-1999; 990S-0131449.  
PR 30-APR-1999; 990S-0132048.  
PR 04-MAY-1999; 990S-0132407.  
PR 05-MAY-1999; 990S-0132484.  
PR 06-MAY-1999; 990S-0132486.  
PR 07-MAY-1999; 990S-0132487.  
PR 11-MAY-1999; 990S-0132863.  
PR 14-MAY-1999; 990S-0134256.  
PR 14-MAY-1999; 990S-0134218.  
PR 14-MAY-1999; 990S-0134219.  
PR 14-MAY-1999; 990S-0134221.  
PR 14-MAY-1999; 990S-0134221.  
PR 18-MAY-1999; 990S-0134370.  
PR 19-MAY-1999; 990S-0134768.  
PR 20-MAY-1999; 990S-0134941.  
PR 21-MAY-1999; 990S-0135124.  
PR 24-MAY-1999; 990S-0135353.  
PR 25-MAY-1999; 990S-0135629.  
PR 27-MAY-1999; 990S-0136021.  
PR 28-MAY-1999; 990S-0136392.  
PR 01-JUN-1999; 990S-0136782.  
PR 03-JUN-1999; 990S-0137222.  
PR 04-JUN-1999; 990S-0137502.  
PR 07-JUN-1999; 990S-0137724.  
PR 08-JUN-1999; 990S-0138094.  
PR 10-JUN-1999; 990S-0138540.  
PR 10-JUN-1999; 990S-0138847.  
PR 14-JUN-1999; 990S-0139119.  
PR 16-JUN-1999; 990S-0139452.  
PR 16-JUN-1999; 990S-0139453.  
PR 17-JUN-1999; 990S-0139492.  
PR 18-JUN-1999; 990S-0139454.  
PR 18-JUN-1999; 990S-0139455.  
PR 18-JUN-1999; 990S-0139456.  
PR 18-JUN-1999; 990S-0139457.  
PR 18-JUN-1999; 990S-0139458.  
PR 18-JUN-1999; 990S-0139459.  
PR 18-JUN-1999; 990S-0139460.  
PR 18-JUN-1999; 990S-0139461.  
PR 18-JUN-1999; 990S-0139462.  
PR 18-JUN-1999; 990S-0139463.  
PR 18-JUN-1999; 990S-0139750.  
PR 18-JUN-1999; 990S-0139763.  
PR 21-JUN-1999; 990S-0139817.  
PR 22-JUN-1999; 990S-0139899.  
PR 23-JUN-1999; 990S-0140353.  
PR 23-JUN-1999; 990S-0140354.  
PR 24-JUN-1999; 990S-0140695.  
PR 28-JUN-1999; 990S-0140823.  
PR 29-JUN-1999; 990S-0140991.  
PR 30-JUN-1999; 990S-0141287.  
PR 01-JUL-1999; 990S-0141842.  
PR 01-JUL-1999; 990S-0142154.  
PR 02-JUL-1999; 990S-0142055.  
PR 06-JUL-1999; 990S-0142390.  
PR 08-JUL-1999; 990S-0142803.  
PR 09-JUL-1999; 990S-0142920.  
  
PR 12-JUL-1999; 990S-0142977.  
PR 13-JUL-1999; 990S-0143542.  
PR 14-JUL-1999; 990S-0143624.  
PR 15-JUL-1999; 990S-0144005.  
PR 16-JUL-1999; 990S-0144085.  
PR 16-JUL-1999; 990S-0144086.  
PR 19-JUL-1999; 990S-0144325.  
PR 19-JUL-1999; 990S-0144331.  
PR 19-JUL-1999; 990S-0144332.  
PR 19-JUL-1999; 990S-0144333.  
PR 19-JUL-1999; 990S-0144334.  
PR 19-JUL-1999; 990S-0144335.  
PR 20-JUL-1999; 990S-0144352.  
PR 20-JUL-1999; 990S-0144632.  
PR 21-JUL-1999; 990S-0144884.  
PR 21-JUL-1999; 990S-0144814.  
PR 21-JUL-1999; 990S-0145086.  
PR 21-JUL-1999; 990S-0145088.  
PR 22-JUL-1999; 990S-0145085.  
PR 22-JUL-1999; 990S-0145087.  
PR 22-JUL-1999; 990S-0145089.  
PR 22-JUL-1999; 990S-0145192.  
PR 23-JUL-1999; 990S-0145145.  
PR 23-JUL-1999; 990S-0145218.  
PR 23-JUL-1999; 990S-0145224.  
PR 26-JUL-1999; 990S-0145276.  
PR 27-JUL-1999; 990S-0145913.  
PR 27-JUL-1999; 990S-0145918.  
PR 27-JUL-1999; 990S-0145919.  
PR 28-JUL-1999; 990S-0145951.  
PR 02-AUG-1999; 990S-0146386.  
PR 02-AUG-1999; 990S-0146388.  
PR 02-AUG-1999; 990S-0146389.  
PR 03-AUG-1999; 990S-0147038.  
PR 04-AUG-1999; 990S-0147204.  
PR 04-AUG-1999; 990S-0147302.  
PR 05-AUG-1999; 990S-0147192.  
PR 05-AUG-1999; 990S-0147260.  
PR 06-AUG-1999; 990S-0147303.  
PR 06-AUG-1999; 990S-0147416.  
PR 09-AUG-1999; 990S-0147493.  
PR 09-AUG-1999; 990S-0147935.  
PR 10-AUG-1999; 990S-0148171.  
PR 11-AUG-1999; 990S-0148319.  
PR 12-AUG-1999; 990S-0148341.  
PR 13-AUG-1999; 990S-0148565.  
PR 13-AUG-1999; 990S-0148684.  
PR 16-AUG-1999; 990S-0149368.  
PR 17-AUG-1999; 990S-0149175.  
PR 18-AUG-1999; 990S-0149426.  
PR 20-AUG-1999; 990S-0149722.  
PR 20-AUG-1999; 990S-0149723.  
PR 20-AUG-1999; 990S-0149929.  
PR 23-AUG-1999; 990S-0149902.  
PR 23-AUG-1999; 990S-0149930.  
PR 25-AUG-1999; 990S-0150566.  
PR 26-AUG-1999; 990S-0150884.  
PR 27-AUG-1999; 990S-0151065.  
PR 27-AUG-1999; 990S-0151066.  
PR 27-AUG-1999; 990S-0151067.  
PR 30-AUG-1999; 990S-0151303.  
PR 31-AUG-1999; 990S-015138.  
PR 01-SEP-1999; 990S-0151930.  
PR 07-SEP-1999; 990S-0152363.  
PR 10-SEP-1999; 990S-0153070.  
PR 13-SEP-1999; 990S-0153758.  
PR 15-SEP-1999; 990S-0154018.  
PR 16-SEP-1999; 990S-0154039.  
PR 20-SEP-1999; 990S-0154779.  
PR 22-SEP-1999; 990S-0155139.  
PR 23-SEP-1999; 990S-0155486.  
PR 24-SEP-1999; 990S-0155659.  
PR 28-SEP-1999; 990S-0156458.



29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157753.  
PR 06-OCT-1999; 99US-0157865.  
PR 07-OCT-1999; 99US-0158029.  
PR 08-OCT-1999; 99US-0158232.  
PR 12-OCT-1999; 99US-0158369.  
PR 13-OCT-1999; 99US-0159293.  
PR 13-OCT-1999; 99US-0159294.  
PR 13-OCT-1999; 99US-0159295.  
PR 14-OCT-1999; 99US-0159329.  
PR 14-OCT-1999; 99US-0159330.  
PR 14-OCT-1999; 99US-0159331.  
PR 14-OCT-1999; 99US-0159637.  
PR 14-OCT-1999; 99US-0159638.  
PR 18-OCT-1999; 99US-0159584.  
PR 21-OCT-1999; 99US-0160741.  
PR 21-OCT-1999; 99US-0160767.  
PR 21-OCT-1999; 99US-0160768.  
PR 21-OCT-1999; 99US-0160770.  
PR 21-OCT-1999; 99US-0160814.  
PR 21-OCT-1999; 99US-0160815.  
PR 22-OCT-1999; 99US-0160980.  
PR 22-OCT-1999; 99US-0160981.  
PR 22-OCT-1999; 99US-0160989.  
PR 25-OCT-1999; 99US-0161404.  
PR 25-OCT-1999; 99US-0161405.  
PR 25-OCT-1999; 99US-0161406.  
PR 26-OCT-1999; 99US-0161359.  
PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161992.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.

Query Match 1.7%; Score 17; DB 21; Length 513;  
Best Local Similarity 100.0%; Pred. No. 65;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 222 tgctgcacccctgcac 238  
|||||  
DB 481 tgctgcacccctgcac 497

RESULT 30  
AAC93440/c  
ID AAC93440 standard; cDNA: 552 BP.

AC AAC93440;  
XX  
DT 16-FEB-2001 (first entry)

DE Human secreted protein gene 19 SEQ ID NO:29.

XX Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic;  
XX antiproliferative; cytoskeletal; cardiant; vasotropic; cerebroprotective;  
XX neurotropic; neuroprotective; antibacterial; virucide; fungicide;  
XX ophthalmological; vulnery; autoimmune disease; Rheumatoid arthritis;  
XX hyperproliferative disorders; cancer; cardiovascular disorder;  
XX cardiac arrest; cerebrovascular disorder; nervous system disorder;  
XX Alzheimer's disease; ocular disorder; wound healing; skin aging; ss.

OS Homo sapiens.  
XX  
XX WO200061625-A1.  
XX  
XX 19-OCT-2000.  
PD  
XX  
XX 06-APR-2000; 2000MO-US08981.  
PF  
XX  
XX 09-APR-1999; 99US-0128701.  
PR  
XX 20-JAN-2000; 2000US-0177166.

XX (HUMA-) HUMAN GENOME SCI INC.  
PA (ROSE/) ROSEN C A.  
XX  
XX Rosen CA, Ruben SM, Komatsoulis G;  
PI WPI; 2000-619226/59.  
DR P-PDB; AAB51747.  
XX  
XX New nucleic acid molecules encoding 48 human secreted proteins for  
PT diagnosing, preventing, treating or ameliorating medical conditions and  
PT used as food additives or preservatives -  
XX  
PS Claim 1; Page 423-424; 500pp; English.

XX Polynucleotide sequences AAC93442 - AAC93449 represent cDNA encoding  
CC human secreted proteins AAB51724 - AAB51777. Sequences AAB51778 -  
CC AAB51825 represent alternative polypeptides encoded by the genes, and  
CC amino acid sequences to which they are homologous. The genes and proteins  
CC have activities dependent on the tissues and cells in which they are  
CC expressed. Examples of their activities include immunosuppressive;  
CC antiarthritic; antirheumatic; antiproliferative; neuroprotective; antibacterial;  
CC vasotropic; cerebroprotective; neurotropic; cytoskeletal; cardiant;  
CC virucide; fungicide; ophthalmological; and vulnery. The secreted  
CC proteins, polynucleotides, antagonists and agonists may be useful in  
CC treating, preventing and/or diagnosing diseases and disorders such as  
CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative  
CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders  
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischemia,  
CC angogenesis, nervous system disorders e.g. Alzheimer's disease,  
CC infections caused by bacteria, viruses and fungi and ocular disorders  
CC e.g. corneal infection. The polypeptides can also be used to aid wound  
CC healing and epithelial cell proliferation, to prevent skin aging due to  
CC sunburn, to maintain organs before transplantation, for supporting cell  
CC culture of primary tissues, to regenerate tissues and in chemotaxis. The  
CC polypeptides can also be used as a food additive or preservative to  
CC increase or decrease storage capabilities, fat content, lipid, protein,  
CC carbohydrate, vitamins, minerals, cofactors and other nutritional  
CC components. Oligonucleotide AAC93413 - AAC93421 and peptide AAB51723 are  
CC used in the isolation and characterisation of the proteins and  
XX polynucleotides of the invention.

SO Sequence 552 BP; 94 A;167 C; 181 G; 102 T; 8 other;

Query Match 1.7%; Score 17; DB 21; Length 552;  
Best Local Similarity 100.0%; Pred. No. 65;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 680 agggcgaggtcaccag 696  
|||||  
DB 356 AGGGCGAGGTTCACAG 340

RESULT 31  
AAF13645/c  
ID AAF13645 standard; cDNA: 662 BP.

AC AAF13645;  
XX  
DT 13-MAR-2001 (first entry)

DE Aspergillus oryzae EST SEQ ID NO:6168.

XX Multiple gene expression; filamentous fungal cell; EST;  
XX expressed sequence tag; Fusarium venenatum; Aspergillus niger;  
XX Aspergillus oryzae; Trichoderma reesei; identification; recombination;  
XX culture condition; environmental stress; spore morphogenesis;  
XX metabolic pathway engineering; catabolic pathway engineering; ss.

OS Aspergillus oryzae.  
XX  
XX WO200056762-A2.

XX 28-SEP-2000.  
 XX 22-MAR-2000; 2000WO-US07781.  
 PF 22-MAR-1999; 99US-0273623.  
 XX 22-MAR-1999; 99US-0273623.  
 PR (NOVO ) NOVO NORDISK BIOTECH INC.  
 PA (NOVO ) NOVO NORDISK AS.  
 XX Berka RM, Rey MM, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;  
 PI WPI: 2000-594572/56.  
 DR Monitoring differential expression of genes in filamentous fungal cells  
 PT uses fluorescence-labeled nucleic acids isolated from the cells and a  
 PT substrate of expressed sequence tags -  
 XX Claim 88; Page 2541; 3161pp; English.  
 XX The present invention describes a method for monitoring differential  
 CC expression of genes in a first filamentous fungal (FF) cell relative to  
 CC expression of the same genes in one or more second filamentous fungal  
 CC cells. The method uses fluorescence-labeled nucleic acids isolated from  
 CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs  
 CC are used in the methods for monitoring differential expression of genes  
 CC in a first filamentous fungal (FF) cell relative to expression of the  
 CC same genes in one or more second filamentous fungal cells. Monitoring  
 CC the global expression of genes from FF cells allows the production  
 CC potential of the microorganisms to be improved. New genes may be  
 CC discovered, possible functions of unknown open reading frames can be  
 CC identified and gene copy number variation and stability can be  
 CC monitored. The expression of genes can be used to study how FF cells  
 CC adapt to changes in culture conditions, environmental stress, spore  
 CC morphogenesis, recombination, metabolic or catabolic pathway  
 CC engineering. Using ESTs provides several advantages over genomic or  
 CC random cDNA clones including elimination of redundancy as one spot on an  
 CC array equals one gene or open reading frame, and organisation of the  
 CC microarrays based on function of the gene products to facilitate  
 CC analysis of the results. AAF07478 to AAF11247 represents ESTs from  
 CC Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus  
 CC niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and  
 CC AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are  
 CC all specifically claimed in the present invention.  
 XX Sequence 662 BP; 148 A; 168 C; 175 G; 171 T; 0 other;  
 SQ

Query Match 1.7%; Score 17; DB 21; Length 662;  
 Best Local Similarity 100.0%; Pred. No. 65;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 712 gattcgcatacaccac 728  
 ||||||||||||||||  
 DB 378 GAGTCGTCATACCAA 362

RESULT 32  
 AAV16884  
 ID AAV16884 standard; DNA: 673 BP.  
 XX AAV16884;  
 AC  
 XX 07-AUG-1998 (first entry)  
 DT  
 XX Human prostate cancer marker UC Band #31.  
 DE  
 XX Prostate cancer; human; marker; diagnosis; treatment; probe; ss.  
 KW  
 XX Homo sapiens.  
 OS  
 XX  
 PN M09804689-A1.  
 XX

PD 05-FEB-1998.  
 XX 31-JUL-1996; 96WO-US12516.  
 PF 31-JUL-1996; 96WO-US12516.  
 XX 31-JUL-1996; 96WO-US12516.  
 PR (UROC-) UROCOR INC.  
 PA An G, O'hara SM, Ralph D, Veltri R;  
 PI WPI: 1998-130681/12.  
 DR Human prostate cancer marker - useful for detection and treatment of  
 PT human prostate cancer  
 PT Claim 1; Page 135; 229pp; English.  
 XX This represents a marker sequence for human prostate cancer. Isolated  
 CC nucleic acid segments shown in AAV16881 to AAV16885, AAV16890 to  
 CC AAV16903, AAV26351 and AAV26352 which can act as human prostate cancer  
 CC markers are provided in the specification. It also provides methods for  
 CC identifying markers for human prostate cancer and for detection of  
 CC prostate cancer cells. The markers can be identified by amplifying human  
 CC prostate RNA to provide nucleic acid amplification products, separating  
 CC the products and identifying those RNA that are differentially expressed  
 CC between human prostate cancers versus normal or benign human prostate.  
 CC prostate cancer cells in a sample can be detected by detecting a nucleic  
 CC acid in a sample, the nucleic acid being a prostate cancer marker.  
 CC primers and probes derived from this marker can be used for the detection  
 CC of prostate cancer cells in a sample. Antibodies against the protein  
 CC encoded by the marker nucleic acid fragments, inhibitors of the protein  
 CC and oligonucleotides antisense to the markers can be used in the  
 CC treatment of prostate cancer. The antibodies can also be used for the  
 CC diagnosis of human prostate cancer.  
 XX Sequence 673 BP; 222 A; 140 C; 145 G; 166 T; 0 other;  
 SQ

Query Match 1.7%; Score 17; DB 19; Length 673;  
 Best Local Similarity 100.0%; Pred. No. 65;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 537 gaaccaacagagagaag 553  
 ||||||||||||||||  
 DB 542 gaaccaacagagagaag 558

RESULT 33  
 AAX26019  
 ID AAX26019 standard; DNA: 673 BP.  
 XX AAX26019;  
 AC  
 XX 20-MAY-1999 (first entry)  
 DT  
 XX Prostate disease marker gene fragment UC Band #31.  
 DE  
 XX Prostate cancer; benign prostatic hyperplasia; marker gene; tumour;  
 KW differentiation; Reverse Transcription Polymerase Chain Reaction;  
 KW diagnostic; progression; cancer; metastasis; human; RT-PCR; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US5882864-A.  
 XX 16-MAR-1999.  
 PD  
 XX 31-JUL-1996; 96US-0692787.  
 PF 31-JUL-1996; 96US-0692787.  
 XX 31-JUL-1996; 96US-0692787.  
 PR 31-JUL-1996; 96US-0692787.  
 XX  
 PA (UROC-) UROCOR INC.

```
XX An G, O'Hara SM, Ralph D, Veltre R;
PI WPI; 1999-214055/18.
XX
XX Diagnosing prostate cancer and benign prostatic hyperplasia cells
PT using oligonucleotide probes specific for marker genes associated
PT with tumor differentiation and progression in Reverse Transcription
PT Polymerase Chain Reaction analysis
XX
XX Claim 1; Columns 71-72; 74pp; English.
XX
XX The invention relates to methods for diagnosing prostate cancer or benign
XX prostatic hyperplasia cells in a biological sample. The method uses
XX oligonucleotide probes specific for marker genes associated with tumor
XX differentiation and progression in Reverse Transcription Polymerase Chain
XX Reaction (RT-PCR) analysis. The methods are diagnostic techniques useful
XX for detecting and monitoring the progression of benign prostatic
XX hyperplasia and human prostate cancer (the most prevalent form of cancer
XX and a major cause of death in males) prior to the tumor undergoing
XX metastasis, therefore allowing the optimal method of treatment to be
XX determined before the condition becomes life threatening. The present
XX sequence represents a claimed marker gene fragment.
XX
XX Sequence 673 BP; 222 A; 140 C; 145 G; 166 T; 0 other;
XX
XX
XX Query Match 1.7%; Score 17; DB 20; Length 673;
XX Best Local Similarity 100.0%; Pred. No. 65;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 537 gaaccacacagagag 553
XX |||||
XX 542 gaaccacacagagag 558
XX
XX
XX RESULT 34
XX AA287504
XX ID AA287504 standard; cDNA; 673 BP.
XX AC AA287504;
XX
XX 19-APR-2000 (first entry)
XX
XX Prostate, breast and bladder cancers detecting biomarker UC Band #31.
XX
XX Nucleic acid marker; biomarker; tumour; prostate cancer; bladder cancer;
XX benign prostatic hyperplasia; BPH; breast cancer; human; immunodetection;
XX diagnosis; ss.
XX
XX Homo sapiens.
XX
XX WO964631-A1.
XX
XX 16-DEC-1999.
XX
XX 11-JUN-1999; 99WO-US13151.
XX
XX 12-JUN-1998; 98US-0097199.
XX
XX (UROC-) UROCOR INC.
XX
XX An G, O'Hara SM, Ralph D, Veltre R;
XX
XX WPI; 2000-116557/10.
XX
XX Novel RNA biomarkers for diagnosis, prognosis and management of
XX prostate, breast and bladder cancer
XX
XX Claim 1; Page 165; 191pp; English.
XX
XX The invention provides nucleic acid markers of prostate, breast and
XX bladder cancer. The markers are indicators of malignant transformation of
```

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CC prostate, breast and bladder tissues and are diagnostic of the potential
CC for metastatic spread of malignant prostate tumours. The nucleic acid can
CC also be used as targets for therapeutic intervention in prostate cancer,
CC benign prostatic hyperplasia (BPH), bladder cancer or breast cancer. The
CC markers may be used to design specific probes and primers, for the rapid
CC analysis of prostate, bladder or breast biopsy samples. The probes and
CC primers may also be used for in situ hybridization or in situ PCR
CC detection and diagnosis. They may also be used to identify and isolate
CC full length gene sequences from various DNA libraries. Antibodies
CC against the polypeptide products of the markers can be used to treat
CC prostate cancer, bladder cancer or breast cancer. The encoded proteins
CC may be used to detect antibodies. The proteins and antibodies can be
CC used in immunodetection methods for detecting or quantifying the cancers,
CC and for clinical diagnosis of these cancers. The antibodies may also be
CC used for radioimaging to quantify and localize the encoded proteins.
XX
XX Sequence 673 BP; 222 A; 140 C; 145 G; 166 T; 0 other;
XX
XX
XX Query Match 1.7%; Score 17; DB 21; Length 673;
XX Best Local Similarity 100.0%; Pred. No. 65;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 537 gaaccacacagagag 553
XX |||||
XX 542 gaaccacacagagag 558
XX
XX
XX RESULT 35
XX AA233534
XX ID AA233534 standard; cDNA; 697 BP.
XX AC AA233534;
XX
XX 08-DEC-1999 (first entry)
XX
XX Human prostate cancer-associated EST 58.
XX
XX Expressed sequence tag; EST; prostate; tumor; treatment; gene therapy;
XX cancer; tissue specificity; human; ss.
XX
XX Homo sapiens.
XX
XX DE19811194-A1.
XX
XX 16-SEP-1999.
XX
XX 10-MAR-1998; 98DE-1011194.
XX
XX 10-MAR-1998; 98DE-1011194.
XX
XX (META-) METAGEN GES GENOMFORSCHUNG MBH.
XX
XX Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E, Rosenthal A;
XX WPI; 1999-519629/44.
XX
XX P-P-SDB; AAT48440.
XX
XX New nucleic acid expressed at high level in normal prostatic tissue and
XX encoded polypeptides, used to treat cancer and screen for therapeutic
XX agents
XX
XX Claim 1a; 119; 194pp; German.
XX
XX This invention describes novel nucleic acid sequences (A) that are
XX expressed at high level in normal prostatic tissue. Polypeptides (I)
XX encoded by (A) are used: (a) for identifying agents for treatment of
XX prostatic cancer and (b) for therapy of prostate cancer, optionally
XX where expressed by gene therapy methods. (A) is also used to isolate
XX full-length genes (for gene therapy) and for recombinant production of
XX (I), which can be used to raise specific antibodies. (A) are identified
XX by assembly of ESTs (expressed sequence tags) before these are analyzed
XX for expression pattern (tissue specificity). This approach eliminates
```

CC many of the false results, as regards tissue specificity, associated  
CC with known methods that use single (usually short) ESTs. AAZ3477-235540  
CC represent expressed sequence tags described in the method of the  
CC invention.

XX  
SQ Sequence 697 BP; 223 A; 140 C; 196 G; 138 T; 0 other;

Query Match 1.7%; Score 17; DB 20; Length 697;  
Best Local Similarity 100.0%; Pred. No. 65;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 aacagcagccagcagccaa 129  
IIIIIIIIIIIIIIIIIIII  
Db 110 aacagcagccagcagccaa 126

RESULT 36

AAC39218  
ID AAC39218 standard; DNA; 763 BP.

XX AAC39218;

DF 17-OCT-2000 (first entry)

XX Arabidopsis thaliana DNA fragment SEQ ID NO: 23810.

XX Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway;

KW metabolic pathway; promoter; termination sequence; ss.

OS Arabidopsis thaliana.

PN EP1033405-A2.

XX 06-SEP-2000.

PD 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0128845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130449.  
PR 23-APR-1999; 99US-0130510.  
PR 28-APR-1999; 99US-0130891.  
PR 30-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
PR 30-APR-1999; 99US-0132407.  
PR 04-MAY-1999; 99US-0132484.  
PR 05-MAY-1999; 99US-0132485.  
PR 06-MAY-1999; 99US-0132486.  
PR 06-MAY-1999; 99US-0132487.  
PR 07-MAY-1999; 99US-0132863.  
PR 11-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134218.  
PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.

PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139492.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144632.  
PR 20-JUL-1999; 99US-0144884.  
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AC AAC99839;  
XX  
XX 13-MAR-2001 (first entry)  
DT  
XX  
DE Human secreted protein gene 22 SEQ ID NO:32.  
XX  
KW Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;  
KW antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;  
KW cerebroprotective; nootropic; neuroprotective; antibacterial; vitrucide;  
KW fungicide; ophthalmological; gene therapy; pathological condition;  
KW autoimmune disease; rheumatoid arthritis; hyperproliferative disorder;  
KW neoplasm; cardiovascular disorder; cardiac arrest; cerebral ischaemia;  
KW cerebrovascular disorder; angiogenesis; nervous system disorder;  
KW Alzheimer's disease; infection; ocular disorder; corneal infection;  
KW wound healing; skin aging; food additive; preservative;  
KW Chromosome 11; ss.  
XX  
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XX  
PN WO200070042-A1.  
XX  
PD 23-NOV-2000.  
XX  
PF 11-MAY-2000. 2000MO-US12788.  
XX  
XX 13-MAY-1999: 99US-0134068.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Ruben SM, Moore PA, Young PE, Komatsu G, Blise CE;  
PI Duan RD, Florence KA, Soppet DR;  
XX  
DR WPI: 2000-679828/66.  
DR P-PSDB; AAB56098.  
XX  
PT Isolated nucleic acid molecule encoding a human secreted protein is  
PT used in preventing, treating or ameliorating a medical condition -  
XX  
PS Claim 1; Page 868; 1065pp; English.  
XX  
CC The polynucleotide sequences given in AAC99818 to AAC99977 encode the  
CC human secreted proteins given in AAB56077 to AAB56362. Human secreted  
CC proteins have activities based on the tissues and cells the genes are  
CC expressed in. Examples of activities include: immunosuppressive;  
CC antirheumatic; antiproliferative; cytostatic; cardiant;  
CC vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial;  
CC vitrucide; fungicide; and ophthalmological. The human secreted  
CC polynucleotides and proteins can be used to prevent, treat or ameliorate  
CC a medical condition in e.g. humans, mice, rabbits, goats, horses, cats,  
CC dogs, chickens or sheep. They are also used in diagnosing a pathological  
CC condition or susceptibility to a pathological condition. Disorders which  
CC are diagnosed or treated include autoimmune diseases e.g. rheumatoid  
CC arthritis, hyperproliferative disorders e.g. neoplasms of the breast or  
CC liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular  
CC disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders  
CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and  
CC fungi and ocular disorders e.g. corneal infection. The proteins can also  
CC be used to aid wound healing and epithelial cell proliferation, to  
CC prevent skin aging due to sunburn, to maintain organs before

CC transplantation, for supporting cell culture of primary tissues, to  
CC regenerate tissues and in chemotaxis. The proteins can also be used as a  
CC food additive or preservative to increase or decrease storage  
CC capabilities. AAC99809 to AAC99817 and AAB56076 represent sequences used  
CC in the exemplification of the present invention.

XX SQ Sequence 800 BP; 154 A; 187 C; 154 G; 305 T; 0 other;

Query Match 1.7%; Score 17; DB 21; Length 800;  
Best Local Similarity 100.0%; Pred. NO. 64;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 743 AACAGCAGCCAGCCCAA 727

## RESULT 38

AAC42507  
ID AAC42507 standard; DNA; 1148 BP.

XX AAC42507;

DT 17-OCT-2000 (first entry)

XX Arabidopsis thaliana DNA fragment SEQ ID NO: 35818.

XX Hybridisation assay: genetic mapping; gene expression control;

KM protein identification; signal transduction pathway;

KM metabolic pathway; promoter; termination sequence; ss.

XX Arabidopsis thaliana.

XX EPI03405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301439.

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PR 05-MAR-1999; 99US-0123180.  
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Query Match 1.7%; Score 17; DB 21; Length 1273;  
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DT 17-OCT-2000 (first entry)  
XX  
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XX Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway;  
KW metabolic pathway; promoter; termination sequence; ss.  
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XX Arabidopsis thaliana.  
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PR 25-MAY-1999; 99US-0136021.  
PR 28-MAY-1999; 99US-0136392.  
PR 01-JUN-1999; 99US-0136782.  
PR 03-JUN-1999; 99US-0137222.  
PR 04-JUN-1999; 99US-0137528.  
PR 07-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139492.  
PR 18-JUN-1999; 99US-0139454.

PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144632.  
PR 20-JUL-1999; 99US-0144884.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145085.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.  
PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145919.  
PR 27-JUL-1999; 99US-0145918.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 02-AUG-1999; 99US-0146389.  
PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.  
PR 10-AUG-1999; 99US-0147935.  
PR 11-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148319.  
PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148684.  
PR 16-AUG-1999; 99US-0149368.

PR 17-AUG-1999; 99US-0149175.  
 PR 18-AUG-1999; 99US-0149426.  
 PR 20-AUG-1999; 99US-0149722.  
 PR 20-AUG-1999; 99US-0149723.  
 PR 20-AUG-1999; 99US-0149929.  
 PR 23-AUG-1999; 99US-0149902.  
 PR 23-AUG-1999; 99US-0149930.  
 PR 25-AUG-1999; 99US-0150566.  
 PR 26-AUG-1999; 99US-0150884.  
 PR 27-AUG-1999; 99US-0151065.  
 PR 27-AUG-1999; 99US-0151066.  
 PR 27-AUG-1999; 99US-0151080.  
 PR 30-AUG-1999; 99US-0151303.  
 PR 31-AUG-1999; 99US-015138.  
 PR 01-SEP-1999; 99US-0151930.  
 PR 07-SEP-1999; 99US-0152363.  
 PR 10-SEP-1999; 99US-0153070.  
 PR 13-SEP-1999; 99US-0153758.  
 PR 15-SEP-1999; 99US-0154018.  
 PR 16-SEP-1999; 99US-0154039.  
 PR 20-SEP-1999; 99US-0154779.  
 PR 22-SEP-1999; 99US-0155139.  
 PR 23-SEP-1999; 99US-0155486.  
 PR 24-SEP-1999; 99US-0155659.  
 PR 28-SEP-1999; 99US-0156458.  
 PR 29-SEP-1999; 99US-0156596.  
 PR 04-OCT-1999; 99US-0157117.  
 PR 05-OCT-1999; 99US-0157753.  
 PR 06-OCT-1999; 99US-0157865.  
 PR 07-OCT-1999; 99US-0158029.  
 PR 08-OCT-1999; 99US-0158232.  
 PR 12-OCT-1999; 99US-0158369.  
 PR 13-OCT-1999; 99US-0159293.  
 PR 13-OCT-1999; 99US-0159294.  
 PR 13-OCT-1999; 99US-0159295.  
 PR 14-OCT-1999; 99US-0159329.  
 PR 14-OCT-1999; 99US-0159330.  
 PR 14-OCT-1999; 99US-0159337.  
 PR 14-OCT-1999; 99US-0159637.  
 PR 14-OCT-1999; 99US-0159638.  
 PR 18-OCT-1999; 99US-0159584.  
 PR 21-OCT-1999; 99US-0160741.  
 PR 21-OCT-1999; 99US-0160767.  
 PR 21-OCT-1999; 99US-0160768.  
 PR 21-OCT-1999; 99US-0160770.  
 PR 21-OCT-1999; 99US-0160814.  
 PR 21-OCT-1999; 99US-0160815.  
 PR 22-OCT-1999; 99US-0160880.  
 PR 22-OCT-1999; 99US-0160881.  
 PR 22-OCT-1999; 99US-0160881.  
 PR 25-OCT-1999; 99US-0160989.  
 PR 25-OCT-1999; 99US-0161404.  
 PR 25-OCT-1999; 99US-0161405.  
 PR 25-OCT-1999; 99US-0161406.  
 PR 26-OCT-1999; 99US-0161359.  
 PR 26-OCT-1999; 99US-0161360.  
 PR 26-OCT-1999; 99US-0161361.  
 PR 28-OCT-1999; 99US-0161920.  
 PR 28-OCT-1999; 99US-0161992.  
 PR 28-OCT-1999; 99US-0161993.  
 PR 29-OCT-1999; 99US-0162142.  
 PR 29-OCT-1999; 99US-0162142.

Query Match 1.7%; Score 17; DB 21; Length 1277;  
 Best Local Similarity 100.0%; Pred. No. 64;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 222 tgctgcatccctgcacat 238  
 Db 524 tgctgcatccctgcacat 540

RESULT 41  
 AAV64526/c  
 ID AAV64526 standard; DNA; 1338 BP.

XX AAV64526;  
 AC  
 XX  
 XX 27-JAN-1999 (first entry)  
 DT  
 DE M. tuberculosis immunogenic polypeptide XP31 DNA.  
 XX  
 XX Tuberculosis; immunogenic; soluble; antigen; protective immunity; TB;  
 KW vaccine; pharmaceutical; infection; diagnosis; ss.  
 XX  
 OS Mycobacterium tuberculosis.  
 XX  
 PN WO9816646-A2.  
 XX  
 PD 23-APR-1998.  
 XX  
 PF 07-OCT-1997; 97WO-US18293.  
 XX  
 PR 13-MAR-1997; 97US-0818112.  
 PR 11-OCT-1996; 96US-0730510.  
 XX  
 PA (CORI-) CORIXA CORP.  
 XX  
 PI Campos-Neto A, Dillon DC, Houghton R, Lodes MJ;  
 PI Reed SG, Skelky YAW, Twardzik DR, Vedvick TS;  
 XX  
 DR WPI; 1998-261042/23.  
 XX  
 PT Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - used  
 PT to develop products for the detection of M. tuberculosis infection  
 PT and for diagnosis, treatment and prevention of tuberculosis  
 XX  
 XX Claim 31a; Page 162-163; 230pp; English.  
 XX  
 CC This sequence encodes an immunogenic portion of a soluble Mycobacterium  
 CC tuberculosis (MT) antigen which can be used in a method for inducing  
 CC protective immunity against tuberculosis (TB). This sequence can be  
 CC formulated into vaccines and/or pharmaceutical compositions for  
 CC immunising against M. tuberculosis infection or may be used for the  
 CC diagnosis of tuberculosis.  
 XX  
 SO Sequence 1338 BP; 199 A; 432 C; 485 G; 222 T; 0 other;

Query Match 1.7%; Score 17; DB 19; Length 1338;  
 Best Local Similarity 100.0%; Pred. No. 64;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 505 gccagcgcgccctgcac 521  
 Db 1147 gccagcgcgccctgcac 1131

RESULT 42  
 AAV44417/c  
 ID AAV44417 standard; DNA; 1338 BP.  
 AC  
 XX  
 XX AAV44417;  
 AC  
 XX  
 DT 09-NOV-1998 (first entry)  
 XX  
 DE Mycobacterium tuberculosis antigen XP31 DNA.  
 XX  
 XX Tuberculosis; infection; diagnosis; antigen; XP31; ss.  
 KW  
 OS Mycobacterium tuberculosis strain Erdman.  
 XX  
 PN WO9816645-A2.  
 XX  
 PD 23-APR-1998.  
 XX  
 PF 07-OCT-1997; 97WO-US18214.  
 XX

PR 13-MAR-1997: 97US-0818111.  
PR 11-OCT-1996; 96US-0729622.  
XX  
XX (CORI-) CORIXA CORP.  
XX Campos-Melo A, Dillon DC, Houghton R, Lodes MJ;  
PI Reed SG, Skeiky YAW, Twardzik DR, Vedvick TS;  
XX WPI, 1998-251292/22.  
DR  
XX  
PT New isolated Mycobacterium tuberculosis polypeptides and DNA - used  
PT to develop products for the detection of M. tuberculosis infection  
and diagnosis of tuberculosis  
XX  
XX Claim 11a; Page 171-172; 250pp; English.

This DNA sequence codes for a portion of Mycobacterium tuberculosis antigen XP31. It was isolated from a M. tuberculosis strain Erdman genomic DNA expression library using sera from patients having extrapulmonary tuberculosis. The clone bears some similarity to known sequences. The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AA664291-W64379) comprising an antigenic portion of a soluble M. tuberculosis antigen, or an immunogenic portion of an M. tuberculosis antigen, as well as DNA sequences encoding such polypeptides, recombinant expression vectors and transformed or transfected host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient using these polypeptides, antibodies or oligonucleotide probes and primers.

Sequence 1338 BP; 199 A; 432 C; 485 G; 222 T; 0 other;

|         | Query Match              | 1.7%;  | Score 17;     | DB 19; | Length 1338; |
|---------|--------------------------|--------|---------------|--------|--------------|
|         | Best Local Similarity    | 100.0% | Pred. No. 64; |        |              |
| Matches | 17; Conservative         | 0;     | Mismatches    | 0;     | Indels       |
|         |                          |        |               |        | Gaps         |
| OY      | 505 gccacgcgagcctcgtc    | 521    |               |        |              |
|         |                          |        |               |        |              |
| db      | 1147 gccacgcggcgccctcgtc | 1131   |               |        |              |

|            |                                                                  |
|------------|------------------------------------------------------------------|
| RESULT     | 43                                                               |
| AA219327/c |                                                                  |
| ID         | AA219327 standard; DNA; 1338 BP.                                 |
| XX         |                                                                  |
| AC         | AA219327;                                                        |
| XX         |                                                                  |
| DT         | 05-NOV-1999 (first entry)                                        |
| XX         |                                                                  |
| DE         | M. tuberculosis antigen XP31 DNA sequence.                       |
| XX         |                                                                  |
| KW         | Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen; |
| XX         |                                                                  |
| KW         | immunotherapy; diagnosis; immunisation; vaccine; infection;      |
| KW         | immune response; skin test; ss.                                  |
| OS         |                                                                  |
| XX         | Mycobacterium tuberculosis.                                      |
| XX         |                                                                  |
| PN         | W09942076-A2.                                                    |
| XX         |                                                                  |
| PD         | 26-AUG-1999.                                                     |
| XX         |                                                                  |
| PF         | 17-FEB-1999; 99MO-US03268.                                       |
| XX         |                                                                  |
| PR         | 05-MAY-1998; 98US-0072967.                                       |
| XX         |                                                                  |
| PR         | 18-FEB-1998; 98US-0025197.                                       |
| XX         |                                                                  |
| PA         | (CORI-) CORIXA CORP.                                             |
| XX         |                                                                  |
| PI         | Campos-Neto A, Dillon DC, Hendrickson RC, Houghton R;            |
| PI         | Loeser MU, Reed SG, Skeiky YAW, Twardzik DR, Vedralick TS;       |
| XX         |                                                                  |

DR WPI: 1995-527409/44.  
XX  
XX New antigens from Mycobacterium tuberculosis useful in diagnostic  
XX skin tests and protective or therapeutic vaccines or compositions  
PT  
XX  
PS Claim 11: Page 157-158; 299pp; English.  
XX  
XX The present invention describes polypeptides comprising an immunogenic  
CC part of a Mycobacterium tuberculosis antigen (Ag). Also described  
CC are vaccines and fusion protein containing M. tuberculosis Ag's.  
CC M. tuberculosis Ag's, DNAs encoding them, derived fusion proteins and  
CC other polypeptides fragments, can be used in pharmaceutical composition  
CC or vaccines to generate a protective or therapeutic immune response to  
CC M. tuberculosis and as reagents in skin tests for diagnosis of  
CC tuberculosis. Ag can induce proliferation of, or cytokine secretion  
CC by, T, B or natural killer cells and/or macrophages in  
CC tuberculosis-immune subjects. AA219249 to AA219460 and AA219083 to  
CC AA219225 are used in the exemplification of the present invention.  
XX  
XX  
S0 Sequence 1338 BP; 199 A; 432 C; 485 G; 222 T; 0 other:

|    |             |                   |              |             |            |            |
|----|-------------|-------------------|--------------|-------------|------------|------------|
|    | Query Match | Similarity        | 1.7%         | Score 17    | DB 20      | Length 138 |
|    | Best Local  | Similarity        | 100.0%       | Pred No. 64 |            |            |
|    | Matches     | 17                | Conservative | 0           | Mismatches | 0          |
| OY | 505         | gccacgcgagcctcgtc | 521          |             |            |            |
|    |             |                   |              |             |            |            |
| Db | 1147        | gccacgcgagcctcgtc | 1131         |             |            |            |

RESULT 44  
ID AAZ19115/c  
AAZ19115 standard; DNA; 1338 BP.  
AC AAZ19115;  
XX  
DT 05-NOV-1999 (first entry)  
DE M. tuberculosis recombinant antigen DNA encoding XP31.  
XX  
KM Antigen; diagnosis; detection; infection; antibody; immunisation;  
KM vaccine; immunity; ss.  
XX  
OS Mycobacterium tuberculosis.  
XX  
PM W09942118-A2.  
XX  
PD 26-AUG-1999.  
XX  
PF 17-FEB-1999; 99WO-US03365.  
XX  
PR 05-MAY-1998; 98US-0072596.  
PR 18-FEB-1998; 98US-0024753.  
XX  
PA (CORI-) CORIXA CORP.  
PI Campos-Neto A, Dillon DC, Hendrickson RC, Houghton R;  
PI Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR, Vedvick TS;  
XX  
DR WPI: 1999-527416/44.  
XX  
PT New polypeptide comprising antigenic portions of M. tuberculosis  
XX  
PS Claim 11a, Page 202-203; 323pp; English.  
XX  
XX This invention describes novel recombinant antigens and their encoding  
CC nucleic acids derived from Mycobacterium tuberculosis. The novel  
CC polypeptides are useful for detecting M. tuberculosis infection in a  
CC biological sample by detecting antibodies which bind with the  
CC polypeptides, and are useful as vaccines for immunizing against  
CC M. tuberculosis infection. The new detection methods are needed as  
CC current vaccination strategies do not provide 100% immunity.

XX Sequence 1338 BP; 199 A; 432 C; 485 G; 222 T; 0 other;  
SQ

Query Match  
1.7%; Score 17; DB 20; Length 1338;  
Best Local Similarity 100.0%; Pred. No. 64;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 505 gccagcgcgcgtcgtc 521  
|||||  
DB 1147 GCCAGCGCGGCTCGTC 1131

## RESULT 45

AAC78035  
ID AAC78035 standard; cDNA; 1470 BP.

AC AAC78035;

DT 08-FEB-2001 (first entry)

DE Human cancer associated gene sequence SEQ ID NO:429.

XX  
XX Human; cancer associated gene; cancer antigen; detection; cancer;  
KM diagnosis; cytostatic; proliferative; vulnerrary; immunomodulator;  
KM antidiabetic; antiaesthetic; antirheumatic; antihypertic; antiviral;  
KM antiinflammatory; antihypertic; antiallergic; antibacterial; cardiant;  
KM dermatological; neuroprotective; thrombolytic; coagulant; noctropic;  
KM vasotrophic; antiproliferative; antineoplastic; gene therapy; inflammation;  
KM immune disorder; haematopoietic cell disorder; autoimmune disorder;  
KM allergic reaction; graft versus host disease; organ rejection;  
KM haemostatic; thrombolytic; cardiovascular disorder; infection;  
KM neurological disease; drug screening; ss.

OS Homo sapiens.

PN WO200055350-A1.

PD 21-SEP-2000.

PF 08-MAR-2000; 2000MO-US05882.

PR 12-MAR-1999; 99US-0124270.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Ruben SM;

DR WPI: 2000-587533/55.

DR P-PSDB: AAB43826.

PT Novel isolated nucleic acids comprising sequences encoding peptides

PT useful for treating or diagnosing e.g. cancer -

PT Claim 1; Page 970; 2352pp; English.

XX AACT7607 to AAC78448 encode the human cancer associated proteins given  
CC in AAB43398 to AAB44239. The proteins can have activities based on the  
CC tissues and cells the genes are expressed in. Example of activities  
CC include: cytostatic; proliferative; vulnerrary; immunomodulator;  
CC antidiabetic; antiaesthetic; antirheumatic; antihypertic;  
CC antiinflammatory; antihypertic; antiallergic; antibacterial; antiviral;  
CC dermatological; neuroprotective; cardiant; thrombolytic; coagulant;  
CC noctropic; vasotrophic; antiproliferative; antineoplastic; gene therapy;  
CC polynucleotides and polypeptides can be used for preventing, treating or  
CC ameliorating medical conditions and diagnosing pathological conditions.  
CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from  
CC the present invention may be used to treat immune disorders by activating  
CC or inhibiting the proliferation, differentiation or mobilisation of  
CC immune cells, to treat disorders of haematopoietic cells, autoimmune  
CC disorders, allergic reactions, graft versus host disease and organ  
CC rejection, modulate haemostatic or thrombolytic activity, modulate  
CC inflammation, cancers, cardiovascular disorders, neurological disease and

CC bacterial or viral infections. The peptides, nucleotides, antibodies,  
CC agonists and antagonists may be also be used in drug screens. AAC78449 to  
CC AAC78457 and AAB44240 represent sequences used in the exemplification of  
CC the present invention.

XX Sequence 1470 BP; 336 A; 380 C; 470 G; 277 T; 7 other;  
SQ

Query Match  
1.7%; Score 17; DB 21; Length 1470;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 812 tgacagagctgcagcag 828  
|||||  
DB 1015 tgacagagctgcagcag 1031

## RESULT 46

AAC79935  
ID AAC79935 standard; cDNA; 1647 BP.

AC AAC79935;

DT 12-FEB-2001 (first entry)

DE Human secreted protein encoding cDNA for gene 38.

XX  
XX Secreted protein; human; immunosuppressive; antirheumatic;  
KM antiproliferative; cytostatic; cardiant; vasotrophic; cerebroprotective;  
KM noctropic; neuroprotective; antibacterial; virucide; fungicide;  
KM ophthalmological; gene therapy; treatment; autoimmune disease; infection;  
KM cardiovascular disorder; nervous system disorder; ocular disorder;  
KM wound healing; epithelial cell proliferation; skin aging; mental state;  
KM transplantation; metabolism modulation; ss.

OS Homo sapiens.

PN WO200055200-A1.

PD 21-SEP-2000.

PF 09-MAR-2000; 2000MO-US06042.

PR 12-MAR-1999; 99US-0124143.

PR 03-DEC-1999; 99US-0168663.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Ruben SM, Komatsoulis G;

DR WPI: 2000-656008/63.

DR P-PSDB: AAB44954.

PT Isolated human secretory proteins, nucleic acids encoding them and

PT antibodies directed against them, useful for diagnosing and treating

PT disorders related to the proteins such as cancer, Alzheimer's disease

PT and Parkinsons -

PT Claim 1a; Page 370-371; 453pp; English.

XX This invention describes a novel isolated polypeptide (I) and its  
CC encoding nucleic acid molecule (II) which have immunosuppressive,  
CC antirheumatic, antiproliferative, cytostatic, cardiant,  
CC vasotrophic, cerebroprotective, neuroprotective, antibacterial,  
CC virucide, fungicide and ophthalmological activity and which can be used  
CC for gene therapy. (I) and (II) are used to prevent, treat or ameliorate  
CC a medical condition in e.g. humans, mice, rabbits, goats, horses, cats,  
CC dogs, chickens or sheep. (I) and (II) are also used in diagnosing a  
CC pathological condition or susceptibility to a pathological condition. The  
CC antibodies to (II) can also be used in alleviating symptoms associated  
CC with the disorders and in diagnostic immunoassays e.g. radioimmunoassays  
CC or enzyme linked immunosorbent assays (ELISA). Disorders which are  
CC diagnosed or treated include autoimmune diseases e.g. Rheumatoid



PI Stimmons CR:  
 XX WPI: 2001-147338/15.  
 DR P-PSDB; AAY97667.  
 XX  
 PT Novel maize ethylene signalling pathway EIN3 gene useful for modulating  
 PT the level of EIN3 in maize plants, including crowding tolerance, growth  
 PT in impacted soils, flooding tolerance and disease resistance  
 XX  
 PS Claim 1: Page 82-85; 86pp; English.  
 XX  
 CC This sequence encodes the corn zm EIN3-2 protein. The protein is involved  
 CC in the ethylene signal transduction pathway, and is an EIN3 homologue.  
 CC An expression cassette comprising the DNA sequence is useful for  
 CC modulating the level of EIN3 in a plant, in particular a maize plant. The  
 CC maize genes are nuclear transcription factors that promote the  
 CC ethylene-mediated responses, including crowding tolerance, seed set and  
 CC development, growth in impacted soils, flooding tolerance, maturation and  
 CC senescence and disease resistance. Diminishment of ethylene action in  
 CC plant, in particular cereals such as maize, by reducing the expression or  
 CC activity of the DNA promotes tolerance to close spacing with reduced  
 CC stress and yield loss. The DNA is useful as a probe or amplification  
 CC primer in the detection, quantitation or isolation of gene transcripts.  
 CC in detecting deficiencies in the level of mRNA in screening for desired  
 CC transgenic plants, for detecting mutations in gene, for monitoring  
 CC upregulation of expression or changes in enzyme activity in screening  
 CC assays, orthologs, or paralog of the gene, or for site directed  
 CC mutagenesis in eukaryotic cells. The nucleic acid can also be used for  
 CC recombinant expression of polypeptides or as immunogens in the  
 CC preparation and/or screening of antibodies. The proteins can be employed  
 CC in assays for enzyme agonists or antagonists of enzyme function, or as  
 CC immunogens or antigens to obtain antibodies specifically immunoreactive  
 CC with the protein. Plants expressing the DNA germinate better in compacted  
 CC soils and in flooded conditions or water-logged soils, resulting in  
 CC higher stand counts.  
 XX  
 SQ Sequence 2459 BP; 587 A; 747 C; 696 G; 429 T; 0 other:  
 XX  
 Query Match 1.7%; Score 17; DB 22; Length 2459;  
 Best Local Similarity 100.0%; Pred. No. 63;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 817 gagctgcagcagagccg 833  
 ||||||||||||||||  
 Db 570 gagctgcagcagagccg 586  
 XX  
 RESULT 49  
 AAX14998/C  
 ID AAX14998 standard; DNA; 2545 BP.  
 XX  
 AC AAX14998;  
 XX  
 DT 15-APR-1999 (first entry)  
 XX  
 DE DNA encoding a monokine induced by gamma-interferon (MIG).  
 XX  
 KW Monokine induced by gamma-interferon; MIG; CXK chemokine; metastasis;  
 KW angiogenesis inhibitor; angiotensin inducer; tumour growth inhibition;  
 KW haemangiomas; rheumatoid arthritis; atherosclerosis; meningioma;  
 KW idiopathic pulmonary fibrosis; benign prostatic hypertrophy; psoriasis;  
 KW vascular restenosis; arteriovenous malformation; neovascular glaucoma;  
 KW angiofibroma; haemophilic joint; hypertrophic scar; Osler-Weber syndrome;  
 KW pyogenic granuloma retrolental fibroplasia; scleroderma; trachoma;  
 KW vascular adhesion; synovitis; dermatitis; endometriosis; pterygium;  
 KW diabetic retinopathy; neovascularisation; chronic bronchitis;  
 KW adult respiratory distress syndrome; ARDS; pseudogout;  
 KW cystic fibrosis; ss.  
 XX  
 KW Homo sapiens.  
 OS  
 XX  
 FH Key Location/Qualifiers

FT CDS 40..417  
 FT /\*tag= a  
 FT /product= MIG  
 XX  
 PN US5871723-A.  
 XX  
 PD 16-FEB-1999.  
 XX  
 PF 06-JUN-1995; 95US-0468819.  
 XX  
 PR 06-JUN-1995; 95US-0468819.  
 XX  
 PA (UNMI ) UNIV MICHIGAN.  
 PI Kunkel SL, Polverini PJ, Strieter RW;  
 DR WPI: 1999-165569/14.  
 DR P-PSDB; AAW96710.  
 XX  
 PT Use of chemokines with a conserved Cys Xaa Cys (CXC) sequence -  
 PT which do not contain amino acid sequence ELR, for inhibiting  
 PT angiogenesis in tumours, rheumatoid arthritis, restenosis or  
 PT glaucoma  
 XX  
 PS Example 13; Columns 123-126; 145pp; English.  
 XX  
 CC The present sequence encodes a monokine induced by gamma-interferon  
 CC (MIG). MIG is a CXK chemokine that is an inhibitor of angiogenesis.  
 CC The specification describes methods for inhibiting angiogenesis or for  
 CC inducing angiostasis, using chemokines (with a conserved Cys Xaa Cys  
 CC (CXC) sequence at the N-terminal) other than platelet factor-4, and  
 CC which do not contain the amino acid sequence ELR. The methods are useful  
 CC for inhibiting tumour growth and metastasis and for treating diseases  
 CC such as haemangiomas, rheumatoid arthritis, atherosclerosis and  
 CC idiopathic pulmonary fibrosis (IPF), benign prostatic hypertrophy (BPH),  
 CC vascular restenosis, arteriovenous malformations (AVM), meningioma,  
 CC neovascular glaucoma, psoriasis, angiofibroma, haemophilic joints,  
 CC hypertrophic scars, Osler-Weber syndrome, pyogenic granuloma retrolental  
 CC fibroplasia, scleroderma, trachoma, vascular adhesions, synovitis,  
 CC dermatitis, endometriosis, pterygium, diabetic retinopathy  
 CC neovascularisation associated with corneal injury or grafts, adult  
 CC respiratory distress syndrome (ARDS), chronic bronchitis, pseudogout  
 CC and cystic fibrosis.  
 XX  
 SQ Sequence 2545 BP; 755 A; 581 C; 457 G; 752 T; 0 other:  
 XX  
 Query Match 1.7%; Score 17; DB 20; Length 2545;  
 Best Local Similarity 100.0%; Pred. No. 63;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 787 ctgaactgggttaga 803  
 ||||||||||||||||  
 Db 277 CTGAACTGCGTTTACA 261  
 XX  
 RESULT 50  
 AAA74878/C  
 ID AAA74878 standard; DNA; 2545 BP.  
 XX  
 AC AAA74878;  
 XX  
 DT 17-JAN-2001 (first entry)  
 XX  
 DE Human chemokine coding sequence spg ID NO: 39.  
 XX  
 KW Macrophage recruitment; chemokine derivative; MCP-1; osteoporosis;  
 KW monocyte chemoattractant protein-1; inflammation; atherosclerosis; HIV;  
 KW AIDS; stroke; psoriasis; autoimmune disease; hypertension; endotoxaemia;  
 KW basophil-mediated disease; myocardial infarction; acute ischaemia;  
 KW rheumatoid arthritis; contraception; ds.  
 XX  
 KW Homo sapiens.  
 OS

|    |     |                                                                          |
|----|-----|--------------------------------------------------------------------------|
| XX | Key | Location/Qualifiers                                                      |
| FH | CDS | 40..417                                                                  |
| FT |     | /tag= a                                                                  |
| FT |     | /product= "human chemokine"                                              |
| PN |     | MO200042071-A2.                                                          |
| XX |     |                                                                          |
| PD |     | 20-JUL-2000.                                                             |
| XX |     |                                                                          |
| PF |     | 12-JAN-2000; 2000WO-US00821.                                             |
| XX |     |                                                                          |
| PR |     | 12-JAN-1999; 99US-0229071.                                               |
| XX |     | 17-MAR-1999; 99US-0271192.                                               |
| PR |     | 01-DEC-1999; 99US-0452406.                                               |
| XX |     |                                                                          |
| PA |     | (NEOR-) NEORX CORP.                                                      |
| PI |     | Granger DJ, Tatalick LM;                                                 |
| XX |     |                                                                          |
| DR |     | WPI: 2000-499101/44.                                                     |
| DR |     | P-PSDB; AAB15803.                                                        |
| XX |     |                                                                          |
| PT |     | New peptide 3, amide and heterocyclic compounds and saccharide           |
| PT |     | conjugates used for inhibiting chemokine induced activity and for        |
| PT |     | treating e.g. stroke, vascular diseases, autoimmune diseases and tumour  |
| PT |     | growth -                                                                 |
| XX |     |                                                                          |
| PS |     | Disclosure; Page 356-358; 387pp; English.                                |
| XX |     |                                                                          |
| CC |     | The present invention concerns the identification of a number of         |
| CC |     | chemokines which can be used to produce derivatives, agonists and        |
| CC |     | antagonists which are then useful in disease treatment. The chemokines   |
| CC |     | include sequences AAB15785-B15794, AAB15803-B15813 and AAB15831-B15848.  |
| CC |     | These chemokine derivatives can be used to treat diseases such as        |
| CC |     | autoimmune diseases, atherosclerosis, osteoporosis, HIV infection and    |
| CC |     | AIDS, psoriasis, inflammatory diseases, hypertension, basophil-mediated  |
| CC |     | diseases, endotoxaemia, myocardial infarction, acute ischaemia and       |
| CC |     | rheumatoid arthritis, and can be used to prevent strokes and as          |
| CC |     | contraceptives. The chemokine coding sequences AA47488-A7488 can be      |
| CC |     | used in gene therapy for the same diseases, as well as in the production |
| CC |     | of animal models.                                                        |
| XX |     |                                                                          |
| SO |     | Sequence 2545 BP; 755 A; 581 C; 457 G; 752 T; 0 other;                   |

|    |     |                   |     |
|----|-----|-------------------|-----|
| QY | 787 | ctgaatctgggtttaga | 803 |
|    |     |                   |     |
| DB | 277 | ctgaatctgggtttaga | 261 |

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| Query Match           | 1.7%;           | Score 17;     | DB 21;    | Length 2545; |
| Best Local Similarity | 100.0%;         | Pred. No. 63; |           |              |
| Matches 17;           | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0;      |

Search completed: September 21, 2001, 16:27:43  
Job time: 9633 sec

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 256: gb\_est187:\*  
 257: gb\_est188:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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| 2          | 20    | 2.0         | 222    | AA645779 | AA645779 vnl0h04..r |
| 3          | 20    | 2.0         | 414    | AM268708 | AM268708 xv35b05.x  |
| 4          | 20    | 2.0         | 438    | AT769658 | AT769658 wj25d02.x  |
| 5          | 20    | 2.0         | 436    | AT028162 | AT028162 ov90d02.x  |
| 6          | 20    | 2.0         | 483    | AM269670 | AM269670 xv36d11.x  |
| 7          | 20    | 2.0         | 480    | AT594177 | AT594177 vnl0h04..y |
| 8          | 20    | 2.0         | 917    | BB893506 | BB893506 601438060  |
| 9          | 19    | 1.9         | 468    | AO511509 | AO511509 HS_5074.B  |
| 10         | 19    | 1.9         | 523    | AO337527 | AO337527 HS_5017.A  |
| 11         | 19    | 1.9         | 656    | A2497878 | A2497878 TM0334G24  |
| 12         | 19    | 1.9         | 657    | AO938059 | AO938059 NB6-908R   |
| 13         | 19    | 1.9         | 713    | CNS04812 | AL325737 mm95d03..y |
| 14         | 19    | 1.9         | 747    | AI325737 | AI325737 Tetradon   |
| 15         | 19    | 1.9         | 842    | A2668255 | AL2668255 ENTKX52TF |
| 16         | 19    | 1.9         | 891    | CNS0370E | AL266639 Tetradon   |
| 17         | 18    | 1.8         | 235    | BB043716 | BB043716 BB043716   |
| 18         | 18    | 1.8         | 241    | AV292150 | AV292150 AV292150   |
| 19         | 18    | 1.8         | 244    | AV526879 | AV526879 AV526879   |
| 20         | 18    | 1.8         | 261    | AA584777 | AA584777 EST67411   |
| 21         | 18    | 1.8         | 264    | AV527317 | AV527317 AV527317   |
| 22         | 18    | 1.8         | 294    | Z29054   | Z29054 ATTS2067 OF  |
| 23         | 18    | 1.8         | 301    | AV208201 | AV208201 AV208201   |
| 24         | 18    | 1.8         | 312    | AA095509 | AA095509 14744..seq |
| 25         | 18    | 1.8         | 318    | 191      | 218479 ATTS0855 AC  |
| 26         | 18    | 1.8         | 327    | 122      | AM896020 QV4-NN003  |
| 27         | 18    | 1.8         | 331    | 188      | T21227              |
| 28         | 18    | 1.8         | 334    | 104      | AI991901 ws42b06..x |
| 29         | 18    | 1.8         | 334    | 119      | AM682518 EST01367   |
| 30         | 18    | 1.8         | 340    | 150      | BF521901 UI-R-BT0   |
| 31         | 18    | 1.8         | 342    | 136      | BE520970 M16A2STM   |
| 32         | 18    | 1.8         | 365    | 31       | AV527474            |
| 33         | 18    | 1.8         | 368    | 189      | T42951 6214.Lambda  |
| 34         | 18    | 1.8         | 370    | 191      | Z47675 ATTS4531 St  |
| 35         | 18    | 1.8         | 376    | 30       | AV430174 AV430174   |
| 36         | 18    | 1.8         | 391    | 31       | AV526330 AV526330   |
| 37         | 18    | 1.8         | 391    | 159      | N65689 20729.Lambda |
| 38         | 18    | 1.8         | 392    | 157      | D78804 HUN516H08B   |
| 39         | 18    | 1.8         | 392    | 226      | AO253544            |
| 40         | 18    | 1.8         | 398    | 31       | AV527255            |
| 41         | 18    | 1.8         | 404    | 31       | AV526564            |
| 42         | 18    | 1.8         | 441    | 188      | T21720 3728.Lambda  |
| 43         | 18    | 1.8         | 443    | 158      | H77242 17673.Lambda |
| 44         | 18    | 1.8         | 446    | 225      | AO228766 HS_2020.A  |
| 45         | 18    | 1.8         | 461    | 159      | N65546 20586.Lambda |
| 46         | 18    | 1.8         | 463    | 104      | AI991951 ws43d04.x  |
| 47         | 18    | 1.8         | 463    | 151      | BF612300 daa17a11.  |
| 48         | 18    | 1.8         | 465    | 140      | BE811867 PMO-AN003  |
| 49         | 18    | 1.8         | 474    | 244      | A2462258 1M0269023  |
| 50         | 18    | 1.8         | 476    | 20       | AI466074 xv39b02..y |
| 51         | 18    | 1.8         | 482    | 234      | AO847780 LMAJFV1_1  |
| 52         | 18    | 1.8         | 487    | 234      | AO849674 LMAJFV1_1  |
| 53         | 18    | 1.8         | 489    | 6        | AA395581 27378.Lam  |
| 54         | 18    | 1.8         | 489    | 166      | BE351801 894051G09  |
| 55         | 18    | 1.8         | 493    | 164      | BE215806 HV_CEBD000 |
| 56         | 18    | 1.8         | 493    | 31       | AV527484            |
| 57         | 18    | 1.8         | 498    | 136      | BE487307 175980.BA  |
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| 59         | 18    | 1.8         | 500    | 31       | AV527890 AV527890   |
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| 61         | 18    | 1.8         | 503    | 31       | AV527784 AV527784   |
| 62         | 18    | 1.8         | 504    | 14       | AA982948 ua22h06..r |
| 63         | 18    | 1.8         | 505    | 188      | T22194 4202.Lambda  |
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| 66         | 18    | 1.8         | 516    | 188      | R64762 13366.Lambda |
| 67         | 18    | 1.8         | 525    | 188      | T21563 3571.Lambda  |
| 68         | 18    | 1.8         | 527    | 112      | AM168137            |
| 69         | 18    | 1.8         | 529    | 159      | N38270              |
| 70         | 18    | 1.8         | 531    | 31       | AV528061            |
| 71         | 18    | 1.8         | 536    | 16       | AI158964            |
| 72         | 18    | 1.8         | 539    | 104      | AI995890            |
| 73         | 18    | 1.8         | 556    | 174      | BG147743            |
| 74         | 18    | 1.8         | 565    | 31       | AV567359            |
| 75         | 18    | 1.8         | 570    | 108      | AU164787            |
| 76         | 18    | 1.8         | 579    | 158      | H36018              |
| 77         | 18    | 1.8         | 583    | 31       | AV526136            |
| 78         | 18    | 1.8         | 592    | 158      | H76069              |
| 79         | 18    | 1.8         | 598    | 151      | BF620011            |
| 80         | 18    | 1.8         | 599    | 1        | AA042763            |
| 81         | 18    | 1.8         | 618    | 107      | AU101340            |
| 82         | 18    | 1.8         | 621    | 242      | AZ351625            |
| 83         | 18    | 1.8         | 682    | 165      | BE291467            |
| 84         | 18    | 1.8         | 707    | 162      | BE037926            |
| 85         | 18    | 1.8         | 707    | 152      | BG323623            |
| 86         | 18    | 1.8         | 711    | 247      | AZ631126            |
| 87         | 18    | 1.8         | 712    | 251      | AZ687529            |
| 88         | 18    | 1.8         | 722    | 141      | BE892353            |
| 89         | 18    | 1.8         | 722    | 162      | BE038966            |
| 90         | 18    | 1.8         | 727    | 162      | BE038427            |
| 91         | 18    | 1.8         | 731    | 144      | BF120897            |
| 92         | 18    | 1.8         | 754    | 138      | BE689492            |
| 93         | 18    | 1.8         | 807    | 21       | AI528777            |
| 94         | 18    | 1.8         | 862    | 146      | BF267443            |
| 95         | 18    | 1.8         | 866    | 150      | BF526531            |
| 96         | 18    | 1.8         | 898    | 230      | AO901727            |
| 97         | 18    | 1.8         | 909    | 225      | CNS01XEB            |
| 98         | 18    | 1.8         | 919    | 221      | CNS030F7            |
| 99         | 18    | 1.8         | 920    | 154      | BG479157            |
| 100        | 18    | 1.8         | 952    | 222      | CNS057PS            |
| 101        | 18    | 1.8         | 968    | 220      | BE741337            |
| 102        | 18    | 1.8         | 986    | 220      | CNS03SRQ            |
| 103        | 18    | 1.8         | 1009   | 221      | CNS0305J            |
| 104        | 18    | 1.8         | 1056   | 222      | CNS05EBA            |
| 105        | 18    | 1.8         | 1078   | 106      | AL543701            |
| 106        | 18    | 1.8         | 1081   | 222      | CNS054X1            |
| 107        | 18    | 1.8         | 1101   | 192      | AK006925            |
| 108        | 18    | 1.8         | 1464   | 144      | BF118779            |
| 109        | 18    | 1.8         | 1481   | 175      | BG250472            |
| 110        | 17    | 1.7         | 72     | 158      | H88159              |
| 111        | 17    | 1.7         | 122    | 159      | N70934              |
| 112        | 17    | 1.7         | 136    | 158      | H59904              |
| 113        | 17    | 1.7         | 164    | 23       | AI701300            |
| 114        | 17    | 1.7         | 165    | 1        | AA002343            |
| 115        | 17    | 1.7         | 206    | 1        | AA042040            |
| 116        | 17    | 1.7         | 207    | 28       | AV278443            |
| 117        | 17    | 1.7         | 208    | 174      | BG158928            |
| 118        | 17    | 1.7         | 212    | 122      | AM896035            |
| 119        | 17    | 1.7         | 219    | 238      | AZ083101            |
| 120        | 17    | 1.7         | 226    | 8        | AA473731            |
| 121        | 17    | 1.7         | 230    | 191      | Z41347              |
| 122        | 17    | 1.7         | 240    | 26       | AV196116            |
| 123        | 17    | 1.7         | 241    | 11       | AM647187            |
| 124        | 17    | 1.7         | 241    | 155      | C05473              |
| 125        | 17    | 1.7         | 242    | 121      | AM809963            |
| 126        | 17    | 1.7         | 244    | 114      | AM313247            |
| 127        | 17    | 1.7         | 244    | 144      | BF116745            |
| 128        | 17    | 1.7         | 244    | 168      | BF730909            |
| 129        | 17    | 1.7         | 248    | 189      | T84122              |
| 130        | 17    | 1.7         | 251    | 7        | AA416280            |
| 131        | 17    | 1.7         | 251    | 187      | N87803              |
| 132        | 17    | 1.7         | 253    | 13       | AA887431            |
| 133        | 17    | 1.7         | 255    | 11       | AA741155            |
| 134        | 17    | 1.7         | 256    | 27       | AV260749            |
| 135        | 17    | 1.7         | 260    | 141      | BE860963            |
| 136        | 17    | 1.7         | 264    | 6        | AA382428            |
| 137        | 17    | 1.7         | 266    | 161      | BB563790            |
| 138        | 17    | 1.7         | 266    | 6        | AA383032            |
| 139        | 17    | 1.7         | 266    | 162      | BB604316            |
| 140        | 17    | 1.7         | 267    | 11       | AA741789            |
|            |       |             |        |          | AM168137 xg60d04..x |
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|            |       |             |        |          | AI158964 u142g05..x |
|            |       |             |        |          | AI995890 701549071  |
|            |       |             |        |          | BG147743 mab53h05.  |
|            |       |             |        |          | AV567359 AV567359   |
|            |       |             |        |          | AU164787 AU164787   |
|            |       |             |        |          | H36018 14540.Lambda |
|            |       |             |        |          | AV526136 AV526136   |
|            |       |             |        |          | H76069 17774.Lambda |
|            |       |             |        |          | BF620011 HVSMC000   |
|            |       |             |        |          | AA042763 25019 CD4  |
|            |       |             |        |          | AU101340 AU101340   |
|            |       |             |        |          | AZ351625 1M0089634  |
|            |       |             |        |          | BE291467 601085211  |
|            |       |             |        |          | BE037926 AA06E04.A  |
|            |       |             |        |          | BG323623 602422094  |
|            |       |             |        |          | AZ631126 1M0485G09  |
|            |       |             |        |          | AZ687529 2M0178H23  |
|            |       |             |        |          | BE892353 601433812  |
|            |       |             |        |          | BE038966 AB07H04.A  |
|            |       |             |        |          | BE038427 AAL7D03.A  |
|            |       |             |        |          | BF120897 60157705   |
|            |       |             |        |          | BE689492 uw55c05..y |
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|            |       |             |        |          | AL334451 Tetradon   |
|            |       |             |        |          | AL543701 Tetradon   |
|            |       |             |        |          | AL321310 Tetradon   |
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|            |       |             |        |          | N87803 K0130F Humna |
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|            |       |             |        |          | AA741155 n201h02..s |
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|            |       |             |        |          | BB604316 BB604316   |
|            |       |             |        |          | AA741789 Lmtv39p3/  |

|     |    |     |     |     |           |                      |       |    |     |     |     |           |                      |
|-----|----|-----|-----|-----|-----------|----------------------|-------|----|-----|-----|-----|-----------|----------------------|
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| 148 | 17 | 1.7 | 287 | 131 | BB318793  | BB318793             | C 221 | 17 | 1.7 | 392 | 113 | AA260776  | AA260776 um67c08..y  |
| 149 | 17 | 1.7 | 288 | 143 | BF061066  | BF061066 7180b03..x  | C 222 | 17 | 1.7 | 394 | 119 | AA647355  | AA647355 EST325898   |
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| 151 | 17 | 1.7 | 291 | 125 | BB086802  | BB086802             | C 224 | 17 | 1.7 | 395 | 18  | AI286530  | AI286530 u18b5h10..y |
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| 154 | 17 | 1.7 | 295 | 115 | AA407061  | AA407061 UI-HF-BLO   | C 227 | 17 | 1.7 | 398 | 114 | AA297283  | AA297283 UI-HF-BMO-  |
| 155 | 17 | 1.7 | 298 | 10  | AA701335  | AA701335 z159g11..s  | C 228 | 17 | 1.7 | 400 | 7   | AA431145  | AA431145 zw71e10..r  |
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| 157 | 17 | 1.7 | 301 | 5   | AA315628  | AA315628 EST18745    | C 230 | 17 | 1.7 | 400 | 121 | AA687045  | AA687045 ps8b10..y   |
| 158 | 17 | 1.7 | 305 | 8   | AA499594  | AA499594 v904f08..r  | C 231 | 17 | 1.7 | 400 | 223 | AQ054381  | AQ054381 C1T-HSP-2   |
| 159 | 17 | 1.7 | 307 | 119 | AA707347  | AA707347 832006G07   | C 232 | 17 | 1.7 | 402 | 118 | AA587625  | AA587625 ST60F08 P   |
| 160 | 17 | 1.7 | 307 | 151 | BF593469  | BF593469 7903a10..x  | C 233 | 17 | 1.7 | 402 | 115 | AA378416  | AA378416 RC3-H7022   |
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| 165 | 17 | 1.7 | 320 | 169 | BF760649  | BF760649 CM1-CT063   | C 238 | 17 | 1.7 | 406 | 112 | AA193438  | AA193438 x175b08..x  |
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| 167 | 17 | 1.7 | 329 | 158 | H56634    | H56634 y18b10..r1    | C 240 | 17 | 1.7 | 408 | 233 | AQ772736  | AQ772736 HS-2019_B   |
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| 175 | 17 | 1.7 | 340 | 155 | CO4433    | CO4433 CO4433 Huma   | C 248 | 17 | 1.7 | 417 | 235 | AA0912690 | AA0912690 nbe60038G  |
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| 194 | 17 | 1.7 | 361 | 32  | AA698101  | AA698101             | C 267 | 17 | 1.7 | 426 | 18  | AI309230  | AI309230 qo68b05..x  |
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| 201 | 17 | 1.7 | 372 | 111 | AAW053009 | AAW053009 614077H07  | C 274 | 17 | 1.7 | 433 | 32  | AA665130  | AA665130 AV665130    |
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| C 287 | 17 | 1.7 | 443 | 187 | N95764    | N95764 z65c03.s1    | 360 | 17 | 1.7 | 502 | 22  | A1561151 | A1561151 tg37a10.x |
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| C 289 | 17 | 1.7 | 444 | 189 | T80744    | T80744 yd92c06.r1   | 362 | 17 | 1.7 | 502 | 137 | BE595042 | BE595042 p11_45_A0 |
| C 290 | 17 | 1.7 | 445 | 110 | AM014376  | AM014376 UI-H-B10-  | 363 | 17 | 1.7 | 503 | 240 | A2220281 | A2220281 Sheared D |
| C 291 | 17 | 1.7 | 446 | 19  | A1361966  | A1361966 qy37g06.x  | 364 | 17 | 1.7 | 503 | 241 | A2299040 | A2299040 RPT-23-1  |
| C 292 | 17 | 1.7 | 446 | 19  | A1379114  | A1379114 t659f02.x  | 365 | 17 | 1.7 | 504 | 141 | BE842356 | BE842356 MR4-ST012 |
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| C 294 | 17 | 1.7 | 448 | 138 | BE66683   | BE66683-150283 MA   | 367 | 17 | 1.7 | 507 | 110 | AV756064 | AV756064 AV756064  |
| C 295 | 17 | 1.7 | 450 | 117 | AM517272  | AM517272 xg08c02.x  | 368 | 17 | 1.7 | 509 | 18  | A1316056 | A1316056 u616h02.y |
| C 296 | 17 | 1.7 | 452 | 21  | A1554616  | A1554616 t626c09.x  | 369 | 17 | 1.7 | 510 | 4   | AA221041 | AA221041 mv62h12.r |
| C 297 | 17 | 1.7 | 453 | 139 | BE759515  | BE759515 an_2338 A  | 370 | 17 | 1.7 | 513 | 9   | AA595851 | AA595851 nn05d10.s |
| C 298 | 17 | 1.7 | 453 | 141 | BE859435  | BE859435 UI-M-AP0-  | 371 | 17 | 1.7 | 513 | 109 | N56635   | N56635 yw*73h03.r1 |
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| C 300 | 17 | 1.7 | 456 | 19  | A1341973  | A1341973 q898a04.x  | 373 | 17 | 1.7 | 515 | 23  | A1691039 | A1691039 t613g11.x |
| C 301 | 17 | 1.7 | 457 | 20  | A1446668  | A1446668 t111f04.x  | 374 | 17 | 1.7 | 516 | 20  | A1471980 | A1471980 t185b11.x |
| C 302 | 17 | 1.7 | 457 | 22  | A1571352  | A1571352 t45b05.x   | 375 | 17 | 1.7 | 517 | 7   | AA411035 | AA411035 zv40b06.s |
| C 303 | 17 | 1.7 | 458 | 1   | AA002916  | AA002916 mg38e10.r  | 376 | 17 | 1.7 | 518 | 145 | BE146275 | BE146275 TCAG31.TY |
| C 304 | 17 | 1.7 | 458 | 159 | N55559    | N55559 yv49e03.s1   | 377 | 17 | 1.7 | 519 | 19  | A1346483 | A1346483 qp51a02.x |
| C 305 | 17 | 1.7 | 459 | 17  | A1195909  | A1195909 ue51b11.r  | 378 | 17 | 1.7 | 519 | 104 | AJ397440 | AJ397440 AJ397440  |
| C 306 | 17 | 1.7 | 459 | 190 | W20518    | W20518 zb26g02.r1   | 379 | 17 | 1.7 | 521 | 13  | AA865735 | AA865735 oH41g10.s |
| C 307 | 17 | 1.7 | 460 | 241 | AA295346  | AA295346 RPT-23-1   | 380 | 17 | 1.7 | 521 | 106 | AL587744 | AL587744 AL587744  |
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| C 310 | 17 | 1.7 | 464 | 155 | BG555936  | BG555936 df23f06.x  | 383 | 17 | 1.7 | 524 | 119 | AM654937 | AM654937 105443 MA |
| C 311 | 17 | 1.7 | 465 | 106 | AL554955  | AL554955 AL554955   | 384 | 17 | 1.7 | 524 | 138 | BE665288 | BE665288 153467 MA |
| C 312 | 17 | 1.7 | 465 | 187 | R23666    | R23666 y932a09.r1   | 385 | 17 | 1.7 | 526 | 102 | A1831691 | A1831691 w150h12.x |
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| C 314 | 17 | 1.7 | 468 | 22  | A1586781  | A1586781 4A6061B05  | 387 | 17 | 1.7 | 527 | 173 | BG103350 | BG103350 RH122-18  |
| C 315 | 17 | 1.7 | 468 | 143 | BF042315  | BF042315 BP250011B  | 388 | 17 | 1.7 | 530 | 23  | A1697165 | A1697165 t606e03.x |
| C 316 | 17 | 1.7 | 469 | 152 | BC370615  | BC370615 u066b01.y  | 389 | 17 | 1.7 | 530 | 154 | BG502333 | BG502333 602550216 |
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| C 318 | 17 | 1.7 | 470 | 23  | A1674357  | A1674357 w638f04.x  | 391 | 17 | 1.7 | 532 | 19  | A1369027 | A1369027 qw27f05.x |
| C 319 | 17 | 1.7 | 470 | 112 | AM140903  | AM140903 EST280837  | 392 | 17 | 1.7 | 533 | 171 | BE932609 | BE932609 RC5-NT018 |
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| C 321 | 17 | 1.7 | 471 | 258 | FR0048019 | FR0048019 Fugu rubr | 394 | 17 | 1.7 | 535 | 30  | AV391380 | AV391380 AV391380  |
| C 322 | 17 | 1.7 | 472 | 102 | A1447169  | A1447169 m94e06.x   | 395 | 17 | 1.7 | 536 | 31  | AV599712 | AV599712 AV599712  |
| C 323 | 17 | 1.7 | 473 | 102 | A1818876  | A1818876 w113a02.x  | 396 | 17 | 1.7 | 538 | 144 | BE111764 | BE111764 7135b10.x |
| C 324 | 17 | 1.7 | 474 | 136 | BE494727  | BE494727 WHE1257.A  | 397 | 17 | 1.7 | 538 | 165 | BE238825 | BE238825 946009E12 |
| C 325 | 17 | 1.7 | 475 | 21  | A1553844  | A1553844 t629f03.x  | 398 | 17 | 1.7 | 539 | 119 | AM720808 | AM720808 833007R02 |
| C 326 | 17 | 1.7 | 475 | 145 | BE152034  | BE152034 u223e08.y  | 399 | 17 | 1.7 | 541 | 32  | AV664061 | AV664061 AV664061  |
| C 327 | 17 | 1.7 | 476 | 22  | A1580492  | A1580492 t113e11.x  | 400 | 17 | 1.7 | 542 | 121 | AM810602 | AM810602 MK4-ST012 |
| C 328 | 17 | 1.7 | 477 | 102 | A1818992  | A1818992 w160f01.x  | 401 | 17 | 1.7 | 544 | 232 | AO677569 | AO677569 HS_5529.A |
| C 329 | 17 | 1.7 | 477 | 136 | BE501650  | BE501650 h61h05.x   | 402 | 17 | 1.7 | 546 | 135 | BE657930 | BE657930 EML_39.DO |
| C 330 | 17 | 1.7 | 479 | 144 | BF130957  | BF130957 601819779  | 403 | 17 | 1.7 | 547 | 138 | BE665798 | BE665798 154964 MA |
| C 331 | 17 | 1.7 | 479 | 188 | R99845    | R99845 yq68f11.r1   | 404 | 17 | 1.7 | 548 | 122 | AM668454 | AM668454 EST380530 |
| C 332 | 17 | 1.7 | 480 | 13  | AA916735  | AA916735 oH84b07.s  | 405 | 17 | 1.7 | 552 | 175 | BC263515 | BC263515 WHE2342.H |
| C 333 | 17 | 1.7 | 481 | 9   | AA571593  | AA571593 vm07b12.r  | 406 | 17 | 1.7 | 552 | 246 | A2591195 | A2591195 IM0401104 |
| C 334 | 17 | 1.7 | 481 | 12  | AA819761  | AA819761 UI-R-A0-a  | 407 | 17 | 1.7 | 554 | 17  | A1183507 | A1183507 q442f04.x |
| C 335 | 17 | 1.7 | 481 | 236 | AO977390  | AO977390 RPT-23-3   | 408 | 17 | 1.7 | 556 | 32  | AV665131 | AV665131 AV665131  |
| C 336 | 17 | 1.7 | 482 | 6   | AA397099  | AA397099 mx84b12.r  | 409 | 17 | 1.7 | 557 | 7   | AA456966 | AA456966 aa09g03.s |
| C 337 | 17 | 1.7 | 482 | 158 | H30789    | H30789 y079f07.r1   | 410 | 17 | 1.7 | 557 | 19  | A1347912 | A1347912 qp60e07.x |
| C 338 | 17 | 1.7 | 483 | 17  | A1230840  | A1230840 EST227535  | 411 | 17 | 1.7 | 559 | 173 | BG084490 | BG084490 H3101E06- |
| C 339 | 17 | 1.7 | 483 | 165 | BE301059  | BE301059 Da84d08.x  | 412 | 17 | 1.7 | 563 | 12  | AA833332 | AA833332 u005h03.r |
| C 340 | 17 | 1.7 | 485 | 15  | A1084920  | A1084920 q1f17g12.x | 413 | 17 | 1.7 | 563 | 138 | BE665781 | BE665781 154938 MA |
| C 341 | 17 | 1.7 | 485 | 170 | BF871631  | BF871631 OVO-ET014  | 414 | 17 | 1.7 | 567 | 190 | W72164   | W72164 zd77f10.r1  |
| C 342 | 17 | 1.7 | 487 | 148 | BF444277  | BF444277 262084 MA  | 415 | 17 | 1.7 | 569 | 112 | AM171153 | AM171153 f138a10.x |
| C 343 | 17 | 1.7 | 487 | 154 | BG516219  | BG516219 ETE5ted55  | 416 | 17 | 1.7 | 569 | 227 | AO338323 | AO338323 HS_5010.B |
| C 344 | 17 | 1.7 | 488 | 142 | BE987729  | BE987729 UI-M-CGP0  | 417 | 17 | 1.7 | 571 | 120 | AM743969 | AM743969 ut26b04.y |
| C 345 | 17 | 1.7 | 490 | 143 | BG39824   | BG39824 OVI_29.E0   | 418 | 17 | 1.7 | 574 | 9   | AA619825 | AA619825 v161d05.s |
| C 346 | 17 | 1.7 | 491 | 122 | AM952892  | AM952892 EST364962  | 419 | 17 | 1.7 | 575 | 137 | BE583063 | BE583063 7-5F-MY P |
| C 347 | 17 | 1.7 | 491 | 144 | BF122166  | BF122166 601755833  | 420 | 17 | 1.7 | 577 | 240 | W73840   | W73840 zd50d01.r1  |
| C 348 | 17 | 1.7 | 492 | 245 | A2521734  | A2521734 RPT-11-1   | 421 | 17 | 1.7 | 577 | 192 | A2357838 | A2357838 1M0099M08 |
| C 349 | 17 | 1.7 | 493 | 13  | AA879755  | AA879755 uv98c07.r  | 422 | 17 | 1.7 | 579 | 245 | A2357695 | A2357695 RPT-23-1  |
| C 350 | 17 | 1.7 | 493 | 13  | AA879755  | AA879755 uv98c07.r  | 423 | 17 | 1.7 | 580 | 105 | AL506266 | AL506266 AL506266  |
| C 351 | 17 | 1.7 | 495 | 19  | A1346125  | A1346125 qP48g12.x  | 424 | 17 | 1.7 | 583 | 30  | AV441561 | AV441561 AV441561  |
| C 352 | 17 | 1.7 | 496 | 7   | AA467505  | AA467505 ve01c09.r  | 425 | 17 | 1.7 | 584 | 151 | BF616788 | BF616788 HYSMEC001 |
| C 353 | 17 | 1.7 | 496 | 111 | AM106034  | AM106034 um22c05.y  | 426 | 17 | 1.7 | 586 | 111 | AM076317 | AM076317 614065E04 |
| C 354 | 17 | 1.7 | 497 | 138 | BE246612  | BE246612 uuz2c09.y  | 427 | 17 | 1.7 | 588 | 151 | BF593498 | BF593498 7g03f03.x |
| C 355 | 17 | 1.7 | 497 | 14  | AI006640  | AI006640 ue16g09.y  | 428 | 17 | 1.7 | 588 | 166 | BE372802 | BE372802 601224318 |
| C 356 | 17 | 1.7 | 500 | 150 | BF544886  | BF544886 UI-R-A0-a  | 429 | 17 | 1.7 | 589 | 111 | AM106080 | AM106080 um22h02.y |
| C 357 | 17 | 1.7 | 500 | 236 | AO987028  | AO987028 RPT-23-2   | 430 | 17 | 1.7 | 589 | 166 | BE332979 | BE332979 us96h01.y |
| C 358 | 17 | 1.7 | 500 |     |           |                     | 431 | 17 | 1.7 | 589 |     |          |                    |
| C 359 | 17 | 1.7 | 500 |     |           |                     | 432 | 17 | 1.7 | 589 |     |          |                    |

|     |    |     |     |     |           |                     |     |    |     |     |     |          |                     |
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| 433 | 17 | 1.7 | 591 | 110 | AM011638  | AM011638 614011B10  | 506 | 17 | 1.7 | 737 | 138 | BE689383 | BE689383 uw54a03.y  |
| 434 | 17 | 1.7 | 592 | 156 | C95922    | C95922 C95922 Marc  | 507 | 17 | 1.7 | 738 | 137 | BE602565 | BE602565 HVSME010   |
| 435 | 17 | 1.7 | 593 | 156 | BG542875  | BG542875 602571050  | 508 | 17 | 1.7 | 743 | 110 | AV756180 | AV756180 AV756180   |
| 436 | 17 | 1.7 | 593 | 156 | C95923    | C95923 C95923 Marc  | 509 | 17 | 1.7 | 747 | 221 | CNS04K09 | AT295290 Tetraodon  |
| 437 | 17 | 1.7 | 593 | 165 | BE237905  | BE237905 894038H08  | 510 | 17 | 1.7 | 749 | 110 | AV755280 | AV755280 AV755280   |
| 438 | 17 | 1.7 | 593 | 167 | BE448856  | BE448856 ut8rf09.y  | 511 | 17 | 1.7 | 754 | 106 | AL556341 | AL556341 AL556341   |
| 439 | 17 | 1.7 | 593 | 242 | A2374514  | A2374514 1M0127M17  | 512 | 17 | 1.7 | 768 | 233 | AV756335 | AV756335 HS_-5387_B |
| 440 | 17 | 1.7 | 597 | 32  | AV708855  | AV708855 AV708855   | 513 | 17 | 1.7 | 769 | 110 | AV756181 | AV756181 AV756181   |
| 441 | 17 | 1.7 | 600 | 247 | A2648402  | A2648402 1M0517120  | 514 | 17 | 1.7 | 774 | 165 | BE276529 | BE276529 601144155  |
| 442 | 17 | 1.7 | 601 | 16  | AL133257  | AL133257 HA1855 Hu  | 515 | 17 | 1.7 | 775 | 23  | AT668760 | AT668760 TENG01065  |
| 443 | 17 | 1.7 | 603 | 117 | AM546477  | AM546477 L0008G06-  | 516 | 17 | 1.7 | 781 | 147 | BP347365 | BP347365 602020650  |
| 444 | 17 | 1.7 | 606 | 226 | A0257474  | A0257474 nbxb0018E  | 517 | 17 | 1.7 | 783 | 139 | BE731340 | BE731340 601566471  |
| 445 | 17 | 1.7 | 610 | 226 | A0269963  | A0269963 HS_-2061_B | 518 | 17 | 1.7 | 784 | 141 | BE870867 | BE870867 601449172  |
| 446 | 17 | 1.7 | 612 | 165 | BE291736  | BE291736 601084456  | 519 | 17 | 1.7 | 784 | 173 | BG111059 | BG111059 602284744  |
| 447 | 17 | 1.7 | 617 | 14  | AA968297  | AA968297 uc71908.y  | 520 | 17 | 1.7 | 787 | 227 | A0367152 | A0367152 toxb00010  |
| 448 | 17 | 1.7 | 617 | 122 | AM912093  | AM912093 ufa1f06.y  | 521 | 17 | 1.7 | 798 | 155 | BG571948 | BG571948 602593296  |
| 449 | 17 | 1.7 | 618 | 8   | AA543452  | AA543452 vJ82805.r  | 522 | 17 | 1.7 | 799 | 172 | BP966263 | BP966263 602269786  |
| 450 | 17 | 1.7 | 618 | 32  | AV717648  | AV717648 AV717648   | 523 | 17 | 1.7 | 802 | 20  | AT125555 | AT125555 md64e12.y  |
| 451 | 17 | 1.7 | 618 | 141 | BE908096  | BE908096 601500326  | 524 | 17 | 1.7 | 804 | 144 | BF065096 | BF065096 HV_CEB002  |
| 452 | 17 | 1.7 | 619 | 22  | AT622195  | AT622195 486037E01  | 525 | 17 | 1.7 | 805 | 175 | BG254933 | BG254933 602369382  |
| 453 | 17 | 1.7 | 619 | 154 | BG472976  | BG472976 602514920  | 526 | 17 | 1.7 | 807 | 221 | CNS04P75 | AT301730 Tetraodon  |
| 454 | 17 | 1.7 | 621 | 137 | BE566092  | BE566092 601339091  | 527 | 17 | 1.7 | 812 | 170 | BF862243 | BF862243 603032P09  |
| 455 | 17 | 1.7 | 625 | 18  | AT1316963 | AT1316963 uJ24G10.y | 528 | 17 | 1.7 | 814 | 153 | BG386185 | BG386185 602455370  |
| 456 | 17 | 1.7 | 625 | 152 | BG354973  | BG354973 006851ea   | 529 | 17 | 1.7 | 815 | 220 | CNS02N73 | AT205032 Tetraodon  |
| 457 | 17 | 1.7 | 626 | 142 | BE960901  | BE960901 601648138  | 530 | 17 | 1.7 | 816 | 220 | CNS02SKH | AL211994 Tetraodon  |
| 458 | 17 | 1.7 | 632 | 140 | BE776997  | BE776997 MY_-23-D-0 | 531 | 17 | 1.7 | 817 | 108 | AU132858 | AU132858 AU132858   |
| 459 | 17 | 1.7 | 636 | 256 | B54011    | B54011 C1T-HSP-201  | 532 | 17 | 1.7 | 827 | 139 | BE740344 | BE740344 601594648  |
| 460 | 17 | 1.7 | 637 | 122 | AM898205  | AM898205 RC3-NN006  | 533 | 17 | 1.7 | 834 | 141 | BE890675 | BE890675 601431090  |
| 461 | 17 | 1.7 | 638 | 152 | BG370097  | BG370097 LMA105 V8  | 534 | 17 | 1.7 | 834 | 144 | BF121069 | BF121069 601757895  |
| 462 | 17 | 1.7 | 640 | 138 | BE648606  | BE648606 UT-M-78005 | 535 | 17 | 1.7 | 836 | 192 | AK003202 | AK003202 Mus muscu  |
| 463 | 17 | 1.7 | 640 | 243 | AZ407409  | AZ407409 1M0178805  | 536 | 17 | 1.7 | 837 | 141 | BE902094 | BE902094 601674864  |
| 464 | 17 | 1.7 | 644 | 242 | AZ356482  | AZ356482 1M0097006  | 537 | 17 | 1.7 | 843 | 137 | BE570924 | BE570924 601329290  |
| 465 | 17 | 1.7 | 646 | 247 | AZ646241  | AZ646241 1M051206   | 538 | 17 | 1.7 | 846 | 137 | BE568051 | BE568051 601341567  |
| 466 | 17 | 1.7 | 648 | 1   | AA044836  | AA044836 zk74d10.r  | 539 | 17 | 1.7 | 847 | 142 | BE968978 | BE968978 601649494  |
| 467 | 17 | 1.7 | 648 | 24  | AT183384  | AT183384 614011B10  | 540 | 17 | 1.7 | 847 | 155 | BG541098 | BG541098 602570264  |
| 468 | 17 | 1.7 | 648 | 241 | AZ333758  | AZ333758 1M0061E22  | 541 | 17 | 1.7 | 856 | 154 | BG491500 | BG491500 602535816  |
| 469 | 17 | 1.7 | 650 | 20  | AT458014  | AT458014 tJ66d09.x  | 542 | 17 | 1.7 | 857 | 221 | CNS04HLZ | AT291104 Tetraodon  |
| 470 | 17 | 1.7 | 652 | 236 | AZ005606  | AZ005606 RPlCI-23-2 | 543 | 17 | 1.7 | 859 | 106 | AL562896 | AL562896 AL562896   |
| 471 | 17 | 1.7 | 655 | 112 | AM133291  | AM133291 se16h07.y  | 544 | 17 | 1.7 | 859 | 174 | BG122071 | BG122071 602349507  |
| 472 | 17 | 1.7 | 658 | 238 | AZ086647  | AZ086647 RPlCI-23-2 | 545 | 17 | 1.7 | 864 | 173 | BG071645 | BG071645 H3101E06-  |
| 473 | 17 | 1.7 | 660 | 225 | AQ161295  | AQ161295 nbxb0006P  | 546 | 17 | 1.7 | 867 | 155 | BG575647 | BG575647 6025986112 |
| 474 | 17 | 1.7 | 661 | 145 | BP185808  | BP185808 601817511  | 547 | 17 | 1.7 | 868 | 174 | BG171410 | BG171410 602321910  |
| 475 | 17 | 1.7 | 663 | 105 | AL505067  | AL505067 AL505067   | 548 | 17 | 1.7 | 873 | 171 | BP966145 | BP966145 602286419  |
| 476 | 17 | 1.7 | 669 | 173 | BG103718  | BG103718 RH1Z2_-39- | 549 | 17 | 1.7 | 873 | 221 | CNS04QVS | AL303121 Tetraodon  |
| 477 | 17 | 1.7 | 670 | 175 | BG269939  | BG269939 Lr_ad_435  | 550 | 17 | 1.7 | 874 | 154 | BG492862 | BG492862 602536894  |
| 478 | 17 | 1.7 | 673 | 144 | BE109949  | BE109949 7172d07.x  | 551 | 17 | 1.7 | 874 | 221 | CNS03O81 | AT255627 Tetraodon  |
| 479 | 17 | 1.7 | 679 | 175 | BG277421  | BG277421 ux43f02.y  | 552 | 17 | 1.7 | 882 | 238 | AZ139107 | AZ139107 SP_0178_B  |
| 480 | 17 | 1.7 | 681 | 105 | AL134536  | AL134536 DKF2P5470  | 553 | 17 | 1.7 | 883 | 154 | BG496771 | BG496771 602538752  |
| 481 | 17 | 1.7 | 684 | 242 | AZ381186  | AZ381186 1M0137006  | 554 | 17 | 1.7 | 883 | 220 | CNS0328Y | AT224539 Tetraodon  |
| 482 | 17 | 1.7 | 687 | 32  | AV703541  | AV703541 AV703541   | 555 | 17 | 1.7 | 884 | 146 | BF214404 | BF214404 601845532  |
| 483 | 17 | 1.7 | 687 | 108 | AU163906  | AU163906 AU163906   | 556 | 17 | 1.7 | 888 | 221 | CNS03205 | BE216490 Tetraodon  |
| 484 | 17 | 1.7 | 688 | 248 | AZ745238  | AZ745238 RPlCI-24-1 | 557 | 17 | 1.7 | 890 | 256 | BI18933  | BI18933 T25J19-5P6  |
| 485 | 17 | 1.7 | 689 | 110 | AV764439  | AV764439 AV764439   | 558 | 17 | 1.7 | 908 | 106 | AL543596 | AL543596 AL543596   |
| 486 | 17 | 1.7 | 690 | 1   | AA044591  | AA044591 zk67b09.r  | 559 | 17 | 1.7 | 912 | 140 | BE780307 | BE780307 601468288  |
| 487 | 17 | 1.7 | 692 | 170 | BP864927  | BP864927 963056A02  | 560 | 17 | 1.7 | 920 | 142 | BE967994 | BE967994 601648877  |
| 488 | 17 | 1.7 | 696 | 241 | AZ299137  | AZ299137 RPlCI-23-1 | 561 | 17 | 1.7 | 920 | 168 | BF698603 | BF698603 602126119  |
| 489 | 17 | 1.7 | 700 | 105 | AL504499  | AL504499 AL504499   | 562 | 17 | 1.7 | 931 | 140 | BE791889 | BE791889 601586177  |
| 490 | 17 | 1.7 | 701 | 144 | BE132470  | BE132470 601820395  | 563 | 17 | 1.7 | 935 | 145 | BF209695 | BF209695 601874229  |
| 491 | 17 | 1.7 | 704 | 155 | BG574361  | BG574361 602596290  | 564 | 17 | 1.7 | 936 | 22  | AT622966 | AT622966 TENG0580   |
| 492 | 17 | 1.7 | 705 | 147 | BE342791  | BE342791 602015065  | 565 | 17 | 1.7 | 941 | 221 | CNS03VM7 | AT262606 Tetraodon  |
| 493 | 17 | 1.7 | 705 | 165 | BE289763  | BE289763 601092348  | 566 | 17 | 1.7 | 942 | 139 | BE746162 | BE746162 601578375  |
| 494 | 17 | 1.7 | 708 | 154 | BG534551  | BG534551 602553795  | 567 | 17 | 1.7 | 943 | 221 | CNS04AML | AL282054 Tetraodon  |
| 495 | 17 | 1.7 | 714 | 18  | AT294394  | AT294394 LP07755.5  | 568 | 17 | 1.7 | 945 | 175 | BG251395 | BG251395 602364041  |
| 496 | 17 | 1.7 | 715 | 155 | BG587261  | BG587261 EST489032  | 569 | 17 | 1.7 | 947 | 221 | CNS04PR3 | AL301656 Tetraodon  |
| 497 | 17 | 1.7 | 719 | 138 | BE647951  | BE647951 UI-M-BH1-  | 570 | 17 | 1.7 | 949 | 145 | BF162577 | BF162577 601770219  |
| 498 | 17 | 1.7 | 719 | 241 | AZ212005  | AZ212005 1M0027109  | 571 | 17 | 1.7 | 950 | 222 | CNS05GAX | AT336066 Tetraodon  |
| 499 | 17 | 1.7 | 721 | 108 | AU139136  | AU139136 AU139136   | 572 | 17 | 1.7 | 951 | 142 | BE970769 | BE970769 601680124  |
| 500 | 17 | 1.7 | 724 | 32  | AV645822  | AV645822 AV645822   | 573 | 17 | 1.7 | 955 | 166 | BE379383 | BE379383 601237054  |
| 501 | 17 | 1.7 | 725 | 248 | AZ705723  | AZ705723 RPlCI-23-2 | 574 | 17 | 1.7 | 956 | 106 | AL578626 | AL578626 AL578626   |
| 502 | 17 | 1.7 | 727 | 220 | CNS02122  | AL176372 Tetraodon  | 575 | 17 | 1.7 | 959 | 141 | BE905703 | BE905703 601495715  |
| 503 | 17 | 1.7 | 732 | 152 | BG328692  | BG328692 602427965  | 576 | 17 | 1.7 | 966 | 221 | CNS04EBO | AT1206447 Tetraodon |
| 504 | 17 | 1.7 | 733 | 32  | AV717926  | AV717926 AV717926   | 577 | 17 | 1.7 | 968 | 220 | CNS02OAE | AT206447 Tetraodon  |
| 505 | 17 | 1.7 | 734 | 233 | AQ781202  | AQ781202 HS_3138_A  | 578 | 17 | 1.7 | 970 | 143 | BF038563 | BF038563 601459827  |

|       |    |     |      |     |           |           |             |    |     |     |     |           |
|-------|----|-----|------|-----|-----------|-----------|-------------|----|-----|-----|-----|-----------|
| 579   | 17 | 1.7 | 979  | 173 | BG106112  | 602289934 | C 652       | 16 | 1.6 | 218 | 116 | AM451421  |
| 580   | 17 | 1.7 | 980  | 141 | BE903833  | 601677192 | C 653       | 16 | 1.6 | 220 | 22  | AI623890  |
| 581   | 17 | 1.7 | 980  | 172 | BG030132  | 602297315 | C 654       | 16 | 1.6 | 223 | 171 | BF901675  |
| C 582 | 17 | 1.7 | 983  | 220 | CNS0347U  | AL2277091 | Tetraodon   | 16 | 1.6 | 225 | 12  | AA786141  |
| C 583 | 17 | 1.7 | 990  | 146 | BF215841  | 601861357 | C 655       | 16 | 1.6 | 225 | 111 | AM087469  |
| C 584 | 17 | 1.7 | 996  | 220 | CNS03861  | AL232227  | Tetraodon   | 16 | 1.6 | 225 | 111 | AM087469  |
| C 585 | 17 | 1.7 | 998  | 220 | CNS0360B  | AL2320276 | Tetraodon   | 16 | 1.6 | 225 | 241 | AZ290667  |
| C 586 | 17 | 1.7 | 1001 | 106 | AL561843  | AL561843  | C 658       | 16 | 1.6 | 226 | 103 | AI916712  |
| C 587 | 17 | 1.7 | 1015 | 192 | AK002864  | AK002864  | C 659       | 16 | 1.6 | 226 | 161 | BM582536  |
| 588   | 17 | 1.7 | 1021 | 192 | AK003834  | AK003834  | C 660       | 16 | 1.6 | 226 | 23  | AI652100  |
| 589   | 17 | 1.7 | 1022 | 190 | W14751    | W14751    | C 661       | 16 | 1.6 | 227 | 23  | AI652100  |
| 590   | 17 | 1.7 | 1023 | 152 | BG329221  | BG329221  | C 662       | 16 | 1.6 | 230 | 29  | AV350839  |
| 591   | 17 | 1.7 | 1028 | 221 | CNS03LAK  | AL249221  | Tetraodon   | 16 | 1.6 | 231 | 241 | AZ479121  |
| 592   | 17 | 1.7 | 1032 | 175 | BG249520  | BG249520  | C 663       | 16 | 1.6 | 234 | 251 | AZ900753  |
| C 593 | 17 | 1.7 | 1033 | 220 | CNS02GAL  | AL196086  | Tetraodon   | 16 | 1.6 | 235 | 30  | AV418718  |
| C 594 | 17 | 1.7 | 1083 | 222 | CNS0547M  | AL337243  | Tetraodon   | 16 | 1.6 | 236 | 222 | FR0018439 |
| 595   | 17 | 1.7 | 1084 | 222 | CNS04XJS  | AL311761  | Tetraodon   | 16 | 1.6 | 240 | 23  | AI683779  |
| 596   | 17 | 1.7 | 1087 | 175 | BG259333  | BG259333  | C 668       | 16 | 1.6 | 240 | 249 | AZ752706  |
| C 597 | 17 | 1.7 | 1101 | 219 | CNS00OND  | AL071401  | Drosophila  | 16 | 1.6 | 241 | 8   | AA477167  |
| C 598 | 17 | 1.7 | 1101 | 219 | CNS00G3V  | AL071401  | Drosophila  | 16 | 1.6 | 242 | 147 | BF373590  |
| C 599 | 17 | 1.7 | 1101 | 222 | CNS054OZ  | BF584626  | 602098650   | 16 | 1.6 | 242 | 170 | BF822858  |
| C 600 | 17 | 1.7 | 1126 | 150 | BF584626  | W29158    | mb96a1.r1   | 16 | 1.6 | 242 | 170 | BF822858  |
| 601   | 17 | 1.7 | 1127 | 190 | W29158    | BG113345  | 602284950   | 16 | 1.6 | 243 | 104 | AI978307  |
| 602   | 17 | 1.7 | 1144 | 141 | BE891148  | BG113345  | 602284950   | 16 | 1.6 | 246 | 161 | BM583147  |
| 603   | 17 | 1.7 | 1146 | 174 | BE891148  | BF208266  | 601871378   | 16 | 1.6 | 247 | 136 | BE516407  |
| C 604 | 17 | 1.7 | 1175 | 145 | BF208266  | AK006059  | Mus muscu   | 16 | 1.6 | 248 | 101 | AA654103  |
| C 605 | 17 | 1.7 | 1196 | 192 | AK006059  | BE420590  | HMM000.E0   | 16 | 1.6 | 249 | 10  | AA654103  |
| 606   | 17 | 1.7 | 1319 | 167 | BE420590  | BG393682  | 602412105   | 16 | 1.6 | 252 | 25  | AV154082  |
| C 607 | 17 | 1.7 | 1418 | 193 | BG393682  | AK017315  | Mus muscu   | 16 | 1.6 | 253 | 248 | AZ728927  |
| C 608 | 17 | 1.7 | 1593 | 152 | AK017315  | BF237917  | 601842495   | 16 | 1.6 | 256 | 113 | AM214673  |
| C 609 | 17 | 1.7 | 1607 | 146 | BF237917  | BF572286  | 602077730   | 16 | 1.6 | 258 | 228 | AO388893  |
| 610   | 17 | 1.7 | 1690 | 150 | BF572286  | BG109738  | 602280875   | 16 | 1.6 | 260 | 140 | BE810749  |
| 611   | 17 | 1.7 | 1889 | 173 | BG109738  | AG022992  | Oryza sat   | 16 | 1.6 | 260 | 223 | AQ027837  |
| 612   | 16 | 1.6 | 59   | 219 | AG022992  | AZ761435  | IM0555F15   | 16 | 1.6 | 261 | 126 | BE118069  |
| C 613 | 16 | 1.6 | 107  | 249 | AZ761435  | T81602    | Yd30a09.r1  | 16 | 1.6 | 261 | 134 | BE528278  |
| C 614 | 16 | 1.6 | 113  | 162 | BE028205  | BE231005  | 253045.BA   | 16 | 1.6 | 265 | 161 | BB601852  |
| 615   | 16 | 1.6 | 121  | 189 | BE028205  | AZ922798  | SIC055G10   | 16 | 1.6 | 267 | 237 | AZ020088  |
| 616   | 16 | 1.6 | 138  | 251 | AZ922798  | BE301846  | BD01C05.Y   | 16 | 1.6 | 268 | 187 | R16206    |
| C 618 | 16 | 1.6 | 139  | 165 | BE301846  | BF534229  | 602047720   | 16 | 1.6 | 269 | 12  | AA825331  |
| C 619 | 16 | 1.6 | 141  | 133 | BF534229  | BF55383   | OV4-HT053   | 16 | 1.6 | 272 | 120 | AA825331  |
| C 620 | 16 | 1.6 | 142  | 150 | BF55383   | BF656411  | FM1-AT053   | 16 | 1.6 | 274 | 130 | BB412379  |
| 621   | 16 | 1.6 | 149  | 145 | BF656411  | AZ918325  | 1006004A0   | 16 | 1.6 | 275 | 133 | BB412379  |
| C 622 | 16 | 1.6 | 154  | 251 | AZ918325  | R84043    | 16002.lambd | 16 | 1.6 | 276 | 2   | AA096629  |
| C 623 | 16 | 1.6 | 157  | 188 | R84043    | A1410706  | EST38999    | 16 | 1.6 | 276 | 106 | AT002342  |
| C 624 | 16 | 1.6 | 160  | 19  | A1410706  | BB581731  | BB581731    | 16 | 1.6 | 277 | 246 | AZ587088  |
| C 625 | 16 | 1.6 | 160  | 161 | BB581731  | AZ371012  | IM0122F19   | 16 | 1.6 | 279 | 107 | AU029833  |
| 626   | 16 | 1.6 | 165  | 242 | AZ371012  | AA422595  | vd29e06.s   | 16 | 1.6 | 279 | 121 | AM853559  |
| C 627 | 16 | 1.6 | 168  | 7   | AA422595  | H48834    | YR34a03.r1  | 16 | 1.6 | 279 | 245 | AZ500749  |
| 628   | 16 | 1.6 | 171  | 158 | H48834    | BB600875  | BB600875    | 16 | 1.6 | 280 | 109 | AV076081  |
| C 629 | 16 | 1.6 | 171  | 161 | BB600875  | A1611757  | lvu7H02.x   | 16 | 1.6 | 280 | 109 | AV076081  |
| C 630 | 16 | 1.6 | 171  | 161 | BB600875  | BE174271  | OV1-HT057   | 16 | 1.6 | 280 | 109 | AV076081  |
| C 631 | 16 | 1.6 | 190  | 22  | AI611757  | BB448586  | BB448586    | 16 | 1.6 | 280 | 131 | BB319896  |
| C 632 | 16 | 1.6 | 191  | 164 | BE174271  | BB582796  | BB582796    | 16 | 1.6 | 281 | 161 | BB572232  |
| C 633 | 16 | 1.6 | 192  | 134 | BB448586  | BE005753  | RC2-BN012   | 16 | 1.6 | 282 | 114 | AM322270  |
| 634   | 16 | 1.6 | 192  | 161 | BB582796  | BG243388  | 602356835   | 16 | 1.6 | 282 | 162 | BE603068  |
| C 635 | 16 | 1.6 | 197  | 162 | BE005753  | BF139810  | 601785791   | 16 | 1.6 | 283 | 190 | W63249    |
| C 636 | 16 | 1.6 | 202  | 175 | BG243388  | BE932425  | OV3-HT063   | 16 | 1.6 | 284 | 172 | BG014672  |
| C 637 | 16 | 1.6 | 203  | 145 | BF139810  | BB584623  | BB584623    | 16 | 1.6 | 285 | 5   | AA319807  |
| C 638 | 16 | 1.6 | 204  | 161 | BB584623  | AT002383  | AT002383    | 16 | 1.6 | 285 | 114 | AM293702  |
| C 639 | 16 | 1.6 | 206  | 142 | BB584623  | AM299903  | XS44a03.x   | 16 | 1.6 | 287 | 246 | AZ625139  |
| 640   | 16 | 1.6 | 207  | 106 | AT002383  | AV2339876 | AV2339876   | 16 | 1.6 | 288 | 128 | BB228806  |
| C 641 | 16 | 1.6 | 208  | 114 | AM299903  | BF006796  | 1160585.A   | 16 | 1.6 | 288 | 191 | AZ21331   |
| 642   | 16 | 1.6 | 211  | 27  | AV2339876 | AZ411926  | IM0185K12   | 16 | 1.6 | 289 | 126 | BB117978  |
| C 643 | 16 | 1.6 | 211  | 143 | BF006796  | AI0332589 | ow70h12.s   | 16 | 1.6 | 289 | 235 | AO922536  |
| C 644 | 16 | 1.6 | 211  | 247 | AZ634242  | AV135546  | AV135546    | 16 | 1.6 | 291 | 132 | BB366546  |
| C 645 | 16 | 1.6 | 212  | 243 | AZ411926  | AM125297  | UT-M-BH2    | 16 | 1.6 | 291 | 246 | AZ588220  |
| 646   | 16 | 1.6 | 213  | 15  | AI0332589 | AM915765  | EST347069   | 16 | 1.6 | 292 | 113 | AW230121  |
| C 647 | 16 | 1.6 | 215  | 25  | AV135546  | AV022822  | AV022822    | 16 | 1.6 | 292 | 129 | BB262861  |
| C 648 | 16 | 1.6 | 215  | 111 | AM125297  | BE011597  | CM4-BN022   | 16 | 1.6 | 292 | 134 | BB452180  |
| C 649 | 16 | 1.6 | 215  | 122 | AM915765  |           |             |    |     |     |     |           |
| C 650 | 16 | 1.6 | 217  | 108 | AV022822  |           |             |    |     |     |     |           |
| C 651 | 16 | 1.6 | 217  | 162 | BE011597  |           |             |    |     |     |     |           |

|     |    |     |     |     |          |           |     |    |     |     |     |           |           |            |
|-----|----|-----|-----|-----|----------|-----------|-----|----|-----|-----|-----|-----------|-----------|------------|
| 725 | 16 | 1.6 | 293 | 8   | AA539651 | LD17930.5 | 798 | 16 | 1.6 | 358 | 144 | BF071087  | BF071087  | s82h01.y   |
| 726 | 16 | 1.6 | 293 | 22  | AI572790 | fn50a04.x | 799 | 16 | 1.6 | 359 | 233 | AO803883  | AO803883  | HS_-2005_A |
| 727 | 16 | 1.6 | 293 | 132 | BB366672 | BB366672  | 800 | 16 | 1.6 | 360 | 26  | AV197870  | AV197870  | AV197870   |
| 728 | 16 | 1.6 | 294 | 162 | BB607769 | BB607769  | 801 | 16 | 1.6 | 360 | 105 | AL118056  | AL118056  | 79224A17   |
| 729 | 16 | 1.6 | 298 | 31  | AV552261 | AV552261  | 802 | 16 | 1.6 | 360 | 105 | CA7720    | CA7720    | Yy1        |
| 730 | 16 | 1.6 | 300 | 26  | AV184952 | AV184952  | 803 | 16 | 1.6 | 360 | 171 | BP934505  | BP934505  | IL5-NT027  |
| 731 | 16 | 1.6 | 300 | 132 | BB384543 | BB384543  | 804 | 16 | 1.6 | 361 | 104 | AI1978332 | AI1978332 | R2154.F.E  |
| 732 | 16 | 1.6 | 301 | 120 | AM804255 | AM804255  | 805 | 16 | 1.6 | 361 | 111 | AM100950  | AM100950  | sd63f06.y  |
| 733 | 16 | 1.6 | 302 | 6   | AA365537 | IL5-UM007 | 806 | 16 | 1.6 | 362 | 247 | A2656736  | A2656736  | 1M0532P24  |
| 734 | 16 | 1.6 | 302 | 21  | AI549953 | AI549953  | 807 | 16 | 1.6 | 362 | 7   | AA438431  | AA438431  | LD12516.5  |
| 735 | 16 | 1.6 | 303 | 160 | W64779   | W64779    | 808 | 16 | 1.6 | 363 | 7   | AA407556  | AA407556  | EST00921   |
| 736 | 16 | 1.6 | 305 | 167 | BE438830 | BE438830  | 809 | 16 | 1.6 | 363 | 114 | AM325063  | AM325063  | TEU04368   |
| 737 | 16 | 1.6 | 307 | 192 | AK00677  | AK00677   | 810 | 16 | 1.6 | 365 | 170 | BF863084  | BF863084  | IL5-ET011  |
| 738 | 16 | 1.6 | 309 | 126 | AA884053 | AA884053  | 811 | 16 | 1.6 | 366 | 4   | AA265761  | AA265761  | m272B02.r  |
| 739 | 16 | 1.6 | 309 | 126 | BB122236 | BB122236  | 812 | 16 | 1.6 | 370 | 14  | AA969069  | AA969069  | op55a10.s  |
| 740 | 16 | 1.6 | 311 | 109 | AV050449 | AV050449  | 813 | 16 | 1.6 | 370 | 115 | AM360326  | AM360326  | 47888.MAR  |
| 741 | 16 | 1.6 | 313 | 12  | AA822603 | AA822603  | 814 | 16 | 1.6 | 370 | 189 | T99585    | T99585    | y65604.r1  |
| 742 | 16 | 1.6 | 313 | 23  | AI696392 | AI696392  | 815 | 16 | 1.6 | 371 | 23  | AI697579  | AI697579  | wel5A06.x  |
| 743 | 16 | 1.6 | 313 | 109 | AV045222 | AV045222  | 816 | 16 | 1.6 | 371 | 138 | BE675255  | BE675255  | 7f05e02.x  |
| 744 | 16 | 1.6 | 314 | 108 | AV022870 | AV022870  | 817 | 16 | 1.6 | 372 | 9   | AA590263  | AA590263  | vm15h07.r  |
| 745 | 16 | 1.6 | 314 | 191 | 224498   | 224498    | 818 | 16 | 1.6 | 373 | 108 | AV030288  | AV030288  | AV030288   |
| 746 | 16 | 1.6 | 315 | 238 | A218498  | A218498   | 819 | 16 | 1.6 | 374 | 16  | AI153822  | AI153822  | ud49B05.r  |
| 747 | 16 | 1.6 | 316 | 11  | AA770179 | AA770179  | 820 | 16 | 1.6 | 374 | 139 | BE719056  | BE719056  | RC6-HT083  |
| 748 | 16 | 1.6 | 317 | 11  | AA783378 | AA783378  | 821 | 16 | 1.6 | 374 | 148 | BF425274  | BF425274  | sux2e11.y  |
| 749 | 16 | 1.6 | 318 | 173 | BC053704 | BC053704  | 822 | 16 | 1.6 | 374 | 163 | BE101421  | BE101421  | UT-R-B01   |
| 750 | 16 | 1.6 | 320 | 25  | AV106214 | AV106214  | 823 | 16 | 1.6 | 374 | 191 | W93044    | W93044    | zd93f03.s1 |
| 751 | 16 | 1.6 | 320 | 102 | AI806593 | AI806593  | 824 | 16 | 1.6 | 376 | 116 | AM462012  | AM462012  | BP230007B  |
| 752 | 16 | 1.6 | 321 | 116 | AM482389 | AM482389  | 825 | 16 | 1.6 | 376 | 147 | BF366987  | BF366987  | PM2-GN001  |
| 753 | 16 | 1.6 | 322 | 6   | AA353189 | AA353189  | 826 | 16 | 1.6 | 376 | 235 | AO933991  | AO933991  | RPCT-23-2  |
| 754 | 16 | 1.6 | 324 | 103 | AI883581 | AI883581  | 827 | 16 | 1.6 | 377 | 115 | AM401253  | AM401253  | lrmldcst   |
| 755 | 16 | 1.6 | 324 | 250 | A2857898 | A2857898  | 828 | 16 | 1.6 | 378 | 15  | AI024452  | AI024452  | ov38A01.x  |
| 756 | 16 | 1.6 | 326 | 258 | P422L    | P422L     | 829 | 16 | 1.6 | 379 | 2   | AA134777  | AA134777  | zm80f05.r  |
| 757 | 16 | 1.6 | 329 | 24  | AI770014 | AI770014  | 830 | 16 | 1.6 | 381 | 223 | AO027089  | AO027089  | CIT-HSP-2  |
| 758 | 16 | 1.6 | 329 | 138 | BE672691 | BE672691  | 831 | 16 | 1.6 | 381 | 223 | AO028370  | AO028370  | CIT-HSP-2  |
| 759 | 16 | 1.6 | 330 | 110 | AV746311 | AV746311  | 832 | 16 | 1.6 | 381 | 250 | A2859332  | A2859332  | 2M0165A13  |
| 760 | 16 | 1.6 | 331 | 14  | AA946593 | AA946593  | 833 | 16 | 1.6 | 382 | 3   | AA201950  | AA201950  | LD04091.5  |
| 761 | 16 | 1.6 | 331 | 158 | H53514   | H53514    | 834 | 16 | 1.6 | 382 | 144 | BF115581  | BF115581  | uy90g10.y  |
| 762 | 16 | 1.6 | 332 | 123 | AM996535 | AM996535  | 835 | 16 | 1.6 | 382 | 223 | AO057463  | AO057463  | CIT-HSP-2  |
| 763 | 16 | 1.6 | 333 | 111 | AM102228 | AM102228  | 836 | 16 | 1.6 | 383 | 112 | AM430242  | AM430242  | 69466.MAR  |
| 764 | 16 | 1.6 | 333 | 158 | H90383   | H90383    | 837 | 16 | 1.6 | 383 | 226 | AO292706  | AO292706  | HS_-2212_B |
| 765 | 16 | 1.6 | 335 | 1   | AA008393 | AA008393  | 838 | 16 | 1.6 | 386 | 2   | AA105799  | AA105799  | mm03c11.r  |
| 766 | 16 | 1.6 | 335 | 23  | AI645058 | AI645058  | 839 | 16 | 1.6 | 386 | 16  | AI158599  | AI158599  | ud29e05.r  |
| 767 | 16 | 1.6 | 335 | 168 | BF709340 | BF709340  | 840 | 16 | 1.6 | 386 | 105 | AL510254  | AL510254  | AL510254   |
| 768 | 16 | 1.6 | 335 | 190 | W33553   | W33553    | 841 | 16 | 1.6 | 387 | 251 | A2927302  | A2927302  | 476.d1874  |
| 769 | 16 | 1.6 | 335 | 191 | 225082   | 225082    | 842 | 16 | 1.6 | 388 | 112 | AM177000  | AM177000  | CMO-CY010  |
| 770 | 16 | 1.6 | 336 | 15  | AI065368 | AI065368  | 843 | 16 | 1.6 | 388 | 187 | R23786    | R23786    | yh34c07.r1 |
| 771 | 16 | 1.6 | 336 | 114 | AM291945 | AM291945  | 844 | 16 | 1.6 | 389 | 22  | AI631514  | AI631514  | wa89h09.x  |
| 772 | 16 | 1.6 | 336 | 160 | BB541584 | BB541584  | 845 | 16 | 1.6 | 389 | 139 | BE724104  | BE724104  | 198805.MA  |
| 773 | 16 | 1.6 | 339 | 13  | AA938349 | AA938349  | 846 | 16 | 1.6 | 390 | 1   | AA034582  | AA034582  | m149f09.r  |
| 774 | 16 | 1.6 | 339 | 141 | BE860869 | BE860869  | 847 | 16 | 1.6 | 390 | 114 | AM282576  | AM282576  | LG1-310_H  |
| 775 | 16 | 1.6 | 340 | 105 | AL511056 | AL511056  | 848 | 16 | 1.6 | 391 | 7   | AA407050  | AA407050  | EST02034   |
| 776 | 16 | 1.6 | 340 | 146 | BE286341 | BE286341  | 849 | 16 | 1.6 | 391 | 169 | BF811493  | BF811493  | CM2-CJ017  |
| 777 | 16 | 1.6 | 341 | 14  | AA965555 | AA965555  | 850 | 16 | 1.6 | 391 | 235 | AO872539  | AO872539  | nbe80050N  |
| 778 | 16 | 1.6 | 342 | 170 | BF883586 | BF883586  | 851 | 16 | 1.6 | 391 | 251 | A2880172  | A2880172  | RPCT-23-2  |
| 779 | 16 | 1.6 | 343 | 102 | AI847406 | AI847406  | 852 | 16 | 1.6 | 394 | 146 | BE058596  | BE058596  | uq73401.y  |
| 780 | 16 | 1.6 | 343 | 138 | BE635322 | BE635322  | 853 | 16 | 1.6 | 394 | 162 | DE058596  | DE058596  | sm18B11.y  |
| 781 | 16 | 1.6 | 343 | 258 | TA33E05P | TA33E05P  | 854 | 16 | 1.6 | 395 | 10  | AA680351  | AA680351  | z11id06.s  |
| 782 | 16 | 1.6 | 344 | 103 | AI918776 | AI918776  | 855 | 16 | 1.6 | 395 | 119 | AM716428  | AM716428  | h2b1D0m.r  |
| 783 | 16 | 1.6 | 344 | 119 | AM721113 | AM721113  | 856 | 16 | 1.6 | 395 | 242 | A2341528  | A2341528  | 1M0073N19  |
| 784 | 16 | 1.6 | 344 | 248 | A2713132 | A2713132  | 857 | 16 | 1.6 | 396 | 156 | C27966    | C27966    | C27966     |
| 785 | 16 | 1.6 | 344 | 249 | A2772746 | A2772746  | 858 | 16 | 1.6 | 396 | 172 | BP986883  | BP986883  | CM1-GN016  |
| 786 | 16 | 1.6 | 345 | 12  | AA844266 | AA844266  | 859 | 16 | 1.6 | 396 | 237 | A2048323  | A2048323  | LMAJFV1_1  |
| 787 | 16 | 1.6 | 348 | 163 | BE126193 | BE126193  | 860 | 16 | 1.6 | 397 | 18  | AI298958  | AI298958  | qul3904.x  |
| 788 | 16 | 1.6 | 350 | 3   | AA178238 | AA178238  | 861 | 16 | 1.6 | 399 | 7   | AA454208  | AA454208  | z48e10.s   |
| 789 | 16 | 1.6 | 351 | 116 | AM480447 | AM480447  | 862 | 16 | 1.6 | 399 | 16  | AI116992  | AI116992  | uz26d11.y  |
| 790 | 16 | 1.6 | 352 | 114 | AM288649 | AM288649  | 863 | 16 | 1.6 | 399 | 170 | BF833779  | BF833779  | RC1-HT088  |
| 791 | 16 | 1.6 | 353 | 9   | AA574335 | AA574335  | 864 | 16 | 1.6 | 399 | 224 | AO072463  | AO072463  | HS_-3024_A |
| 792 | 16 | 1.6 | 353 | 158 | H42425   | H42425    | 865 | 16 | 1.6 | 400 | 224 | AO143095  | AO143095  | HS_-3064_A |
| 793 | 16 | 1.6 | 354 | 2   | AA096628 | AA096628  | 866 | 16 | 1.6 | 401 | 146 | BF286220  | BF286220  | EST7450811 |
| 794 | 16 | 1.6 | 355 | 113 | AM214689 | AM214689  | 867 | 16 | 1.6 | 402 | 2   | AA133814  | AA133814  | z132f12.r  |
| 795 | 16 | 1.6 | 356 | 119 | AM663133 | AM663133  | 868 | 16 | 1.6 | 402 | 143 | BF007087  | BF007087  | 1477161.A  |
| 796 | 16 | 1.6 | 357 | 119 | AM722110 | AM722110  | 869 | 16 | 1.6 | 403 | 244 | A2481215  | A2481215  | 1M0303M18  |
| 797 | 16 | 1.6 | 358 | 140 | BE819977 | BE819977  | 870 | 16 | 1.6 | 404 | 114 | AM296863  | AM296863  | UT-H-BI2-  |



|       |    |     |     |     |           |                     |       |    |     |     |     |           |                      |
|-------|----|-----|-----|-----|-----------|---------------------|-------|----|-----|-----|-----|-----------|----------------------|
| C 871 | 16 | 1.6 | 404 | 136 | BE524462  | BE524462 MS055TM    | C 944 | 16 | 1.6 | 432 | 18  | A1268354  | A1268354 qm05a03.x   |
| C 872 | 16 | 1.6 | 405 | 167 | BE448697  | BE448697 ut48d01.y  | C 945 | 16 | 1.6 | 432 | 117 | AM558166  | AM558166 L0291d11-   |
| C 873 | 16 | 1.6 | 404 | 13  | AA921685  | AA921685 o190d01.s  | C 946 | 16 | 1.6 | 432 | 190 | W58944    | W58944 m053f03.t1    |
| C 874 | 16 | 1.6 | 405 | 17  | A1209184  | A1209184 g929a04.x  | C 947 | 16 | 1.6 | 432 | 225 | AQ173762  | AQ173762 HS_3194.A   |
| C 875 | 16 | 1.6 | 405 | 119 | AW708575  | AW708575 c7e12ne.r  | C 948 | 16 | 1.6 | 433 | 107 | AU016059  | AU016059 AU016059    |
| C 876 | 16 | 1.6 | 405 | 240 | AZ251691  | AZ251691 RPCI-23-9  | C 949 | 16 | 1.6 | 434 | 17  | A1213439  | A1213439 z1h07a1.r   |
| C 877 | 16 | 1.6 | 406 | 14  | AA965723  | AA965723 o4e05a1.r  | C 950 | 16 | 1.6 | 434 | 17  | A1226957  | A1226957 u102c01.y   |
| C 878 | 16 | 1.6 | 406 | 17  | A1196706  | A1196706 u153d01.y  | C 951 | 16 | 1.6 | 434 | 190 | W34045    | W34045 ma84c12.t1    |
| C 879 | 16 | 1.6 | 407 | 4   | AA262248  | AA262248 z770g01.s  | C 952 | 16 | 1.6 | 435 | 13  | AA889761  | AA889761 a150e01.s   |
| C 880 | 16 | 1.6 | 407 | 12  | AA816828  | AA816828 LD17393.5  | C 953 | 16 | 1.6 | 435 | 13  | AV632197  | AV632197 AV632197    |
| C 881 | 16 | 1.6 | 407 | 107 | AU091598  | AU091598 AU091598   | C 954 | 16 | 1.6 | 435 | 156 | C20361    | C20361 C20361 R1ce   |
| C 882 | 16 | 1.6 | 407 | 135 | BE499769  | BE499769 WHE0975.D  | C 955 | 16 | 1.6 | 435 | 167 | BE438853  | BE438853 BCD1661.W   |
| C 883 | 16 | 1.6 | 407 | 226 | AQ213957  | AQ213957 HS_2246.B  | C 956 | 16 | 1.6 | 436 | 21  | A1509561  | A1509561 vx02a08.r   |
| C 884 | 16 | 1.6 | 408 | 148 | BF425618  | BF425618 sut57b04.y | C 957 | 16 | 1.6 | 436 | 166 | BE335083  | BE335083 v9e2f08.y   |
| C 885 | 16 | 1.6 | 409 | 223 | AQ014497  | AQ014497 CIT-HSP-2  | C 958 | 16 | 1.6 | 437 | 149 | BF473527  | BF473527 WHE0929.D   |
| C 886 | 16 | 1.6 | 409 | 241 | AZ302507  | AZ302507 GSSTc1247  | C 959 | 16 | 1.6 | 437 | 237 | AZ026774  | AZ026774 RPCI-23-2   |
| C 887 | 16 | 1.6 | 409 | 250 | AZ834445  | AZ834445 2M0117F11  | C 960 | 16 | 1.6 | 437 | 244 | AZ468944  | AZ468944 1M0282007   |
| C 888 | 16 | 1.6 | 409 | 250 | AZ846355  | AZ846355 2M0146F03  | C 961 | 16 | 1.6 | 437 | 248 | AZ700927  | AZ700927 RPCI-23-1   |
| C 889 | 16 | 1.6 | 410 | 220 | CNS02DP3  | AL192720 Tetraodon  | C 962 | 16 | 1.6 | 438 | 141 | BE847233  | BE847233 uW24b07.y   |
| C 890 | 16 | 1.6 | 412 | 30  | AV409651  | AV409651 AV409651   | C 963 | 16 | 1.6 | 438 | 154 | BG516181  | BG516181 E1ESTed54   |
| C 891 | 16 | 1.6 | 412 | 102 | A1811649  | A1811649 tw44c05.x  | C 964 | 16 | 1.6 | 438 | 190 | W77168    | W77168 me59h12.t1    |
| C 892 | 16 | 1.6 | 413 | 17  | A1214297  | A1214297 qt28c12.x  | C 965 | 16 | 1.6 | 439 | 148 | BF423299  | BF423299 Hc.d11_26   |
| C 893 | 16 | 1.6 | 413 | 30  | AV397717  | AV397717 AV397717   | C 966 | 16 | 1.6 | 439 | 190 | W87236    | W87236 m157c06.t1    |
| C 894 | 16 | 1.6 | 413 | 115 | AM429547  | AM429547 67830.MAR  | C 967 | 16 | 1.6 | 439 | 231 | A0644024  | A0644024 RPCI93-DP   |
| C 895 | 16 | 1.6 | 413 | 167 | BE439110  | BE439110 CDO358.MH  | C 968 | 16 | 1.6 | 440 | 23  | A1693021  | A1693021 w410e10.x   |
| C 896 | 16 | 1.6 | 414 | 225 | AQ178372  | AQ178372 HS_2220.A  | C 969 | 16 | 1.6 | 440 | 107 | AU057342  | AU057342 AU057342    |
| C 897 | 16 | 1.6 | 414 | 20  | A1463897  | A1463897 va71b01.y  | C 970 | 16 | 1.6 | 440 | 137 | BE604187  | BE604187 WHE1413-1   |
| C 898 | 16 | 1.6 | 415 | 14  | AA994019  | AA994019 o442d10.s  | C 971 | 16 | 1.6 | 441 | 147 | BF374537  | BF374537 PM4-ST011   |
| C 899 | 16 | 1.6 | 415 | 117 | AM564102  | AM564102 LG1_282.E  | C 972 | 16 | 1.6 | 441 | 239 | AZ153403  | AZ153403 SP_0048.B   |
| C 900 | 16 | 1.6 | 416 | 21  | A1237778  | A1237778 EST234340  | C 973 | 16 | 1.6 | 442 | 105 | AL499702  | AL499702 AL499702    |
| C 901 | 16 | 1.6 | 416 | 21  | A1552688  | A1552688 mm03c11.y  | C 974 | 16 | 1.6 | 442 | 167 | BE452707  | BE452707 894065DP1   |
| C 902 | 16 | 1.6 | 417 | 4   | AA238136  | AA238136 mw97b09.r  | C 975 | 16 | 1.6 | 442 | 225 | AQ184106  | AQ184106 HS_3216.A   |
| C 903 | 16 | 1.6 | 417 | 7   | AA436989  | AA436989 zv54g07.r  | C 976 | 16 | 1.6 | 442 | 15  | A1046134  | A1046134 TENU1220    |
| C 904 | 16 | 1.6 | 417 | 21  | A1524631  | A1524631 Ld11c08.x  | C 977 | 16 | 1.6 | 443 | 19  | A1355294  | A1355294 q7f9h09.x   |
| C 905 | 16 | 1.6 | 417 | 110 | AM035593  | AM035593 EST281331  | C 978 | 16 | 1.6 | 443 | 123 | AM996520  | AM996520 QV3-BN004   |
| C 906 | 16 | 1.6 | 417 | 114 | AM297517  | AM297517 UI-H-BM0-  | C 979 | 16 | 1.6 | 444 | 126 | AQ264072  | AQ264072 CITB1-EL-   |
| C 907 | 16 | 1.6 | 417 | 162 | BE024360  | BE024360 894002E01  | C 980 | 16 | 1.6 | 444 | 257 | B84250    | B84250 RPCI11-22N9   |
| C 908 | 16 | 1.6 | 418 | 115 | AM419046  | AM419046 h416e08.x  | C 981 | 16 | 1.6 | 444 | 227 | B84250    | B84250 RPCI11-22N9   |
| C 909 | 16 | 1.6 | 418 | 151 | BF601076  | BF601076 265952.MA  | C 982 | 16 | 1.6 | 446 | 223 | AQ055188  | AQ055188 CIT-HSP-2   |
| C 910 | 16 | 1.6 | 418 | 167 | BE448310  | BE448310 ut82a01.y  | C 983 | 16 | 1.6 | 447 | 3   | AA213401  | AA213401 z191g12.x   |
| C 911 | 16 | 1.6 | 419 | 8   | AA505554  | AA505554 nh56g03.s  | C 984 | 16 | 1.6 | 447 | 17  | A1180586  | A1180586 uc67b05.r   |
| C 912 | 16 | 1.6 | 419 | 14  | AA965710  | AA965710 o4b06a1.r  | C 985 | 16 | 1.6 | 447 | 17  | AM559241  | AM559241 EST306077   |
| C 913 | 16 | 1.6 | 419 | 141 | BE847940  | BE847940 uw30h12.y  | C 986 | 16 | 1.6 | 447 | 163 | BE106805  | BE106805 UI-R-BT1    |
| C 914 | 16 | 1.6 | 419 | 222 | FR0021169 | AL014046 F.rubridge | C 987 | 16 | 1.6 | 447 | 153 | BE272304  | BE272304 601126035   |
| C 915 | 16 | 1.6 | 419 | 226 | AQ263146  | AQ263146 CITB1-EL-  | C 988 | 16 | 1.6 | 447 | 187 | R34119    | R34119 ynb83a12.t1   |
| C 916 | 16 | 1.6 | 420 | 233 | AQ080822  | AQ080822 HS_3192.A  | C 989 | 16 | 1.6 | 447 | 229 | AQ0513923 | AQ0513923 HS_5152.A  |
| C 917 | 16 | 1.6 | 420 | 30  | AV431288  | AV431288 AV431288   | C 990 | 16 | 1.6 | 448 | 138 | BE624506  | BE624506 uc23a03.y   |
| C 918 | 16 | 1.6 | 420 | 154 | BG516182  | BG516182 E1ESTed54  | C 991 | 16 | 1.6 | 448 | 153 | BG406652  | BG406652 dact14a12.y |
| C 919 | 16 | 1.6 | 420 | 225 | AQ187019  | AQ187019 HS_3122.B  | C 992 | 16 | 1.6 | 449 | 23  | A1657642  | A1657642 fc23b04.y   |
| C 920 | 16 | 1.6 | 421 | 120 | AM755716  | AM755716 s108b12.y  | C 993 | 16 | 1.6 | 449 | 105 | AL500809  | AL500809 AL500809    |
| C 921 | 16 | 1.6 | 421 | 104 | A1979195  | A1979195 w771n05.x  | C 994 | 16 | 1.6 | 449 | 239 | AZ163101  | AZ163101 SP_0073.B   |
| C 922 | 16 | 1.6 | 423 | 234 | AQ0844136 | AQ0844136 LMAUFV1_L | C 995 | 16 | 1.6 | 450 | 9   | AA579544  | AA579544 n117b01.s   |
| C 923 | 16 | 1.6 | 424 | 225 | AQ229268  | AQ229268 HS_2261.B  | C 996 | 16 | 1.6 | 450 | 120 | AM786051  | AM786051 117663.MA   |
| C 924 | 16 | 1.6 | 425 | 12  | AA856459  | AA856459 vx02a08.r  | C 997 | 16 | 1.6 | 450 | 147 | BF311325  | BF311325 601966724   |
| C 925 | 16 | 1.6 | 425 | 234 | AQ0843621 | AQ0843621 nbx00024A | C 998 | 16 | 1.6 | 450 | 142 | BF311325  | BF311325 601966724   |
| C 926 | 16 | 1.6 | 425 | 243 | AZ416587  | AZ416587 1M0191G34  | C 999 | 16 | 1.6 | 450 | 241 | AZ285018  | AZ285018 RPCI-23-1   |
| C 927 | 16 | 1.6 | 426 | 244 | AZ462408  | AZ462408 1M0269K14  | C1000 | 16 | 1.6 | 450 | 241 | AZ285018  | AZ285018 RPCI-23-1   |
| C 928 | 16 | 1.6 | 427 | 225 | AQ180680  | AQ180680 HS_3209.A  |       |    |     |     |     |           |                      |
| C 929 | 16 | 1.6 | 427 | 237 | AZ073851  | AZ073851 RPCI-23-A  |       |    |     |     |     |           |                      |
| C 930 | 16 | 1.6 | 427 | 244 | AZ489703  | AZ489703 1M0322L13  |       |    |     |     |     |           |                      |
| C 931 | 16 | 1.6 | 428 | 1   | AA051534  | AA051534 m152d04.r  |       |    |     |     |     |           |                      |
| C 932 | 16 | 1.6 | 428 | 14  | AA989827  | AA989827 uc79e08.y  |       |    |     |     |     |           |                      |
| C 933 | 16 | 1.6 | 428 | 172 | BF990176  | BF990176 CML-GN016  |       |    |     |     |     |           |                      |
| C 934 | 16 | 1.6 | 428 | 245 | AZ501354  | AZ501354 1M0340K08  |       |    |     |     |     |           |                      |
| C 935 | 16 | 1.6 | 429 | 9   | AA576188  | AA576188 nm50d11.s  |       |    |     |     |     |           |                      |
| C 936 | 16 | 1.6 | 429 | 154 | BG508736  | BG508736 sac859g06. |       |    |     |     |     |           |                      |
| C 937 | 16 | 1.6 | 430 | 116 | AM002436  | AM002436 w61h10.x   |       |    |     |     |     |           |                      |
| C 938 | 16 | 1.6 | 430 | 246 | AZ609405  | AZ609405 1M0434H10  |       |    |     |     |     |           |                      |
| C 939 | 16 | 1.6 | 430 | 258 | P9711.    | AL390677 Leishmani  |       |    |     |     |     |           |                      |
| C 940 | 16 | 1.6 | 431 | 22  | A1600121  | A1600121 EST251824  |       |    |     |     |     |           |                      |
| C 941 | 16 | 1.6 | 431 | 116 | AM461954  | AM461954 BF230007A  |       |    |     |     |     |           |                      |
| C 942 | 16 | 1.6 | 431 | 145 | BF201611  | BF201611 WHE1772_F  |       |    |     |     |     |           |                      |
| C 943 | 16 | 1.6 | 432 | 13  | AA877204  | AA877204 oD09g07.s  |       |    |     |     |     |           |                      |

## ALIGNMENTS

RESULT 1  
 LOCUS BG481731 894 bp mRNA  
 DEFINITION 602528280F1 NIH\_MGC\_21 Homo sapiens cDNA clone IMAGE:4652011 5',  
 mRNA sequence.  
 ACCESSION BG481731  
 VERSION BG481731.1 GI:13414010  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 894)  
AUTHORS NIH-MGC <http://mhc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapds-remail.nih.gov](mailto:cgapds-remail.nih.gov)  
Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: L1C1M435 row: 0 column: 20  
High quality sequence stop: 759.

## FEATURES

source

1. 894  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4652011"  
/clone\_lib="NIH-MGC\_21"  
/tissue\_type="choriocarcinoma"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: placenta; Vector: pOTB7; Site\_1: XhoI;  
Site\_2: EcoRI; CDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GCCACGAG(G). Size-selected 2500bp  
for average insert size 1.8kb. Library constructed by  
Ling Hong in the laboratory of Gerald M. Rubin (University  
of California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."  
BASE COUNT 205 a 248 c 250 g 190 t 1 others  
ORIGIN

Query Match 2.2%; Score 21; DB 154; Length 894;  
Best Local Similarity 100.0%; Pred. No. 2.3;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 932 acatcacgaagggtgaagc 952  
|||||  
DB 825 ACATCACGAAGGGGTGAAGC 845

RESULT 2  
AA645779/c 222 bp mRNA EST 28-OCT-1997  
LOCUS vnl0h04.r1 Stratigene mouse Tcell 937311 Mus musculus CDNA clone  
DEFINITION IMAGE:1020823 5', mRNA sequence.  
ACCESSION AA645779  
VERSION AA645779.1 GI:2572208  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 222)

REFERENCE 1 (bases 1 to 222)  
AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
Gaisel, S., Kucab, T., Lacy, M., Le, M., Martin, J., Morris, M.,  
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,  
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
Waterston, R.  
TITLE The WashU-HMI Mouse EST Project  
JOURNAL Unpublished (1996)  
COMMENT Contact: Marra M/Mouse EST Project  
WashU-HMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: [mouseest@watson.wustl.edu](mailto:mouseest@watson.wustl.edu)  
This clone is available royalty-free through LLNL; contact the

IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
MGI:571599  
Seq primer: -28m13 rev1 ET from Amersham  
High quality sequence stop: 220.

## FEATURES

source

1. 222  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/clone="IMAGE:1020823"  
/clone\_lib="Stratigene mouse Tcell 937311"  
/tissue\_type="Tcell"  
/dev\_stage="M30 CD4+ cells"  
/lab\_host="SOLR (kanamycin resistant)"  
/note="Organ: blood; Vector: pBluescript SK-; Site\_1:  
EcoRI; Site\_2: XhoI; Cloned unidirectionally. Primer:  
Oligo dT. M30 CD4+ cells. Average insert size: 1.0 kb;  
Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGCAG  
3' -3' adaptor sequence: 5' CTCGACGTTTTTTTTTTTTTTT 3'."  
BASE COUNT 72 a 45 c 53 g 52 t  
ORIGIN

Query Match 2.0%; Score 20; DB 10; Length 222;  
Best Local Similarity 100.0%; Pred. No. 7.9;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 781 caactctgaatctggatt 800  
|||||  
DB 21 CAACCTCTGAACTGGCTT 2

RESULT 3  
AM268708/c 414 bp mRNA EST 03-JAN-2000  
LOCUS xv35b05.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens CDNA clone  
DEFINITION IMAGE:2815089 3', mRNA sequence.  
ACCESSION AM268708  
VERSION AM268708.1 GI:6655738  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 414)

REFERENCE 1 (bases 1 to 414)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapds-remail.nih.gov](mailto:cgapds-remail.nih.gov)  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Seq primer: -40UP from Gibco  
High quality sequence stop: 408.

## FEATURES

source

1. 414  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2815089"  
/clone\_lib="Soares\_NFL\_T\_GBC\_S1"  
/lab\_host="DH10B"  
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with  
a modified polylinker; Site\_1: Not I; Site\_2: Eco RI;  
Equal amounts of plasmid DNA from three normalized  
libraries (fetal lung Nhlh19W, testis NHT, and B-cell  
NCI-CGAP-GCB1) were mixed, and ss circles were made in  
vitro. Following HAP purification, this DNA was used as  
tracer in a subtractive hybridization reaction. The driver  
was PCR-amplified cDNAs from pools of 5,000 clones made  
from the same 3 libraries. The pools consisted of  
I.M.A.G.E. clones 297480-302087, 682632-687239,  
726408-728711, and 729096-731399. Subtraction by Bento  
Soares and M. Fatima Bonaldo."

BASE COUNT 87 a 106 c 80 g 141 t  
ORIGIN

Query Match 2.0%; Score 20; DB 113; Length 414;  
Best Local Similarity 100.0%; Pred. No. 8.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 813 gacagagctgcagcagagcc 832  
|||||  
Db 158 GACAGAGCTGCAGCAGAGCC 139

RESULT 4  
LOCUS AI769658 438 bp mRNA EST 21-DEC-1999  
DEFINITION wj2502.x1 NCI-CGAP\_Kid12 Homo sapiens cDNA clone IMAGE:2403843 3',  
mRNA sequence.  
ACCESSION AI769658  
VERSION AI769658.1 GI:5236167  
KEYWORDS EST.

## SOURCE

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 438)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapsb-remail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmett-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
DNA Sequencing by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/dbp/image/image.html  
Insert Length: 536 Std Error: 0.00  
Seq primer: -40UP from Gibco.

## JOURNAL

COMMENT

## FEATURES

source 1..438  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2403843"  
/clone\_lib="NCI-CGAP\_Kid12"  
/issue\_type="2 pooled tumors (clear cell type)"  
/lab\_host="DH10B"  
/note="Organ: Kidney; Vector: p773D-Pac (Pharmacia) with  
a modified polylinker; Site\_1: Not I; Site\_2: Eco RI;  
Plasmid DNA from the normalized library NCI-CGAP\_Kids was  
prepared, and ss circles were made in vitro. Following HAP  
purification, this DNA was used as tracer in a subtractive  
hybridization reaction. The driver was PCR-amplified cDNAs  
from a pool of 5,000 clones made from the same library  
(cloneids 1323912-1323831, 1471368-1472903 and  
1492104-1493255). Subtraction by Bento Soares and M.  
Fatima Bonaldo."

BASE COUNT 93 a 110 c 89 g 146 t  
ORIGIN

Query Match 2.0%; Score 20; DB 24; Length 438;  
Best Local Similarity 100.0%; Pred. No. 8.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 813 gacagagctgcagcagagcc 832  
|||||  
Db 159 GACAGAGCTGCAGCAGAGCC 140

RESULT 5  
LOCUS AI028162/c  
DEFINITION ov90602.x1 Soares-Testis\_NHT Homo sapiens cDNA clone IMAGE:1644554  
3', mRNA sequence.  
ACCESSION AI028162  
VERSION AI028162.1 GI:3245471  
KEYWORDS EST.

## SOURCE

ORGANISM human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 456)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapsb-remail.nih.gov  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo  
, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/dbp/image/image.html  
Insert Length: 835 Std Error: 0.00  
Seq primer: -40m13 fwd. ET from Amersham  
High quality sequence stop: 359.  
Location/Qualifiers  
1..456  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1644554"  
/clone\_lib="Soares-Testis\_NHT"  
/sex="male"  
/lab\_host="DH10B"  
/note="Vector: p773D-Pac (Pharmacia) with a modified  
polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA  
was prepared from mRNA obtained from Clontech Laboratories  
, Inc., and primed with a Not I - oligo(dT) primer [5'  
TGTACCAATCTGACAGCGGCGCCCAATTTTCTTTTCTTTT 3']  
Double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified p773 vector. Library  
went through one round of normalization to Cot5, and was  
constructed by Bento Soares and M. Fatima Bonaldo."

## JOURNAL

COMMENT

## FEATURES

source 1..456  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1644554"  
/clone\_lib="Soares-Testis\_NHT"  
/sex="male"  
/lab\_host="DH10B"  
/note="Vector: p773D-Pac (Pharmacia) with a modified  
polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA  
was prepared from mRNA obtained from Clontech Laboratories  
, Inc., and primed with a Not I - oligo(dT) primer [5'  
TGTACCAATCTGACAGCGGCGCCCAATTTTCTTTTCTTTT 3']  
Double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified p773 vector. Library  
went through one round of normalization to Cot5, and was  
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 102 a 110 c 93 g 151 t  
ORIGIN

Query Match 2.0%; Score 20; DB 15; Length 456;  
Best Local Similarity 100.0%; Pred. No. 8.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 813 gacagagctgcagcagagcc 832  
|||||  
Db 160 GACAGAGCTGCAGCAGAGCC 141

RESULT 6  
LOCUS AM269670/c  
DEFINITION AM269670 483 bp mRNA EST 03-JAN-2000  
IMAGE:2815221 3', mRNA sequence.  
ACCESSION AM269670  
VERSION AM269670.1 GI:6656700  
KEYWORDS EST.

## SOURCE

ORGANISM human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 483)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Seq primer: -40UP from Gibco  
High quality sequence stop: 471.  
Location/Qualifiers

FEATURES  
source  
1. 483  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2815221"  
/clone\_1lb="Soares\_NFL\_T\_GBC\_S1"  
/lab\_host="DH10B"  
/note="Organ: pooled; Vector: p773D-Pac (Pharmacia) with  
a modified polylinker; Site\_1: Not I; Site\_2: Eco RI;  
Equal amounts of plasmid DNA from three normalized  
libraries (fetal lung NbHL19W, testis NHT, and B-cell  
NCI-CGAP GCBI) were mixed, and ss circles were made in  
vitro. Following HAP purification, this DNA was used as  
tracer in a subtractive hybridization reaction. The driver  
was PCR-amplified cDNAs from pools of 5,000 clones made  
from the same 3 libraries.  
I.M.A.G.E. clones 297480-302087, 682632-687239,  
726408-728711, and 729096-731359. Subtraction by Bento  
Soares and M. Fatima Bonaldo."

BASE COUNT 105 a 121 c 100 g 157 t  
ORIGIN

Query Match 2.0%; Score 20; DB 113; Length 483;  
Best Local Similarity 100.0%; Pred. No. 8.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 813 gacagagctgcagcagacc 832  
|||||  
Db 158 GACAGAGCTGCAGCAGACC 139

RESULT 7  
A1594177 490 bp mRNA EST 21-APR-1999  
LOCUS vni0h04.y1 Stratagene mouse Tcell 937311 Mus musculus cDNA clone  
DEFINITION IMAGE:1020823 5', mRNA sequence.  
ACCESSION A1594177  
VERSION A1594177.1 GI:4603225  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sclerogonathi; Muridae; Murinae; Mus.  
1 (bases 1 to 490)  
Marras, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,  
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person  
, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritzer  
, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,  
Waterston, R. and Wilson, R.  
The Mashu-NCI Mouse EST Project 1999  
Unpublished (1999)  
Contact: Marra M/Mashu-NCI Mouse EST Project 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@watson.wustl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
MGI:571599  
This read has been verified (found to hit its original self in the

correct orientation)  
Seq primer: -40RP from Gibco  
High quality sequence stop: 397.  
Location/Qualifiers

FEATURES  
source  
1. 490  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/clone="IMAGE:1020823"  
/clone\_1lb="Stratagene mouse Tcell 937311"  
/tissue\_type="Tcell"  
/dev\_stage="M30 CD4+ cells"  
/lab\_host="SOLR (kanamycin resistant)"  
/note="Organ: Blood; Vector: pBluescript SK-; Site\_1:  
EcoRI; Site\_2: XhoI; Cloned unidirectionally. Primer:  
Oligo dt. M30 CD4+ cells. Average insert size: 1.0 kb;  
Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGCGACGAG  
3' -3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTTCTTTT 3'."

BASE COUNT 174 a 94 c 117 g 105 t  
ORIGIN

Query Match 2.0%; Score 20; DB 22; Length 490;  
Best Local Similarity 100.0%; Pred. No. 8.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 781 caactctgaatctgggttc 800  
|||||  
Db 22 CAACCTCTGCAATCTGGGTTT 3

RESULT 8  
BE893506 917 bp mRNA EST 20-OCT-2000  
LOCUS BE893506/c 601438060F1 NIH\_MGC\_72 Homo sapiens cDNA clone IMAGE:3923007 5',  
DEFINITION mRNA sequence.  
ACCESSION BE893506  
VERSION BE893506.1 GI:10354930  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 917)  
NIH-MGC <http://mgc.ncbi.nlm.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov  
Tissue Procurement: ATCC/DCTD/DTF  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov> row: h column: 16  
Place: LLM9758  
High quality sequence stop: 607.  
Location/Qualifiers

FEATURES  
source  
1. 917  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3923007"  
/clone\_1lb="NIH\_MGC\_72"  
/tissue\_type="melanotic melanoma"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: skin; Vector: pCMV-SPORE6; Site\_1: NotI;  
Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 2 kb. Library constructed by Life  
Technologies."

BASE COUNT 226 a 219 c 319 g 153 t  
ORIGIN

Query Match 2.0%; Score 20; DB 141; Length 917;  
Best Local Similarity 100.0%; Pred. No. 8.4;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 671 accagtcgagggcgaagtc 690  
|||||  
DB 917 ACCAGTCGAGGGCAGGCTT 898

RESULT 9  
LOCUS AO511509/c 468 bp DNA GSS 05-MAY-1999  
DEFINITION HS-5074.B1.C08.SP6B RPCI-11 Human Male BAC Library Homo sapiens  
ACCESSION AO511509 genomic clone Plate=650 COL=15 Row=F, DNA sequence.  
VERSION AO511509.1 GI:4744119  
KEYWORDS GSS.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 468)  
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,  
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and  
Hood,L.  
TITLE Sequence-tagged connectors: A sequence approach to mapping and  
scanning the human genome  
JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)  
MEDLINE 99380589  
COMMENT Contact: Mahairas GG, Wallace JC, Hood L  
High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: jwallace@u.washington.edu  
Clones are derived from the human BAC library RPCI-11. For BAC  
library availability, please contact Pieter de Jong  
(pieterdejong.med.buffalo.edu). Clones may be purchased from  
BACPAC Resources ([http://bacpac.med.buffalo.edu/ordering\\_bac.htm](http://bacpac.med.buffalo.edu/ordering_bac.htm))  
or from Research Genetics (<http://www.htsc.washington.edu>)  
<http://www.htsc.washington.edu> Plate: 650 row: F column: 15  
Seq primer: SP6  
Class: BAC ends  
High quality sequence stop: 468.  
FEATURES  
source  
1. 468  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="Plate=650 COL=15 Row=F"  
/clone\_id="RPCI-11 Human Male BAC Library"  
/sex="male"  
/note="Vector: pBAC3.6; Site.1: EcoRI; Site.2: EcoRI;  
Male blood DNA was isolated from one randomly chosen donor  
and partially digested with a combination of EcoRI and  
EcoRI Methylase. Size selected DNA was cloned into the  
pBAC3.6 vector at EcoRI sites"

BASE COUNT 143 a 92 c 92 g 135 t 6 others

ORIGIN  
Query Match 1.9%; Score 19; DB 229; Length 468;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 580 agtcctgctgcgataaatg 598  
|||||  
DB 39 AGCTCCGTGGCGATATATG 21

RESULT 10  
AO337527

LOCUS AO337527 523 bp DNA GSS 06-MAR-1999  
DEFINITION HS-5017.A2.F02.T7 RPCI11 Human Male BAC Library Homo sapiens  
ACCESSION AO337527 genomic clone Plate=593 COL=4 Row=K, DNA sequence.  
VERSION AO337527.1 GI:4141739  
KEYWORDS GSS.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 523)  
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,  
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and  
Hood,L.  
TITLE Sequence-tagged connectors: A sequence approach to mapping and  
scanning the human genome  
JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)  
MEDLINE 99380589  
COMMENT Contact: Mahairas GG, Wallace JC, Hood L  
High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: jwallace@u.washington.edu  
Clones may be purchased from Research Genetics (<http://www.htsc.washington.edu>)  
BAC end Web Server: <http://www.htsc.washington.edu>  
Plate: 593 row: K column: 4  
Seq primer: T7  
Class: BAC ends  
High quality sequence stop: 523.  
FEATURES  
source  
1. 523  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="Plate=593 COL=4 Row=K"  
/clone\_id="RPCI11 Human Male BAC Library"  
/sex="male"  
/cell\_type="lymphocytes"  
/note="Vector: pBAC3.6; RPCI11 Human Male BAC Library"

BASE COUNT 183 a 151 c 125 g 58 t 6 others

ORIGIN  
Query Match 1.9%; Score 19; DB 227; Length 523;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 347 ggattaatgtaccacaag 365  
|||||  
DB 151 GGATTATATGTCACCAAG 169

RESULT 11  
LOCUS AZ497878/c 656 bp DNA GSS 05-OCT-2000  
DEFINITION IM0334G24R Mouse 10kb plasmid UUC1M library Mus musculus genomic  
ACCESSION AZ497878 clone UUC1M0334G24 R, DNA sequence.  
VERSION AZ497878  
KEYWORDS AZ497878.1 GI:10675204  
SOURCE GSS.  
ORGANISM Mus musculus  
house mouse.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 656)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly  
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)

## COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunne@genetics.utah.edu  
Insert Length: 1000 Std Error: 0.00  
Plate: 0334 row: 6 column: 24  
Seq primer: CACACAGCAACACGTATGACC  
Class: plasmid ends  
High quality sequence stop: 656.  
Location/Qualifiers

FEATURES  
source

1. 656  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUCG1M0334G24"  
/clone\_1lb="Mouse 10kb plasmid UUCG1M library"  
/sex="Male"  
/lab\_host="F. Coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114/gb1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."  
BASE COUNT 155 a 176 c 132 g 192 t 1 others  
ORIGIN

Query Match 1.9%; Score 19; DB 245; Length 656;  
Best Local Similarity 100.0%; Pred. No. 30;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 537 gaaccacacagagaaga 555  
|||||

Db 110 GAACCAACAGGAGAGAA 92

## RESULT 12

AO938059

LOCUS AO938059 657 bp DNA GSS 23-AUG-2000  
DEFINITION NB6-908R Human NOT1 clones Homo sapiens genomic, DNA sequence.  
ACCESSION AO938059  
VERSION AO938059.1 GI:7214437  
KEYWORDS GSS.  
SOURCE human.  
ORGANISM Homo sapiens

Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
1 (bases 1 to 657)

REFERENCE 1 Zabarovskiy, E.R., Glazutulin, R., Podowski, R.M., Zabarovska, V.V., Xie

Protopopov, A., Kashuba, V., Ernberg, I., Winberg, G. and Wahlstedt, C.  
Not1 clones in the analysis of the human genome  
Nucleic Acids Res. 28 (7), 1635-1639 (2000)

JOURNAL 20175728  
CONTACT: Podowski RM

Center for Genomics Research

Karolinska Institute  
17177 Stockholm, Sweden

Tel: +46-8-728-6372

Fax: +46-8-337983

Email: Raf.Podowski@cgr.ki.se

Class: Not1 site.

FEATURES  
source

1. 657  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_1lb="Human Not1 clones"  
BASE COUNT 102 a 236 c 201 g 117 t 1 others  
ORIGIN

Query Match 1.9%; Score 19; DB 235; Length 657;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 280 gccgcgcgcgcgcgcgcgc 298  
|||||

Db 4 GCCGCGCGCGATCGCTG 22

## RESULT 13

CNS0481Z/C

LOCUS CNS0481Z/C 713 bp DNA GSS 19-MAY-2000  
DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone  
089u07 of library G from Tetraodon nigroviridis, genomic survey  
sequence.  
ACCESSION AL278720.1 GI:8015082  
KEYWORDS GSS: genome survey sequence.  
SOURCE Tetraodon nigroviridis.  
ORGANISM Tetraodon nigroviridis

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
Tetraodontidae; Tetraodon.

1 (bases 1 to 713)  
REFERENCE 1 Roest-Crollius, H., Jallion, O., Dasilva, C., Fizames, C., Fisher, C.,  
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and  
Weissenbach, J.

JOURNAL 2 Characterization and repeat analysis of the compact genome of the  
freshwater pufferfish Tetraodon nigroviridis  
Unpublished  
2 (bases 1 to 713)

REFERENCE 1 Roest-Crollius, H., Jallion, O., Dasilva, C., Bouneau, L., Fisher, C.,  
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,  
Saurin, W. and Weissenbach, J.  
Human gene number estimate provided by genome wide analysis using  
Tetraodon nigroviridis DNA sequence  
Unpublished  
3 (bases 1 to 713)

## JOURNAL

Genoscope.

Direct Submission  
Submitted (12-APR-2000) to the EMBL/Genbank/DBJ databases  
This sequence is a single read and was generated as part of a large  
scale clone-end sequencing project of the Tetraodon nigroviridis  
genome. For more information, please take a look at  
http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers

FEATURES  
source

1. 713  
/organism="Tetraodon nigroviridis"  
/db\_xref="taxon:99883"  
/clone\_1lb="G"  
/note="Genoscope sequence ID : C0B6089CG04LPI-end : T7"  
BASE COUNT 1 a 330 c 174 g 180 t 28 others  
ORIGIN

|                       |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                     |           |             |
|-----------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------|-----------|-------------|
| Query Match           | 1.9%                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | Score 19:           | DB 221:   | Length 713: |
| Best Local Similarity | 100.0%                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | Pred. NO. 30:       |           |             |
| Matches 19:           | Conservative 0:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Mismatches 0:       | Indels 0: | Gaps 0:     |
| QY                    | 106                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | aggagaacagcagccag   | 124       |             |
|                       |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                     |           |             |
| Db                    | 650                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | AGGAGAGAACACACGCCAG | 632       |             |
| RESULT 14             |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                     |           |             |
| AI325737              | 747 bp                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | mRNA                | EST       | 23-DEC-1998 |
| LOCUS                 |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                     |           |             |
| DEFINITION            | mm95d03.y1 Stratiogene mouse heart (#937316) Mus musculus cDNA clone IMAGE:536165 5' similar to gb:X1869 ELONGATION FACTOR 1 ALPHA 1 (HUMAN): gb:X13661 Mouse mRNA for elongation factor 1-alpha (MOUSE); mRNA sequence.                                                                                                                                                                                                                                                                                                                                                                                                                   |                     |           |             |
| ACCESSION             | AI325737                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                     |           |             |
| VERSION               | AI325737.1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | GI:4060166          |           |             |
| KEYWORDS              | EST.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |                     |           |             |
| SOURCE                | house mouse.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |                     |           |             |
| ORGANISM              | Mus musculus                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |                     |           |             |
| REFERENCE             | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 747)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |                     |           |             |
| AUTHORS               | Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.                                                                                                                                                                                                                                                                                                                                                                       |                     |           |             |
| TITLE                 | The WashU-HHMI Mouse EST Project                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |                     |           |             |
| JOURNAL               | Unpublished (1996)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                     |           |             |
| COMMENT               | Contact: Marra M/Mouse EST Project<br>WashU-HHMI Mouse EST Project<br>Washington University School of Medicine<br>4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108<br>Tel: 314 286 1800<br>Fax: 314 286 1810<br>Email: mouseest@watson.wustl.edu<br>This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.<br>MGI:323101<br>This read is a RESSEQUENCE of a previously sequenced mouse clone<br>This read has been verified (found to hit its original self in the correct orientation)<br>Seq primer: -40RP from Gibco<br>High quality sequence stop: 114. |                     |           |             |
| FEATURES              | Location/Qualifiers                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |                     |           |             |
| SOURCE                | 1..747                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |                     |           |             |
|                       | /organism="Mus musculus"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                     |           |             |
|                       | /strain="NIH/Swiss"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |                     |           |             |
|                       | /db_xref="taxon:10090"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |                     |           |             |
|                       | /clone="IMAGE:536165"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |                     |           |             |
|                       | /clone_lib="Stratiogene mouse heart (#937316)"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |                     |           |             |
|                       | /sex="pooled"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |                     |           |             |
|                       | /tissue_type="heart"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |                     |           |             |
|                       | /dev_stage="13 day embryos"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                     |           |             |
|                       | /lab_host="SOLR (kanamycin resistant)"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |                     |           |             |
|                       | /note="Organ: heart; Vector: pluscript SK-; Site: 1; Ecoli: Site-2; XhoI: Cloned unidirectionally. Primer: Oligo dT. 93 pooled NIH/Swiss 13 day embryo hearts. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGCGACGAG 3' -3' adaptor sequence: 5' CTCGAGTGTGTGTGTGTGTGT 3'"                                                                                                                                                                                                                                                                                                                               |                     |           |             |
| BASE COUNT            | 208 a                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 182 c               | 148 g     | 208 t       |
| ORIGIN                | 1 others                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                     |           |             |
| Query Match           | 1.9%                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | Score 19:           | DB 18:    | Length 747: |
| Best Local Similarity | 100.0%                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | Pred. NO. 30:       |           |             |
| Matches 19:           | Conservative 0:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Mismatches 0:       | Indels 0: | Gaps 0:     |
| QY                    | 364                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | aggagcgtcgtcagcagc  | 382       |             |
|                       |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                     |           |             |

```

RESULT 15
LOCUS      A2668255      842 bp      DNA      GSS      14-DEC-2000
DEFINITION ENRKSX2TF Entamoeba histolytica Sheared DNA Entamoeba histolytica
            genomic, DNA sequence.
ACCESSION  A2668255
VERSION    A2668255.1 GI:11805401
KEYWORDS   GSS.
SOURCE     Entamoeba histolytica.
ORGANISM   Entamoeba histolytica.
REFERENCE  1 (bases 1 to 842)
AUTHORS   Loftus,B., Van Aken,S. and Fraser,C.
TITLE     Determination of clone end sequences from Entamoeba histolytica
          HM1:IMSS sheared DNA library
JOURNAL   Unpublished (2000)
COMMENT   Contact: Brendan J Loftus
          Department of Eukaryotic Genomics
          The Institute for Genomic Research
          9712 Medical Center Dr., Rockville, MD 20850, USA
          Tel: 301 838 0200
          Fax: 301 838 0208
          Email: b1loftus@ligr.org
          Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
          DNA library
          Seq primer: M13-Forward
          Class: shotgun
          High quality sequence start: 24
          High quality sequence stop: 731.
          Location/Qualifiers
            1..842
              /organism="Entamoeba histolytica"
              /strain="HM1:IMSS"
              /db_xref="taxon:5759"
              /clone_id="Entamoeba histolytica sheared DNA"
              /note="Vector: pHOSt1; Site_1: Bst I; Constructed at The
              Institute for Genomic Research (TIGR), Rockville, MD.
              Genomic DNA isolated from broth cultures of E. histolytica
              using a method described by Clark and Diamond (Clark,
              C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
              method for isolate identification. Exp. Parasitol.
              77:450.). The DNA was mechanically sheared to give a
              tight size distribution (~2 kb). The v + i method used for
              the library construction is described in detail in Smith,
              H.O. and Venter, J.C. (Making small insert libraries for
              whole genome shotgun sequencing projects. In Genome
              Sequencing: A Practical Approach, eds. M. Vaudin and B.
              Barrell, Oxford University Press, 1999)."
```

SOURCE  
ORGANISM Tetraodon nigroviridis.  
Tetraodon nigroviridis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Acanthopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
Tetraodontidae; Tetraodon.  
1 (bases 1 to 891)  
Roest-Crollius,H., Jalllon,O., Dasilva,C., Fizeses,C., Fisher,C.,  
Bonneau,L., Billault,A., Quetler,F., Saurin,W., Bernot,A. and  
Weissenbach,J.  
TITLE  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 891)  
Roest-Crollius,H., Jalllon,O., Dasilva,C., Bonneau,L., Fisher,C.,  
Bernot,A., Fizeses,C., Wincker,P., Brotlier,P., Quetler,F.,  
Saurin,W. and Weissenbach,J.  
COMMENT Human gene number estimate provided by genome wide analysis using  
Tetraodon nigroviridis DNA sequence  
Unpublished  
JOURNAL Direct Submission  
REFERENCE 3 (bases 1 to 891)  
Genoscope.  
TITLE Submitted (12-APR-2000) to the EMBL/Genbank/DBD databases  
JOURNAL This sequence is a single read and was generated as part of a large  
COMMENT genome. For more information, please take a look at  
http://www.genoscope.cns.fr/Tetraodon.  
FEATURES  
SOURCE 1..891  
/organism="Tetraodon nigroviridis"  
/db\_xref="taxon:99883"  
/clone="06bJ20"  
/clone\_1lb="G"  
/note="Genoscope sequence ID : C0B6068DE10SP1-end :  
PUC-ori"  
BASE COUNT 254 a 196 c 213 g 216 t 12 others  
ORIGIN  
Query Match 1.9%; Score 19; DB 221; Length 891;  
Best local Similarity 100.0%; Pred. No. 31;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 231 cccgcacacccccctgtt 249  
|||||  
DB 143 CCTGCATCACCCTCTGT 161  
RESULT 17  
BB043716 235 bp mRNA EST 23-JUN-2000  
LOCUS BB043716 RIKEN full-length enriched, 13 days embryo male testis Mus  
DEFINITION musculus cDNA clone 6030477B18 3' similar to AL133589 Homo sapiens  
mRNA: cDNA DKFZp34J039.1 (from clone DKFZp34J039.1); mRNA sequence.  
ACCESSION BB043716  
VERSION BB043716.1 GI:8450102  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 235)  
Konno,H., Alzawa,K., Akahira,S., Akiyama,J., Atrakawa,T., Carlincl  
P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,  
Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,  
Iizawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,  
Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M.,  
Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,K., Oda,H., Okazaki,Y.,  
Ono,T., Owa,C., Saito,H., Sakai,C., Satou,K., Shibata,K., Shibata  
Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sugahara,Y.,  
Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tomlinaga,N., Toyu  
T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanae,I.

TITLE  
JOURNAL Unpublished (2000)  
COMMENT Contact: Yoshitake Hayashizaki  
Genome Exploration Research Group, Life Science Tsukuba Center,  
Genome Science Laboratory  
The Institute of Physical and Chemical Research (RIKEN), Genomic  
Sciences Center  
3-1-1 Koyada, Tsukuba, Ibaraki 305-0074, Japan  
Tel: +81-298-36-9013  
Fax: +81-298-36-9098  
Email: genome-res@rtc.riken.go.jp,  
URL: http://genome.rtc.riken.go.jp/  
Carlincl,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki  
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
Thermotaxation and thermotaxation of thermolabile enzymes by  
trehalose and its application for the synthesis of full length  
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)  
Itoh,M., Kusunagi,T., Akiyama,J., Shibata,K., Iizawa,M., Kawai,J.,  
Tomaru,Y., Carlincl,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki  
Y. and Hayashizaki,Y.  
Automated filtration-based high-throughput plasmid preparation  
system. Genome Res. 9 (5), 463-470 (1999)  
Carlincl,P. and Hayashizaki,Y.  
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,  
19-44 (1999)  
Please visit our web site (http://genome.rtc.riken.go.jp) for  
further details.  
FEATURES  
SOURCE 1..235  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="6030477B18"  
/clone\_1lb="RIKEN full-length enriched, 13 days embryo  
male testis"  
/sex="male"  
/tissue="testis"  
/dev\_stage="13 days embryo"  
/lab\_host="DH10B"  
/note="Site 1: Sali; Site 2: BamHI; cDNA library was  
prepared and sequenced in Mouse Genome Encyclopedia  
Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in  
RIKEN. Division of Experimental Animal Research in Riken  
contributed to prepare mouse tissues. 1st strand cDNA was  
primed with a primer 15',  
GAGAGAGAGAGATCCAGACCTTTTCTTTTCTTTTCTTTVN 3'. cDNA was  
prepared by using trehalose thermo-activated reverse  
transcriptase and subsequently enriched for full-length by  
cap-trapper. cDNA went through one round of normalization  
to Rot = 5.0 and subtraction to Rot = 100.0. Second strand  
cDNA was prepared with the primer adapter of sequence 15'  
GAGAGAGATTCCTCGACTTAATTAATTCCTCCCCCCCC 3'. cDNA  
was cloned into the XhoI and BamHI sites. Vector: a  
modified pBluescript KS(+) after bulk excision from Lambda  
FLC I. Cloning sites, 5' end: Sali; 3' end: BamHI."  
BASE COUNT 60 a 69 c 41 g 65 t  
ORIGIN  
Query Match 1.8%; Score 18; DB 124; Length 235;  
Best local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 111 agacagcagccagcgcca 128  
|||||  
DB 1 AGAAGCAGCAGCCAGCCCA 18  
RESULT 18  
AV292150/c



```

LOCUS       AV292150      241 bp      mRNA      EST      09-NOV-1999
DEFINITION   AV292150 RIKEN full-length enriched, 6 days neonate head Mus
ACCESSION   AV292150
VERSION     AV292150.1 GI:6306181
KEYWORDS
SOURCE      house mouse.
ORGANISM    Mus musculus.
REFERENCE   1 (bases 1 to 241)
AUTHORS     Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T.,
            Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F.,
            Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai
            C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M.,
            Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,
            Owa,C., Ozawa,Y., Saito,H., Sano,M., Sato,K., Shibata,K., Shibata,
            Y., Shigemoto,Y., Shitaki,T., Sogabe,Y., Sugahara,Y., Suzuki,H.,
            Suzuki,H., Takahashi,F., Tateo,M., Tomioka,N., Tsunoda,Y.,
            Watahiki,A., Watanabe,S., Yamamura,T., Yasunishi,A., Yokota,T.,
            Yoshiki,M., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
            RIKEN Mouse ESTs (Konno,H., et al. 1999)
COMMENT     Unpublished (1999)
            Contact: Yoshihide Hayashizaki
            Genome Exploration Research Group, Life Science Tsukuba Center,
            The Institute of Physical and Chemical Research (RIKEN), Genomic
            Sciences Center
            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
            Tel: +81-298-36-9013
            Fax: +81-298-36-9098
            Email: genome-res@rtc.riken.go.jp,
            URL:http://genome.rtc.riken.go.jp/
            Sasaki,N., Izawa,M., Watahiki,M., Okazaki,Y. and Hayashizaki
            Y.,
            Matsura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
            Y.,
            Transcriptional sequencing: A method for DNA sequencing using RNA
            polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7): 3455-3460 (1998)
            Itoh,M., Kitsuana,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
            Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
            Y. and Hayashizaki,Y.
            Automated filtration-based high-throughput plasmid preparation
            system. Genome Res. 9 (5): 463-470 (1999)
            Carninci,P. and Hayashizaki,Y.
            High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
            19-44 (1999)
            Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
            Location/Qualifiers
                1..241
                /organism="Mus musculus"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="5430416G10"
                /clone_lib="RIKEN full-length enriched, 6 days neonate
                head"
                /sex="mixed"
                /tissue_type="head"
                /dev_stage="6 days neonate"
                /lab_host="DH10B"
                /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                prepared and sequenced in Mouse Genome Encyclopedia
                Project of Genome Exploration Research Group in Riken
                Genomic Sciences Center and Genome Science Laboratory in
                RIKEN. Division of Experimental Animal Research in Riken
                contributed to prepare mouse tissues. 1st strand cDNA was
                primed with a primer [5'
                GAGAGAGAGAGATCCAGAGCTTTTCTTTTCTTTTCTTTVN 3'], cDNA was
                transcribed by using trehalose thermo-activated reverse
                transcriptase and subsequently enriched for full-length by
                cap-trapper. cDNA went through one round of normalization
                to Rot = 10.0 and subtraction to Rot = 100.0. Second
                strand cDNA was prepared with the primer adapter of
                sequence [5' GAGAGAGAGATTCGAGTTAATTAATTAATTCACCCCCCCC
                3']. cDNA was cloned into the XhoI and BamHI sites.
                Vector: a modified plasmid pBluescript KS(+) after bulk excision
                from lambda FLC I. Cloning sites, 5' end: SalI; 3' end:
                BamHI"
BASE COUNT   70 a      37 c      33 g      101 t
ORIGIN
Query Match      1.8%; Score 18; DB 28; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Yy 774 ccaatgaacaactctgaa 791
Db 124 CCATGACACTTCTCGAA 107

RESULT 19
AV526879/c
LOCUS       AV526879      244 bp      mRNA      EST      01-SEP-2000
DEFINITION   AV526879 Arabidopsis thaliana aboveground organs two to six-week
ACCESSION   AV526879
VERSION     AV526879.1 GI:8686407
KEYWORDS
SOURCE      thale cress.
ORGANISM    Arabidopsis thaliana
            Eugaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
            1 (bases 1 to 244)
            A large scale analysis of cDNA in Arabidopsis thaliana: Generation
            of 12,028 non-redundant expressed sequence tags from normalized and
            size-selected cDNA libraries
            DNA Res. 7, 175-180 (2000)
            Contact: Erika Asanizu
            The First Laboratory for Plant Gene Research
            Kazusa DNA Research Institute
            Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
            Email: asanizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
            Location/Qualifiers
                1..244
                /organism="Arabidopsis thaliana"
                /strain="Columbia"
                /db_xref="taxon:3702"
                /clone="AP223f03R"
                /clone_lib="Arabidopsis thaliana aboveground organs two to
                six-week old"
                /tissue_type="aboveground organs"
                /dev_stage="two to six-week old"
                /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                XhoI"
BASE COUNT   74 a      67 c      44 g      59 t
ORIGIN
Query Match      1.8%; Score 18; DB 31; Length 244;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Yy 930 caacatacgaaggggt 947
Db 140 CACATCAGCAGAGGGGTT 123

RESULT 20
AA358477/c
LOCUS       AA358477      261 bp      mRNA      EST      21-APR-1997
DEFINITION   EST67411 Fetal lung III Homo sapiens cDNA 5' end, mRNA sequence.
ACCESSION   AA358477

```

```

VERSION AA358477.1 GI:2010845
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 261)
JOURNAL Adams,M.D., Soares,M.B., Kerlavage,A.R., Fields,C. and Venter,J.C.
MEDLINE Rapid cDNA sequencing (expressed sequence tags) from a
COMMENT directionally cloned human infant brain cDNA library
94004965
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M3 Reverse.

FEATURES
Location/Qualifiers
1..261
/organism="Homo sapiens"
/db_xref="ATCC (Inhost):162671"
/db_xref="taxon:9606"
/clone.lib="Fetal Lung IIT"
/dev_stage="fetus"
/note="organ: lung; Vector: pBluescript SK-; Site_1: EcoRI
; Site_2: XhoI"
BASE COUNT 47 a 77 c 85 g 48 t 4 others
ORIGIN

Query Match 1.8%; Score 18; DB 6; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 gtagctgcgtcctgcgtg 61
|||||
Db 18 gTACGTCGCTCCTCGCTG 1

RESULT 21
AV527317 264 bp mRNA EST 01-SEP-2000
LOCUS AV527317 Arabidopsis thaliana aboveground organs two to six-week
DEFINITION Old Arabidopsis thaliana cDNA clone AP234b05R 5', mRNA sequence.
ACCESSION AV527317
VERSION AV527317.1 GI:8686845
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
TITLE 1 (bases 1 to 264)
JOURNAL Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
MEDLINE A large scale analysis of cDNA in Arabidopsis thaliana: Generation
COMMENT of 12,028 non-redundant expressed sequence tags from normalized and
size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)
20363093
Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
1..264
/organism="Arabidopsis thaliana"

FEATURES
source

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/strain="Columbia"
/db_xref="taxon:3702"
/clone.lib="AP234b05R"
/clone.lib="Arabidopsis thaliana aboveground organs two to
six-week old"
/tissue_type="aboveground organs"
/dev_stage="two to six-week old"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT 85 a 71 c 49 g 59 t
ORIGIN

Query Match 1.8%; Score 18; DB 31; Length 264;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 930 caacatcacgaaggaggt 947
|||||
Db 152 CAACATCAGCAGAGGGGCT 135

RESULT 22
Z29054/c 294 bp mRNA EST 16-DEC-1993
LOCUS Z29054 Arabidopsis thaliana cDNA clone OA067 5' similar to
DEFINITION complex II type III chlorophyll a/b binding prot, mRNA sequence.
ACCESSION Z29054
VERSION Z29054.1 GI:435254
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
TITLE 1 (bases 1 to 294)
JOURNAL CNRS.
AUTHORS The Arabidopsis thaliana transcribed genome: the GDR cDNA program
TITLE Unpublished (1996)
JOURNAL Contact: Krivitzky M., Bonnet R., Jean-Jacques I., Kreis M.,
COMMENT Lecharny A.
Laboratoire de Biologie du Développement des Plantes
Université de Paris Sud
Bat. 450, 91405 Orsay Cedex, France
Email: alain@bdp.u-ps.cirec.fr.
Location/Qualifiers
1..294
/organism="Arabidopsis thaliana"
/strain="ecotype Columbia"
/db_xref="taxon:3702"
/clone.lib="OA067"
/clone.lib="Ora-A"
/tissue_type="green shoots"
/note="Vector: lambda ZAPIT"
BASE COUNT 76 a 78 c 65 g 75 t
ORIGIN

Query Match 1.8%; Score 18; DB 191; Length 294;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 930 caacatcacgaaggaggt 947
|||||
Db 121 CAACATCAGCAGAGGGGCT 104

RESULT 23
AV208201 301 bp mRNA EST 30-OCT-1999
LOCUS AV208201 RIKEN full-length enriched, adult male testis Mus musculus
DEFINITION cDNA clone 1700106B02 3' similar to AF065386 Mus musculus Jun
coactivator Jabi (Jabi) mRNA, mRNA sequence.

```



Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 1 (bases 1 to 318)  
 CNRS.  
 The Arabidopsis thaliana transcribed genome: the GDR cDNA program  
 Unpublished (1996)  
 Contact: Berthomieu P., Guerrier D., Giraudat J.  
 Genetique Moleculaire d'Arabidopsis  
 ISV - UPR40, CNRS  
 Avenue de la Terrasse, 1198 Gif-sur-Yvette Cedex, France  
 Email: Giraudat@cnrs-gif.fr  
 CDS 6. .>318 /product="CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR".  
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 1. .318  
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 /clone\_1lb="AC16H"  
 /tissue\_type="cell suspension culture"  
 /dev\_stage="cycling cells"  
 /note="Vector: lambda ZAPII"  
 /note="Vector: lambda ZAPII"  
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 80 a 86 c 70 g 82 t  
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 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 930 caacatcaggaagggt 947  
 |||||  
 Db 102 CACATCAGCAGCGGT 85  
 |||||  
 RESULT 26  
 AM896020 327 bp mRNA EST 24-MAY-2000  
 LOCUS  
 DEFINITION QV4-NN0039-110500-204-a03 NN0039 Homo sapiens cDNA, mRNA sequence.  
 AM896020  
 VERSION AM896020.1 GI:8060225  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 327)  
 Dias Neto, E., Garcia Correia, R., Verjovski-Almeida, S., Bioness, M.R.,  
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bal, G.S., Simpson, D.H.,  
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,  
 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
 Simpson, A.J.  
 Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 20202663  
 Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=tl2-QV4-NN0039-110  
 500-204-a03&tl3=2000-05-11&tl4=1)  
 500-204-a03&tl3=2000-05-11&tl4=1)  
 Seg primer: puc 18 forward  
 High quality sequence start: 9  
 High quality sequence stop: 132.

Location/Qualifiers  
 1. .327  
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 /db\_xref="taxon:9606"  
 /clone\_1ib="NN0039"  
 /dev\_stage="Adult"  
 /note="Organ: nervous, normal; Vector: puc18; Site\_1: SmaI;  
 Site\_2: SmaI; A mini-library was made by cloning products  
 derived from ORESTES PCR (U.S. Letters Patent application  
 No. 196,716 - Ludwig Institute for Cancer Research)  
 profiles into the pUC 18 vector. Reverse transcription of  
 tissue mRNA and cDNA amplification were performed under  
 low stringency conditions."  
 BASE COUNT  
 107 a 65 c 98 g 57 t  
 ORIGIN  
 Query Match 1.8%; Score 18; DB 122; Length 327;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 544 acagagagaagaagcc 561  
 |||||  
 Db 140 ACAGGAGAGAGAGGCC 157  
 |||||  
 RESULT 27  
 T21227/c 331 bp mRNA EST 06-NOV-1997  
 LOCUS  
 DEFINITION 3235 Lambda-PRL2 Arabidopsis thaliana cDNA clone 93E117, mRNA  
 sequence.  
 T21227  
 VERSION T21227.1 GI:2596344  
 KEYWORDS EST.  
 SOURCE thale cress.  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 1 (bases 1 to 331)  
 Newman, T., debruijn, F.J., Green, P., Keegstra, K., Kende, H., McIntosh,  
 L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M., Retzel,  
 E. and Somerville, C.  
 Genes galore: a summary of methods for accessing results from  
 large-scale partial sequencing of anonymous Arabidopsis cDNA clones  
 Plant Physiol. 106, 1241-1255 (1994)  
 95148729  
 On Nov 6, 1997 this sequence version replaced gi:931743.  
 CONTACT: Thomas Newman  
 MSU-DOE Plant Research Laboratory  
 Michigan State University  
 MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.  
 Lansing, MI  
 Tel: 517-353-0854  
 Fax: 517-353-9168  
 Email: 223j3t@clm.cl.msu.edu  
 Seq primer: T7 dye primer.  
 Location/Qualifiers  
 1. .331  
 /organism="Arabidopsis thaliana"  
 /strain="var Columbia"  
 /db\_xref="taxon:3702"  
 /clone\_1ib="93E117"  
 /clone\_1lb="Lambda-PRL2"  
 /note="Vector: lambda Zip-lox; Site\_1: Sal; Site\_2: Not;  
 Lambda PRL2 is a cDNA library derived from equal  
 quantities of 4 pools of mRNA. The mRNA sources were 1) 7  
 day germinated etiolated seedlings; 2) tissue culture  
 grown roots; 3) staged plants half with 24 hour light  
 cycle, half on 16 hr light, 8 hour dark- rosettes; 4)  
 same plants as 3 but aerial tissue (stems, flowers and  
 siliques). The vector is BRV's lambda Zip-lox. The cDNA  
 inserts were directionally cloned with Sal-Not arms using



MEDLINE 97044477  
COMMENT Contact: Soares, MB  
Program for Rat Gene Discovery and Mapping  
University of Iowa  
451 Eckstein Medical Research Building Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: msoares@blue.weeg.uiowa.edu  
CDNA Library Preparation: M.B. Soares Lab Clone Distribution:  
clones will be available through Research Genetics (www.resgen.com)  
This clone is also available through the I.M.A.G.E. Consortium at  
LLNL (infoimage.llnl.gov). IMAGE ID= 1792965  
Seq primer: M13 forward.

FEATURES  
source  
1. 340  
/organism="Rattus norvegicus"  
/strain="Sprague-Dawley"  
/db\_xref="taxon:10116"  
/clone="UI-R-B70-px-d-11-0-UI"  
/clone\_1lb="UI-R-B70"  
/dev\_stage="adult"  
/lab\_host="DH10B (Life Technologies)"  
/note="Vector: pT7p3D-Pac (Pharmacia) with a modified  
polylinker. Site\_1: Not I. Site\_2: Eco RI. This library  
(UI-R-B70) consists of a mixture of individually tagged  
normalized libraries constructed from rat hippocampus,  
thalamus, mid-brain, medulla, corpus striatum, cerebral  
cortex and testis. The tag used to identify the source  
tissue is a string of 3-6 nucleotides present between the  
Not I site and the oligo-dT track which allows  
identification of the library of origin of a clone within  
the mixture. This library was then subtracted using a  
driver consisting of a mixture of all clones from UI-R-A0,  
UI-R-A1, UI-R-E0, UI-R-E1, UI-R-C0, UI-R-C1, UI-R-C2 and  
UI-R-C2p."

BASE COUNT 82 a 82 c 78 g 98 t  
ORIGIN

Query Match 1.8%; Score 18; DB 150; Length 340;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 812 tgacagagctgcacgaca 829  
|||||  
Db 142 TGACAGAGCTGCACGACA 159

RESULT 31  
BE520970/c 342 bp mRNA EST 19-MAR-2001  
LOCUS M16A2STM Arabidopsis developing seed Arabidopsis thaliana CDNA  
DEFINITION clone M16A2 5', mRNA sequence.  
ACCESSION BE520970  
VERSION BE520970.1 GI:9778948  
KEYWORDS EST.  
SOURCE thale cress.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 342)  
White,J.A., Todd,J., Newman,T., Focks,N., Girke,T., Martinez de  
Illarduya,O., Jaworski,J.G., Ohlrogge,J. and Benning,C.  
A new set of Arabidopsis expressed sequence tags from developing  
seeds. The metabolic pathway from carbohydrates to seed oil  
Plant Physiol. 124 (4), 1582-1594 (2000)  
20367808  
JOURNAL Contact: Benning, C  
MEDLINE Dept. of Biochemistry & Molecular Biology  
COMMENT Michigan State University  
224 Biochemistry, Michigan State University, East Lansing, MI 48824  
, USA

Tel: 517 355 1609  
Fax: 517 353 9334  
Email: benning@msu.edu  
Michigan State University DNA Sequencing Facility Arabidopsis  
Biological Resource Center, The Ohio State University, 309 Botany &  
Zoology Bldg., 1735 Neil Avenue, Columbus, OH 43210 USA, FAX:  
6142920603 TEL: 6142929371.

FEATURES  
source  
1. 342  
/organism="Arabidopsis thaliana"  
/strain="Columbia"  
/db\_xref="taxon:3702"  
/clone="M16A2"  
/clone\_1lb="Arabidopsis developing seed"  
/rissue\_type="seed"  
/dev\_stage="5-13 days after flowering"  
/lab\_host="E.coli"  
/note="Organ: Developing seed; Vector: pBluescript SK-;  
Site\_1: EcoRI; Site\_2: XhoI"  
Location/Qualifiers

BASE COUNT 82 a 90 c 80 g 90 t  
ORIGIN

Query Match 1.8%; Score 18; DB 136; Length 342;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 930 caacatcacgaaggagct 947  
|||||  
Db 108 CAACATCAGCAGAGGCGCT 91

RESULT 32  
AV527474 365 bp mRNA EST 01-SEP-2000  
LOCUS AV527474/c  
DEFINITION Old Arabidopsis thaliana aboveground organs two to six-week  
ACCESSION AV527474  
VERSION AV527474.1 GI:8687002  
KEYWORDS EST.  
SOURCE thale cress.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 365)  
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.  
A large scale analysis of cDNA in Arabidopsis thaliana: Generation  
of 12,028 non-redundant expressed sequence tags from normalized and  
size-selected cDNA libraries  
DNA Res. 7, 175-180 (2000)  
20363093  
JOURNAL Contact: Erika Asamizu  
MEDLINE The first laboratory for plant Gene Research  
COMMENT Kazusa DNA Research Institute  
Yana 1532-3, Kisarazu, Chiba 252-0812, Japan  
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/  
Location/Qualifiers

FEATURES  
source  
1. 365  
/organism="Arabidopsis thaliana"  
/strain="Columbia"  
/db\_xref="taxon:3702"  
/clone="AP237e11r"  
/clone\_1lb="Arabidopsis thaliana aboveground organs two to  
six-week old"  
/rissue\_type="aboveground organs"  
/dev\_stage="two to six-week old"  
/note="Vector: pBluescriptII SK-; Site\_1: EcoRI; Site\_2:  
XhoI"  
Location/Qualifiers

BASE COUNT 103 a 96 c 81 g 85 t  
ORIGIN

Query Match 1.8%; Score 18; DB 31; Length 365;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 930 caacatcagaagggt 947  
 |||  
 Db 142 CAACATCAGGAGGGGT 125

RESULT 33  
 T42951/c 368 bp mRNA EST 06-NOV-1997  
 LOCUS 6214 Lambda-PRL2 Arabidopsis thaliana cDNA clone 118112T7, mRNA  
 DEFINITION sequence.  
 T42951  
 ACCESSION T42951 GI:2597542  
 VERSION  
 KEYWORDS EST.  
 SOURCE thale cress.  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 REFERENCE 1 (bases 1 to 368)  
 AUTHORS Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H., McIntosh  
 ,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M., Retzel  
 ,E. and Somerville,C.  
 Genes galore: a summary of methods for accessing results from  
 large-scale partial sequencing of anonymous Arabidopsis cDNA clones  
 Plant Physiol. 106, 1241-1255 (1994)  
 95148729  
 COMMENT On Nov 6, 1997 this sequence version replaced gi:947584.  
 Contact: Thomas Newman  
 MSU-DOE Plant Research Laboratory  
 Michigan State University  
 MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.  
 Lansing, MI  
 Tel: 517-353-0854  
 Fax: 517-353-9168  
 Email: 22313cneilm.cl.msu.edu  
 Seq primer: 77 dye primer.  
 Location/Qualifiers  
 1..368  
 /organism="Arabidopsis thaliana"  
 /strain="var Columbia"  
 /db\_xref="taxon:3702"  
 /clone="118112T7"  
 /note="Vector: lambda zip-lox; Site\_1: Sal; Site\_2: Not;  
 Lambda PRL2 is a cDNA library derived from equal  
 quantities of 4 pools of mRNA. The mRNA sources were 1) 7  
 day germinated etiolated seedlings; 2) tissue culture  
 grown roots; 3) staged plants half with 24 hour light  
 cycle, half on 16 hr light, 8 hour dark- rosettes; 4)  
 same plants as 3 but aerial tissue (stems, flowers and  
 siliques. The vector is BRU's lambda zip-lox. The cDNA  
 inserts were directionally cloned with Sal-I Not arms using  
 oligo dT primed cDNA."

BASE COUNT 91 a 86 c 83 g 94 t 14 others  
 ORIGIN

Query Match 1.8%; Score 18; DB 189; Length 368;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 930 caacatcagaagggt 947  
 |||  
 Db 139 CAACATCAGGAGGGGT 122

RESULT 34  
 T47675/c 370 bp mRNA EST 17-JAN-1995  
 LOCUS

DEFINITION ATTS4531 Strasbourg-A Arabidopsis thaliana cDNA clone FAFJ47, mRNA  
 sequence.  
 ACCESSION 247675  
 VERSION 247675.1 GI:623714  
 KEYWORDS EST.  
 SOURCE thale cress.  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 REFERENCE 1 (bases 1 to 370)  
 CNRS.  
 The Arabidopsis thaliana transcribed genome: the GDR cDNA program  
 Unpublished (1996)  
 CONTACT: Parmentier Y., Criqui M.C., Durr A., Fleck J.  
 Fleck Jacqueline / U626  
 Biologie Moleculaire des Plantes - CNRS  
 12 Rue du General Zimmer, 67084 Strasbourg Cedex, France  
 Email: ARABANK@MEDOC.U-STRASBG.FR.  
 Location/Qualifiers  
 1..370  
 /organism="Arabidopsis thaliana"  
 /strain="ecotype Columbia"  
 /db\_xref="taxon:3702"  
 /clone="FAFJ47"  
 /note="Vector: Lambda ZAPIT; tissue-sliced leaves of  
 A.thaliana ecotype Columbia; clone library-Strasbourg-A;  
 Cloning vector: Lambda ZAPIT; Physiological condition:  
 leaves strips incubated 2/3/4 days in liquid culture  
 medium."

BASE COUNT 87 a 96 c 85 g 100 t 2 others  
 ORIGIN

Query Match 1.8%; Score 18; DB 191; Length 370;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 930 caacatcagaagggt 947  
 |||  
 Db 96 CAACATCAGGAGGGGT 79

RESULT 35  
 AV430174/c 376 bp mRNA EST 23-AUG-2000  
 LOCUS AV430174 Porphyra yezoensis TU-1 Porphyra yezoensis cDNA clone  
 PL014e12\_r 5', mRNA sequence.  
 DEFINITION AV430174  
 ACCESSION AV430174 GI:8585399  
 KEYWORDS EST.  
 SOURCE Porphyra yezoensis.  
 ORGANISM Porphyra yezoensis  
 Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae;  
 Porphyra.  
 1 (bases 1 to 376)  
 REFERENCE 1  
 Nikaido,I., Asamizu,E., Nakajima,M., Nakamura,Y., Saga,N. and  
 Tabata,S.  
 Generation of 10,154 expressed sequence tags from a leafy  
 gametophyte of a marine red alga, Porphyra yezoensis  
 DNA Res. 7, 223-227 (2000)  
 TITLE The First Laboratory for Plant Gene Research  
 JOURNAL Kazusa DNA Research Institute  
 MEDLINE Yana 1532-3, Kikarazu, Chiba 292-0812, Japan  
 COMMENT Email: asamizukazusa.or.jp. URL: http://www.kazusa.or.jp/en/plant/  
 Location/Qualifiers  
 1..376  
 /organism="Porphyra yezoensis"  
 /strain="TU-1"  
 /db\_xref="taxon:2788"

BASE COUNT 40 a 158 c 121 g 57 t

ORIGIN

Query Match 1.8%; Score 18; DB 30; Length 376;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 596 atcgacagccggcgccg 613  
|||||  
|||||

Db 220 ATGCACACGCCCGGCC 203

RESULT 36  
AV526330/c 391 bp mRNA EST 01-SEP-2000  
LOCUS  
DEFINITION AV526330 Arabidopsis thaliana aboveground organs two to six-week  
ACCESSION AV526330 Old Arabidopsis thaliana cDNA clone AP210d10R 5', mRNA sequence.  
VERSION AV526330.1 GI:8685858  
KEYWORDS EST.  
SOURCE thale cress.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; euroids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 391)  
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.  
A large scale analysis of cDNA in Arabidopsis thaliana: Generation  
of 12,028 non-redundant expressed sequence tags from normalized  
size-selected cDNA libraries  
DNA Res. 7, 175-180 (2000)

REFERENCE  
AUTHORS  
TITLE

JOURNAL  
MEDLINE  
COMMENT 20363093  
Contact: Erika Asamizu  
The First Laboratory for Plant Gene Research  
Kazusa DNA Research Institute  
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan  
Email: asamizuekazusa.or.jp. URL: http://www.kazusa.or.jp/en/plant/.  
Location/Qualifiers

FEATURES  
source  
1. 391  
/organism="Arabidopsis thaliana"  
/strain="Columbia"  
/db\_xref="taxon:3702"  
/clone="AP210d10R"  
/clone\_lib="Arabidopsis thaliana aboveground organs two to  
six-week Old"  
/issue\_type="aboveground organs"  
/dev\_stage="two to six-week Old"  
/note="Vector: pBluescriptII SK-; site\_1: EcoRI; site\_2:  
XhoI"

BASE COUNT 107 a 100 c 87 g 97 t

ORIGIN

Query Match 1.8%; Score 18; DB 31; Length 391;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 930 caacatcagaaggagg 947  
|||||  
|||||

Db 134 CAACATCAGCAGGCGGT 117

RESULT 37  
N65689/c 391 bp mRNA EST 05-JAN-1998  
LOCUS  
DEFINITION 20729 Lambda-PRL2 Arabidopsis thaliana cDNA clone 229K107, mRNA  
sequence.  
ACCESSION N65689

VERSION N65689.1 GI:1217315  
KEYWORDS EST.  
SOURCE thale cress.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; euroids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 391)  
Neman, T., deBrujin, F.J., Green, P., Keegstra, K., Kende, H., McIntosh  
L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomasow, M., Retzel  
E., and Somerville, C.  
Gene galore: a summary of methods for accessing results from  
large-scale partial sequencing of anonymous Arabidopsis cDNA clones  
Plant Physiol. 106, 1241-1255 (1994)

TITLE  
JOURNAL  
MEDLINE  
COMMENT 95148729  
Contact: Thomas Neman  
MSU-DOE Plant Research Laboratory  
Michigan State University  
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.  
Lansing, MI  
Tel: 517-353-0854  
Fax: 517-353-9168  
Email: 22313cpebm.cl.msu.edu  
Seq primer: T7 dye primer.  
Location/Qualifiers

FEATURES  
source  
1. 391  
/organism="Arabidopsis thaliana"  
/strain="var columbia"  
/db\_xref="taxon:3702"  
/clone="229K107"  
/clone\_lib="Lambda-PRL2"  
/note="Vector: lambda zip-lox; site\_1: Sal; site\_2: Not;  
Lambda PRL2 is a cDNA library derived from equal  
quantities of 4 pools of mRNA. The mRNA sources were 1) 7  
day germinated etiolated seedlings; 2) tissue culture  
grown roots; 3) staged plants half with 24 hour light  
cycle, half on 16 hr light, 8 hour dark - rosettes; 4)  
same plants as 3 but aerial tissue (stems, flowers and  
siliques. The vector is BRL's lambda zip-lox. The cDNA  
inserts were directionally cloned with Sal-Not arms using  
oligo dr primed cDNA."

BASE COUNT 100 a 86 c 90 g 100 t 15 others

ORIGIN

Query Match 1.8%; Score 18; DB 159; Length 391;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 930 caacatcagaaggagg 947  
|||||  
|||||

Db 147 CAACATCAGCAGGCGGT 130

RESULT 38  
D78804 392 bp mRNA EST 09-FEB-1996  
LOCUS  
DEFINITION HUM516H08B Human placenta polyA+ (T Fujiiwara) Homo sapiens cDNA  
clone GEN-516H08 5', mRNA sequence.  
ACCESSION D78804  
VERSION D78804.1 GI:1180677  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 392)  
Fujiiwara, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M.,  
Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H., Takaichi  
A., Takeda, S., Watanabe, T., Takahashi, E., Hirai, Y., Maekawa, H.,  
Shin, S. and Nakamura, Y.  
Fujiiwara et al (1995)  
Unpublished (1995)



## COMMENT

Contact: Tsutomu Fujiwara  
Otsuka GEN Research Institute  
Otsuka Pharmaceutical Co. Ltd  
463-10 Kagasuno Kawanchi-cho, Tokushima, Tokushima, 771-01 Japan  
Tel: 0886-65-2888  
Fax: 0886-37-1035.

## FEATURES

## source

Location/Qualifiers  
1..392  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="GEN-516H08"  
/clone\_lib="Human placenta polyA+ (rFujiwara)"  
/tissue\_type="placenta"

## BASE COUNT

90 a 127 c 79 g 96 t

## ORIGIN

Query Match 1.8%; Score 18; DB 157; Length 392;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 230 cccctgcatcacccctg 247  
|||||

Db 8 CCCCTGCATCACCCCTG 25

## RESULT 39

## LOCUS

A0253544 392 bp DNA GSS 10-OCT-1998

HS-2227\_A2.G04.MF CIT Approved Human Genomic Sperm Library D Homo

sapiens genomic clone Plate=2227 Col=8 Row=M, DNA sequence.

## ACCESSION

A0253544

## VERSION

A0253544.1 GI:3724898

## KEYWORDS

## SOURCE

## ORGANISM

human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 392)  
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,  
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and  
Hood,L.  
Sequence-tagged connectors: A sequence approach to mapping and  
scanning the human genome

## TITLE

Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)

## JOURNAL

## MEDLINE

## COMMENT

Contact: Mahairas GG, Wallace JC, Hood L  
High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: jwallace@u.washington.edu  
Sequence Tagged Connector  
Plate: 2227 row: M column: 8  
Class: BAC ends  
High quality sequence stop: 392.

## FEATURES

## source

Location/Qualifiers  
1..392  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="Plate=2227 Col=8 Row=M"  
/clone\_lib="CIT Approved Human Genomic Sperm Library D"  
/sex="male"  
/note="Organ: sperm; Vector: pBelobAC11; BAC clones in  
E-Coli DH10B"

## BASE COUNT

94 a 101 c 67 g 129 t 1 others

## ORIGIN

Query Match 1.8%; Score 18; DB 226; Length 392;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 489 gccagctaataagtgctc 506  
|||||

Db 154 GCCAGCTAATATGTGTGC 137

## RESULT 40

## LOCUS

AV527255 398 bp mRNA EST 01-SEP-2000

AV527255 Arabidopsis thaliana aboveground organs two to six-week

old Arabidopsis thaliana cDNA clone AP23g91R 5', mRNA sequence.

## ACCESSION

## VERSION

AV527255.1 GI:8686783

## KEYWORDS

## SOURCE

thale cress.  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 398)  
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.  
A large scale analysis of cDNA in Arabidopsis thaliana: Generation  
of 12,028 non-redundant expressed sequence tags from normalized and  
size-selected cDNA libraries  
DNA Res. 7, 175-180 (2000)

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## MEDLINE

## COMMENT

Contact: Erika Asamizu  
The First Laboratory for Plant Gene Research  
Kazusa DNA Research Institute  
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan  
Email: asamizu@kazusa.or.jp, URL: <http://www.kazusa.or.jp/en/plant/>.

## FEATURES

## source

Location/Qualifiers  
1..398  
/organism="Arabidopsis thaliana"  
/strain="Columbia"  
/db\_xref="taxon:3702"  
/clone="AP23g91R"  
/clone\_lib="Arabidopsis thaliana aboveground organs two to  
six-week old"  
/tissue\_type="aboveground organs"  
/dev\_stage="two to six-week old"  
/note="Vector: pBluescriptII SK-; Site\_1: EcoRI; Site\_2:  
XhoI"

## BASE COUNT

95 a 102 c 94 g 107 t

## ORIGIN

Query Match 1.8%; Score 18; DB 31; Length 398;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 930 caacatcagaagggagt 947  
|||||

Db 35 CAACATCAGAGGCGGT 18

## RESULT 41

## LOCUS

AV526564 404 bp mRNA EST 01-SEP-2000

AV526564 Arabidopsis thaliana aboveground organs two to six-week

old Arabidopsis thaliana cDNA clone AP216b09R 5', mRNA sequence.

## ACCESSION

## VERSION

AV526564.1 GI:8686092

## KEYWORDS

## SOURCE

thale cress.  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 404)  
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.  
A large scale analysis of cDNA in Arabidopsis thaliana: Generation  
of 12,028 non-redundant expressed sequence tags from normalized and

size-selected cDNA libraries  
DNA Res. 7, 175-180 (2000)  
20363093  
Contact: Erika Asamizu  
The First Laboratory for Plant Gene Research  
Kazusa DNA Research Institute  
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan  
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/  
Location/Qualifiers

FEATURES  
source  
1. 404  
/organism="Arabidopsis thaliana"  
/strain="Columbia"  
/db\_xref="taxon:3702"  
/clone\_1lb="Arabidopsis thaliana aboveground organs two to six-week old"  
/tissue\_type="aboveground organs"  
/dev\_stage="two to six-week old"  
/note="Vector: pBluescriptII SK-; Site\_1: EcoRI; Site\_2: XhoI"

BASE COUNT  
111 a 104 c 90 g 99 t

ORIGIN

Query Match 1.8%; Score 18; DB 31; Length 404;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 930 caacatcacgaaggaggt 947  
|||||

Db 141 CAACATCAGCAGAGGGGT 124

RESULT 42  
T21720/c 441 bp mRNA EST 07-JAN-1998  
LOCUS  
DEFINITION 3728 Lambda-PRL2 Arabidopsis thaliana cDNA clone 97C2177, mRNA  
sequence.  
ACCESSION T21720  
VERSION T21720.1 GI:2757230  
KEYWORDS EST.  
SOURCE thale cress.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidops.  
1 (bases 1 to 441)  
Newman,T., debruijn,F.J., Green,P., Keegstra,K., Kende,H., McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M., Retzel,E. and Somerville,C.  
Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones  
Plant Physiol. 106, 1241-1255 (1994)  
95148729  
On Jan 7, 1998 this sequence version replaced gi:914624.  
Contact: Thomas Newman  
MSU-DOE Plant Research Laboratory  
Michigan State University  
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E. Lansing, MI  
Tel: 517-353-0854  
Fax: 517-353-9168  
Email: 22313tcn@lhm.cl.msu.edu  
Seq primer: T7.  
Location/Qualifiers

FEATURES  
source  
1. 441  
/organism="Arabidopsis thaliana"  
/strain="var Columbia"  
/db\_xref="taxon:3702"  
/clone="97C2177"  
/clone\_1lb="Lambda-PRL2"  
/note="Vector: lambda Zip-lox; Site\_1: Sal; Site\_2: Not; Lambda PRL2 is a cDNA library derived from equal

quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark- rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dt primed cDNA.

BASE COUNT  
115 a 101 c 97 g 113 t 15 others

ORIGIN

Query Match 1.8%; Score 18; DB 188; Length 441;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 930 caacatcacgaaggaggt 947  
|||||

Db 126 CAACATCAGCAGAGGGGT 109

RESULT 43  
H77242/c 443 bp mRNA EST 05-JAN-1998  
LOCUS  
DEFINITION 17673 Lambda-PRL2 Arabidopsis thaliana cDNA clone 205H2377, mRNA  
sequence.  
ACCESSION H77242  
VERSION H77242.1 GI:1054493  
KEYWORDS EST.  
SOURCE thale cress.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidops.  
1 (bases 1 to 443)  
Newman,T., debruijn,F.J., Green,P., Keegstra,K., Kende,H., McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M., Retzel,E. and Somerville,C.  
Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones  
Plant Physiol. 106, 1241-1255 (1994)  
95148729  
Contact: Thomas Newman  
MSU-DOE Plant Research Laboratory  
Michigan State University  
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E. Lansing, MI  
Tel: 517-353-0854  
Fax: 517-353-9168  
Email: 22313tcn@lhm.cl.msu.edu  
Seq primer: T7 dye primer.  
Location/Qualifiers

FEATURES  
source  
1. 443  
/organism="Arabidopsis thaliana"  
/strain="var Columbia"  
/db\_xref="taxon:3702"  
/clone="205H2377"  
/clone\_1lb="Lambda-PRL2"  
/note="Vector: lambda Zip-lox; Site\_1: Sal; Site\_2: Not; Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark- rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dt primed cDNA.

BASE COUNT  
122 a 104 c 95 g 105 t 17 others

ORIGIN

Query Match 1.8%; Score 18; DB 158; Length 443;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 930 caacatcagaagggt 947  
|||||  
Db 153 CAACATCAGAGGGGT 136

RESULT 44  
LOCUS AQ228766/c 446 bp DNA GSS 26-SEP-1998  
DEFINITION HS-2020.A2.H08.T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2020 Col=16 Row=O, DNA sequence.  
ACCESSION AQ228766  
VERSION AQ228766.1 GI:3653995  
KEYWORDS GSS.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 446)  
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.  
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome  
JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)  
MEDLINE 99380589  
COMMENT Contact: Mahairas GG, Wallace JC, Hood L  
High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: jwallace@u.washington.edu  
Sequence Tagged Connector  
Plate: 2020 row: 0 column: 16  
Class: BAC ends  
High quality sequence stop: 446.  
Location/Qualifiers  
source  
1. 446  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="Plate=2020 Col=16 Row=O"  
/clone\_lib="CIT Approved Human Genomic Sperm Library D"  
/sex="male"  
/note="Organ: sperm; Vector: pBelOBAC11; BAC clones in E-Coli DH10B"

BASE COUNT 72 a 131 c 103 g 138 t 2 others  
ORIGIN

Query Match 1.8%; Score 18; DB 225; Length 446;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 816 agagctgcagcagcg 833  
|||||  
Db 232 AGAGCTGCAGCAGCG 215

RESULT 45  
LOCUS N65546/c 461 bp mRNA EST 05-JAN-1998  
DEFINITION 20586 Lambda-PRL2 Arabidopsis thaliana cDNA clone 231J27, mRNA sequence.  
ACCESSION N65546  
VERSION N65546.1 GI:1217172  
KEYWORDS EST.  
SOURCE Thale cress.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

REFERENCE 1 (bases 1 to 461)  
AUTHORS Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H., McIntosh,L., Ohlrogge,J., Ralikel,N., Somerville,S., Thomashow,M., Rezel,E. and Somerville,C.  
TITLE Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones  
JOURNAL Plant Physiol. 106, 1241-1255 (1994)  
MEDLINE 95148729  
COMMENT Contact: Thomas Newman  
MSU-DOE Plant Research Laboratory  
Michigan State University  
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E. Lansing, MI  
Tel: 517-353-0854  
Fax: 517-353-9168  
Email: 22313c@pml.msu.edu  
Seq primer: T7 dye primer.  
Location/Qualifiers  
source  
1. 461  
/organism="Arabidopsis thaliana"  
/strain="var Columbia"  
/db\_xref="taxon:3702"  
/clone="231J27"  
/clone\_lib="Lambda-PRL2"  
/note="Vector: lambda Z1p-Lox; Site 1: Sal; Site 2: Not; Lambda PRL2 is a cDNA library derived from equal 7 quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark- rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Z1p-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dt primed cDNA."

BASE COUNT 118 a 107 c 100 g 119 t 17 others  
ORIGIN

Query Match 1.8%; Score 18; DB 159; Length 461;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 930 caacatcagaagggt 947  
|||||  
Db 144 CAACATCAGAGGGGT 127

RESULT 46  
LOCUS AI991951/c 463 bp mRNA EST 08-MAR-2000  
DEFINITION ws43a04.x1 NCI CGAP\_Brn25 Homo sapiens cDNA IMAGE:249918 3' similar to contains element MSRI repetitive element ;, mRNA sequence.  
ACCESSION AI991951  
VERSION AI991951.1 GI:5838856  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 463)  
AUTHORS NCI/NIHDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTCAP), Tumor Gene Index  
JOURNAL Unpublished (1998)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaaps-remail.nih.gov  
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/brdp/image/image.html  
Insert length: 565 Std Error: 0.00  
Seq primer: -40UP from Gibco.

## FEATURES

source

1. .463  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2499918"  
/clone\_lib="NCI-CGAP\_Brn25"  
/tissue\_type="anaplastic oligodendroglioma"  
/lab\_host="DH10B"  
/note="Organ: brain; Vector: pRT73D-Pac (Pharmacia) with a  
modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dt) primer [5'  
TCTTACCAATCTGAAAGTGGACGGCCGCGCATGCTTTTCTTTTCTTTTCTTTT  
T 3']; double-stranded cDNA was ligated to Eco RI  
adaptors (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of the modified pRT73 vector.  
Library is normalized, and was constructed by Bento  
Soares and M.Fatima Bonaldo."

## BASE COUNT

99 a 102 c 132 g 129 t 1 others

## ORIGIN

## Query Match

Best Local Similarity 100.0%; Pred. No. 1.1e+02; Length 463;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 230 cccctgcatcaccctg 247  
|||||

Db 151 cccctgcatcaccctg 134

## RESULT 47

BF612300

LOCUS

BF612300 463 bp mRNA EST 14-DEC-2000  
daa17a11.y1 NICHD XGC Lul Xenopus laevis cDNA clone IMAGE:4056476

DEFINITION

5' similar to SW:GSP\_TORCA P56101 CYSTEINE STRING PROTEIN ;, mRNA  
sequence.

ACCESSION BF612300  
VERSION BF612300.1 GI:11782798

KEYWORDS

SOURCE

ORGANISM

Xenopus laevis  
African clawed frog.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;

Xenopodinae; Xenopus.  
1 (bases 1 to 463)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index  
Unpublished (1997)

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Martha Rebert, Steven L. Klein, Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: Xenopus clones from this library are available  
through the I.M.A.G.E. Consortium/LLNL at: [infoimage.llnl.gov](http://infoimage.llnl.gov)

Seq primer: -40RP from Gibco

High quality sequence stop: 439.

Location/Qualifiers

FEATURES

source

1. .463  
/organism="Xenopus laevis"  
/db\_xref="taxon:8355"  
/clone="IMAGE:4056476"  
/clone\_lib="NICHD XGC Lul"  
/dev\_stage="adult"

## BASE COUNT

108 a 111 c 138 g 106 t

## ORIGIN

## Query Match

Best Local Similarity 100.0%; Pred. No. 1.1e+02; Length 463;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 453 cgggcaacatgcccagc 470  
|||||

Db 30 cgggcaacatgcccagc 47

## RESULT 48

BE811867

LOCUS

BE811867 465 bp mRNA EST 21-SEP-2000  
PMO-AN0032-110700-001-a12 AN0032 Homo sapiens cDNA, mRNA sequence.

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 463)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,  
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.U.

Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
This sequence was derived from the FADES/ILICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-PMO-AN0032-110>  
700-001-a12et3-2000-07-11et4-1)

Seq primer: puc 18 forward

High quality sequence stop: 266.

Location/Qualifiers

FEATURES

source

1. .465  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="AN0032"  
/dev\_stage="Adult"

/note="Organ: amnion,normal; Vector: puc18; Site.1: SmaI;  
Site.2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the puc 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

BASE COUNT

111 a 160 c 92 g 102 t

ORIGIN

Query Match

1.8%; Score 18; DB 140; Length 465;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 230 cccctgacacccctg 247  
|||||  
Db 138 CCCCTGCATCACCCCTG 155

## RESULT 49

A2462258

LOCUS 474 bp DNA GSS 04-OCT-2000  
DEFINITION IM0269023F Mouse 10kb plasmid U06C1M library Mus musculus genomic  
clone U06C1M0269023 F, DNA sequence.

A2462258

ACCESSION A2462258.1 GI:10620383  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

house mouse.  
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 474)

## REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,  
,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A.  
and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## TITLE

Unpublished (2000)

## JOURNAL

COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0269 row: 0 column: 23  
Seq primer: CGTTCGTAACGACGCCACAC  
Class: plasmid ends  
High quality sequence stop: 474.

## FEATURES

source

Location/Qualifiers

1. 474

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="U06C1M0269023"

/clone\_lib="Mouse 10kb plasmid U06C1M library"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PMD42nv. Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adapter oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 (g14732114|gblaf129072.1) a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT  
ORIGIN

85 a 132 c 135 g 122 t

Query Match 1.8%; Score 18; DB 244; Length 474;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 265 gaagcgcgcctcctg 282  
|||||

Db 219 GCAGCGCGCCTCTGCC 236

## RESULT 50

A1466074

LOCUS 476 bp mRNA EST 09-MAR-1999  
DEFINITION vw39b02.y1 Soares\_mammary\_gland\_NBMVG Mus musculus cDNA clone  
IMAGE:1246155 5' similar to gb:U17574 Mouse mRNA for  
proactosin-binding protein (MOUSE);, mRNA sequence.

ACCESSION A1466074.1 GI:4320104  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

house mouse.  
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 476)

## REFERENCE

AUTHORS

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)

## JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: cgaps-rt@mail.nih.gov  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:659843

This read is a RESSEQUENCE of a previously sequenced mouse clone  
this read has been verified (found to hit its original self in the  
correct orientation)  
Seq primer: -40RP from Glibco  
High quality sequence stop: 317.

## FEATURES

source

Location/Qualifiers

1. 476

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="IMAGE:1246155"

/clone\_lib="Soares\_mammary\_gland\_NBMVG"

/sex="male"

/tissue\_type="mammary gland"

/dev\_stage="4 weeks"

/lab\_host="DH10B"

/note="Organ: mammary gland; Vector: pT73D-Pac (Pharmacia  
) with a modified polylinker; Site 1: Not I; Site 2: Eco  
RI; 1st strand cDNA was primed with a Not I - oligo(dT)  
primer (5'  
TGTACCAATCTGAAGTGGAGCGCGCGAAGGTTTTTTTTTTTTTTTTTTT  
T 3'); double-stranded cDNA was ligated to Eco RI  
adaptors (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of the modified pT73 vector.  
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library  
constructed and normalized by Bento Soares and M. Fatima  
Bonaldo."

BASE COUNT 104 a 132 c 134 g 106 t  
ORIGIN

Query Match 1.8%; Score 18; DB 20; Length 476;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 265 gaagcgcgcctcctg 282  
|||||

Db 380 GCAGCGCGCCTCTGCC 397

Search completed: September 21, 2001, 03:21:19  
Job time: 9395 sec

---

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 21, 2001, 16:24:12 : Search time 84.41 Seconds  
(without alignments)  
2188.931 Million cell updates/sec

Title: US-09-138-735-1\_COPY\_1232\_2207

Perfect score: 976  
Sequence: 1 cagtgacgcgcgtacgcgtc.....tgtgaacgagccattatgt 976

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 324599 seqs, 9465562 residues

Word size : 0

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : Issued\_Patents\_NA:\*  
1: /cgnl\_7/ptodata/1/ina/5A.COMB.seq:\*  
2: /cgnl\_7/ptodata/1/ina/5B.COMB.seq:\*  
3: /cgnl\_7/ptodata/1/ina/6A.COMB.seq:\*  
4: /cgnl\_7/ptodata/1/ina/6B.COMB.seq:\*  
5: /cgnl\_7/ptodata/1/ina/PCRTUS.COMB.seq:\*  
6: /cgnl\_7/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID                | Description       |
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| 1          | 976   | 100.0       | 3402   | 1 US-08-480-917-1    | Sequence 1, Appl  |
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| 3          | 21    | 2.2         | 21     | 1 US-08-480-917-10   | Sequence 10, Appl |
| 4          | 21    | 2.2         | 21     | 1 US-08-480-917-12   | Sequence 12, Appl |
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| 6          | 19    | 1.9         | 11878  | 2 US-08-970-269A-31  | Sequence 31, Appl |
| 7          | 19    | 1.9         | 11883  | 2 US-08-970-269A-28  | Sequence 28, Appl |
| 8          | 18    | 1.8         | 18     | 1 US-08-480-917-5    | Sequence 5, Appl  |
| 9          | 18    | 1.8         | 18     | 1 US-08-480-917-8    | Sequence 8, Appl  |
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| 11         | 18    | 1.8         | 2520   | 2 US-08-340-426D-50  | Sequence 50, Appl |
| 12         | 18    | 1.8         | 2520   | 2 US-08-450-673C-50  | Sequence 50, Appl |
| 13         | 18    | 1.8         | 2520   | 5 PCT-US95-17111A-50 | Sequence 50, Appl |
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| 16         | 17    | 1.7         | 673    | 2 US-08-692-787-4    | Sequence 4, Appl  |
| 17         | 17    | 1.7         | 673    | 4 US-09-097-199-4    | Sequence 4, Appl  |
| 18         | 17    | 1.7         | 2545   | 2 US-08-468-819-72   | Sequence 72, Appl |
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| 20         | 17    | 1.7         | 3337   | 2 US-08-719-822B-1   | Sequence 1, Appl  |
| 21         | 17    | 1.7         | 3337   | 4 US-09-092-458-1    | Sequence 1, Appl  |
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| 25         | 16    | 1.6         | 1185   | 3 US-08-912-205-9    | Sequence 9, Appl  |
| 26         | 16    | 1.6         | 1185   | 4 US-09-440-400-9    | Sequence 9, Appl  |
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| 28  | 16 | 1.6 | 1411  | 1 US-07-952-817-10   | Sequence 10, Appl  |
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| 30  | 16 | 1.6 | 1856  | 2 US-08-360-606B-29  | Sequence 29, Appl  |
| 31  | 16 | 1.6 | 1864  | 2 US-08-673-388-9    | Sequence 9, Appl   |
| 32  | 16 | 1.6 | 1864  | 2 US-08-614-877-9    | Sequence 9, Appl   |
| 33  | 16 | 1.6 | 2190  | 3 US-08-508-761B-5   | Sequence 5, Appl   |
| 34  | 16 | 1.6 | 2214  | 3 US-08-864-038A-1   | Sequence 1, Appl   |
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| 36  | 16 | 1.6 | 3331  | 3 US-08-864-038A-2   | Sequence 2, Appl   |
| 37  | 16 | 1.6 | 3331  | 3 US-08-864-038A-4   | Sequence 4, Appl   |
| 38  | 16 | 1.6 | 4394  | 2 US-08-750-152A-1   | Sequence 1, Appl   |
| 39  | 16 | 1.6 | 5117  | 5 PCT-US95-05512-1   | Sequence 1, Appl   |
| 40  | 16 | 1.6 | 5117  | 5 PCT-US95-13749-3   | Sequence 3, Appl   |
| 41  | 16 | 1.6 | 6545  | 5 US-08-056-200-93   | Sequence 93, Appl  |
| 42  | 16 | 1.6 | 9551  | 2 US-08-800-644-93   | Sequence 1, Appl   |
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| 46  | 15 | 1.5 | 81    | 1 US-08-443-407-14   | Sequence 14, Appl  |
| 47  | 15 | 1.5 | 81    | 1 US-08-443-407-14   | Sequence 14, Appl  |
| 48  | 15 | 1.5 | 81    | 5 PCT-US95-05600-158 | Sequence 158, Appl |
| 49  | 15 | 1.5 | 325   | 3 US-08-994-946A-1   | Sequence 1, Appl   |
| 50  | 15 | 1.5 | 689   | 4 US-09-383-586-2    | Sequence 2, Appl   |
| 51  | 15 | 1.5 | 837   | 4 US-09-123-492A-3   | Sequence 3, Appl   |
| 52  | 15 | 1.5 | 837   | 4 US-08-633-779-1    | Sequence 1, Appl   |
| 53  | 15 | 1.5 | 846   | 3 US-09-154-874-1    | Sequence 1, Appl   |
| 54  | 15 | 1.5 | 1142  | 1 US-08-236-311-9    | Sequence 9, Appl   |
| 55  | 15 | 1.5 | 1142  | 3 US-08-457-918-9    | Sequence 9, Appl   |
| 56  | 15 | 1.5 | 1249  | 3 US-09-082-092-8    | Sequence 8, Appl   |
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| 58  | 15 | 1.5 | 1313  | 1 US-08-176-427B-7   | Sequence 7, Appl   |
| 59  | 15 | 1.5 | 1313  | 2 US-08-356-060A-4   | Sequence 4, Appl   |
| 60  | 15 | 1.5 | 1313  | 4 US-08-460-900C-4   | Sequence 4, Appl   |
| 61  | 15 | 1.5 | 1338  | 4 US-08-855-910-5    | Sequence 5, Appl   |
| 62  | 15 | 1.5 | 1433  | 3 US-08-651-136C-9   | Sequence 9, Appl   |
| 63  | 15 | 1.5 | 1505  | 4 US-08-875-847B-1   | Sequence 1, Appl   |
| 64  | 15 | 1.5 | 1566  | 2 US-08-405-175A-10  | Sequence 10, Appl  |
| 65  | 15 | 1.5 | 1608  | 2 US-08-211-718-8    | Sequence 8, Appl   |
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| 74  | 15 | 1.5 | 1777  | 3 US-08-951-742-5    | Sequence 5, Appl   |
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| 76  | 15 | 1.5 | 1869  | 3 US-09-143-068-1    | Sequence 1, Appl   |
| 77  | 15 | 1.5 | 1869  | 4 US-09-350-268-1    | Sequence 1, Appl   |
| 78  | 15 | 1.5 | 1875  | 2 US-08-642-406A-21  | Sequence 21, Appl  |
| 79  | 15 | 1.5 | 1876  | 4 US-09-082-092-5    | Sequence 5, Appl   |
| 80  | 15 | 1.5 | 1885  | 3 US-08-501-572-5    | Sequence 5, Appl   |
| 81  | 15 | 1.5 | 1885  | 3 US-09-040-444-5    | Sequence 5, Appl   |
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| 84  | 15 | 1.5 | 2501  | 3 US-08-787-739-58   | Sequence 58, Appl  |
| 85  | 15 | 1.5 | 2625  | 6 5457037-4          | Patent No. 5457037 |
| 86  | 15 | 1.5 | 2646  | 1 US-08-365-189-7    | Sequence 7, Appl   |
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| 90  | 15 | 1.5 | 3103  | 3 US-08-944-495-3    | Sequence 3, Appl   |
| 91  | 15 | 1.5 | 3103  | 3 US-09-126-640-2    | Sequence 2, Appl   |
| 92  | 15 | 1.5 | 3103  | 4 US-08-925-588-3    | Sequence 3, Appl   |
| 93  | 15 | 1.5 | 3111  | 3 US-09-487-444-3    | Sequence 3, Appl   |
| 94  | 15 | 1.5 | 3336  | 6 5457037-1          | Patent No. 5457037 |
| 95  | 15 | 1.5 | 3317  | 2 US-08-642-406A-20  | Sequence 20, Appl  |
| 96  | 15 | 1.5 | 3517  | 3 US-08-434-000A-1   | Sequence 1, Appl   |
| 97  | 15 | 1.5 | 3532  | 3 US-08-787-739-90   | Sequence 90, Appl  |
| 98  | 15 | 1.5 | 3532  | 3 US-09-008-979A-7   | Sequence 7, Appl   |
| 99  | 15 | 1.5 | 3981  | 4 US-09-460-618-7    | Sequence 7, Appl   |
| 100 | 15 | 1.5 | 4066  | 4 US-09-298-367B-3   | Sequence 3, Appl   |

|       |    |     |        |   |                   |                    |       |    |     |     |   |                    |                    |
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| C 101 | 15 | 1.5 | 4396   | 4 | US-09-060-410-3   | Sequence 3, Appl1  | 174   | 14 | 1.4 | 486 | 3 | US-08-630-019A-31  | Sequence 31, Appl1 |
| C 102 | 15 | 1.5 | 4883   | 5 | US-08-472-358-1   | Sequence 1, Appl1  | C 175 | 14 | 1.4 | 490 | 4 | US-08-998-416-882  | Sequence 882, App  |
| C 103 | 15 | 1.5 | 4983   | 5 | PCr-US92-05786A-1 | Sequence 1, Appl1  | C 176 | 14 | 1.4 | 501 | 2 | US-08-611-757-37   | Sequence 37, Appl  |
| C 104 | 15 | 1.5 | 4984   | 4 | US-08-687-806-1   | Sequence 1, Appl1  | C 177 | 14 | 1.4 | 505 | 4 | PCr-US95-0598A-37  | Sequence 37, Appl  |
| C 105 | 15 | 1.5 | 5162   | 4 | US-09-298-367B-1  | Sequence 1, Appl1  | C 178 | 14 | 1.4 | 501 | 5 | US-08-916-576B-18  | Sequence 18, Appl  |
| C 106 | 15 | 1.5 | 5162   | 4 | US-09-298-367B-4  | Sequence 4, Appl1  | 179   | 14 | 1.4 | 512 | 2 | US-08-481-658B-45  | Sequence 45, Appl  |
| C 107 | 15 | 1.5 | 5262   | 4 | US-09-298-367B-5  | Sequence 5, Appl1  | 180   | 14 | 1.4 | 512 | 2 | US-08-477-504A-45  | Sequence 45, Appl  |
| C 108 | 15 | 1.5 | 5373   | 3 | US-08-757-223-7   | Sequence 7, Appl1  | 181   | 14 | 1.4 | 512 | 2 | US-08-486-756A-45  | Sequence 45, Appl  |
| C 109 | 15 | 1.5 | 6850   | 4 | US-09-298-367B-2  | Sequence 2, Appl1  | 182   | 14 | 1.4 | 512 | 3 | US-08-485-862B-45  | Sequence 45, Appl  |
| C 110 | 15 | 1.5 | 8533   | 1 | US-07-846-181-6   | Sequence 6, Appl1  | 183   | 14 | 1.4 | 512 | 3 | US-08-787-739-45   | Sequence 45, Appl  |
| C 111 | 15 | 1.5 | 8533   | 1 | US-07-845-989-6   | Sequence 6, Appl1  | 184   | 14 | 1.4 | 512 | 3 | US-08-487-077A-45  | Sequence 45, Appl  |
| C 112 | 15 | 1.5 | 8906   | 2 | US-08-826-267-1   | Sequence 1, Appl1  | 185   | 14 | 1.4 | 512 | 3 | US-08-485-863A-45  | Sequence 45, Appl  |
| C 113 | 15 | 1.5 | 10898  | 2 | US-08-481-658B-5  | Sequence 5, Appl1  | 186   | 14 | 1.4 | 512 | 4 | US-08-485-045D-45  | Sequence 45, Appl  |
| C 114 | 15 | 1.5 | 10898  | 2 | US-08-477-504A-5  | Sequence 5, Appl1  | 187   | 14 | 1.4 | 522 | 1 | US-08-672-569-3    | Sequence 3, Appl1  |
| C 115 | 15 | 1.5 | 10898  | 2 | US-08-486-756A-5  | Sequence 5, Appl1  | C 188 | 14 | 1.4 | 522 | 3 | US-08-906-136A-3   | Sequence 3, Appl1  |
| C 116 | 15 | 1.5 | 10898  | 2 | US-08-485-862B-5  | Sequence 5, Appl1  | C 189 | 14 | 1.4 | 522 | 4 | US-09-363-427-3    | Sequence 3, Appl1  |
| C 117 | 15 | 1.5 | 10898  | 3 | US-08-787-739-5   | Sequence 5, Appl1  | C 190 | 14 | 1.4 | 525 | 3 | US-08-906-136A-1   | Sequence 1, Appl1  |
| C 118 | 15 | 1.5 | 10898  | 3 | US-08-487-077A-5  | Sequence 5, Appl1  | C 191 | 14 | 1.4 | 525 | 4 | US-09-363-427-1    | Sequence 1, Appl1  |
| C 119 | 15 | 1.5 | 10898  | 3 | US-08-485-863A-5  | Sequence 5, Appl1  | 192   | 14 | 1.4 | 532 | 4 | US-07-872-678A-10  | Sequence 10, Appl  |
| C 120 | 15 | 1.5 | 10898  | 4 | US-08-485-045D-5  | Sequence 5, Appl1  | 193   | 14 | 1.4 | 534 | 2 | US-09-098-487-11   | Sequence 11, Appl  |
| C 121 | 15 | 1.5 | 24417  | 2 | US-08-846-762-1   | Sequence 2, Appl1  | C 194 | 14 | 1.4 | 536 | 3 | US-08-705-875A-7   | Sequence 7, Appl1  |
| C 122 | 15 | 1.5 | 36519  | 3 | US-08-923-137-2   | Sequence 2, Appl1  | 195   | 14 | 1.4 | 538 | 1 | US-08-676-967-9    | Sequence 9, Appl1  |
| C 123 | 15 | 1.5 | 50341  | 1 | US-08-247-901C-1  | Sequence 1, Appl1  | 196   | 14 | 1.4 | 538 | 1 | US-08-676-974-9    | Sequence 9, Appl1  |
| C 124 | 15 | 1.5 | 50341  | 2 | US-09-075-904-1   | Sequence 1, Appl1  | 197   | 14 | 1.4 | 538 | 2 | US-09-098-487-9    | Sequence 9, Appl1  |
| C 125 | 15 | 1.5 | 50937  | 4 | US-09-426-436-1   | Sequence 1, Appl1  | 198   | 14 | 1.4 | 540 | 1 | US-08-676-967-6    | Sequence 6, Appl1  |
| C 126 | 15 | 1.5 | 52297  | 4 | US-08-724-394A-20 | Sequence 20, Appl1 | 199   | 14 | 1.4 | 540 | 1 | US-08-676-967-7    | Sequence 7, Appl1  |
| C 127 | 15 | 1.5 | 246240 | 2 | US-08-724-394A-21 | Sequence 21, Appl1 | 200   | 14 | 1.4 | 540 | 1 | US-08-676-967-8    | Sequence 8, Appl1  |
| C 128 | 15 | 1.5 | 246240 | 2 | US-08-724-394A-22 | Sequence 22, Appl1 | 201   | 14 | 1.4 | 540 | 1 | US-08-676-974-6    | Sequence 6, Appl1  |
| C 129 | 15 | 1.5 | 246240 | 2 | US-09-053-866-12  | Sequence 12, Appl1 | 202   | 14 | 1.4 | 540 | 1 | US-08-676-974-7    | Sequence 7, Appl1  |
| C 130 | 14 | 1.4 | 18     | 3 | US-08-889-296A-22 | Sequence 22, Appl1 | 203   | 14 | 1.4 | 540 | 1 | US-08-676-974-8    | Sequence 8, Appl1  |
| C 131 | 14 | 1.4 | 20     | 2 | US-08-848-840A-22 | Sequence 22, Appl1 | 204   | 14 | 1.4 | 540 | 2 | US-09-098-487-6    | Sequence 6, Appl1  |
| C 132 | 14 | 1.4 | 20     | 2 | US-08-961-469A-30 | Sequence 30, Appl1 | 205   | 14 | 1.4 | 540 | 2 | US-09-098-487-7    | Sequence 7, Appl1  |
| C 133 | 14 | 1.4 | 20     | 3 | US-09-128-494-22  | Sequence 22, Appl1 | 206   | 14 | 1.4 | 540 | 2 | US-09-098-487-8    | Sequence 8, Appl1  |
| C 134 | 14 | 1.4 | 20     | 3 | US-09-481-288-4   | Sequence 4, Appl1  | 207   | 14 | 1.4 | 554 | 1 | US-08-330-123A-1   | Sequence 1, Appl1  |
| C 135 | 14 | 1.4 | 30     | 1 | US-08-398-613A-10 | Sequence 10, Appl1 | 208   | 14 | 1.4 | 559 | 2 | US-08-485-778-2    | Sequence 2, Appl1  |
| C 136 | 14 | 1.4 | 37     | 1 | US-08-398-612A-10 | Sequence 10, Appl1 | 209   | 14 | 1.4 | 559 | 3 | US-08-520-550A-2   | Sequence 2, Appl1  |
| C 137 | 14 | 1.4 | 37     | 1 | US-08-398-611A-10 | Sequence 10, Appl1 | 210   | 14 | 1.4 | 560 | 1 | US-08-482-115B-1   | Sequence 1, Appl1  |
| C 138 | 14 | 1.4 | 37     | 1 | US-08-396-851A-10 | Sequence 10, Appl1 | 211   | 14 | 1.4 | 560 | 2 | US-08-660-678A-1   | Sequence 1, Appl1  |
| C 139 | 14 | 1.4 | 37     | 2 | US-08-491-334A-10 | Sequence 10, Appl1 | 212   | 14 | 1.4 | 560 | 2 | US-08-472-802C-2   | Sequence 2, Appl1  |
| C 140 | 14 | 1.4 | 37     | 2 | US-09-027-449-10  | Sequence 10, Appl1 | 213   | 14 | 1.4 | 560 | 3 | US-08-998-416-995  | Sequence 3, Appl1  |
| C 141 | 14 | 1.4 | 37     | 3 | US-08-804-444A-10 | Sequence 10, Appl1 | C 214 | 14 | 1.4 | 567 | 4 | US-09-007-905-6    | Sequence 6, Appl1  |
| C 142 | 14 | 1.4 | 37     | 3 | US-09-026-985-10  | Sequence 10, Appl1 | C 215 | 14 | 1.4 | 599 | 2 | US-08-557-182A-9   | Sequence 9, Appl1  |
| C 143 | 14 | 1.4 | 47     | 1 | US-08-285-440-17  | Sequence 17, Appl1 | C 216 | 14 | 1.4 | 599 | 2 | US-08-705-875A-2   | Sequence 2, Appl1  |
| C 144 | 14 | 1.4 | 47     | 1 | US-08-630-349-9   | Sequence 9, Appl1  | C 217 | 14 | 1.4 | 616 | 4 | US-08-998-416-1055 | Sequence 1055, Ap  |
| C 145 | 14 | 1.4 | 48     | 4 | US-08-916-576B-31 | Sequence 31, Appl1 | C 218 | 14 | 1.4 | 666 | 4 | US-08-998-416-995  | Sequence 995, App  |
| C 146 | 14 | 1.4 | 200    | 1 | US-08-672-569-4   | Sequence 4, Appl1  | 219   | 14 | 1.4 | 703 | 4 | US-08-827-171B-3   | Sequence 3, Appl1  |
| C 147 | 14 | 1.4 | 213    | 4 | US-08-905-223-46  | Sequence 46, Appl1 | C 220 | 14 | 1.4 | 704 | 4 | US-08-998-416-724  | Sequence 724, App  |
| C 148 | 14 | 1.4 | 265    | 3 | US-09-332-934-7   | Sequence 7, Appl1  | C 221 | 14 | 1.4 | 728 | 4 | US-08-998-416-1093 | Sequence 1093, Ap  |
| C 149 | 14 | 1.4 | 270    | 2 | US-08-921-382-16  | Sequence 16, Appl1 | C 222 | 14 | 1.4 | 728 | 4 | US-09-276-531-128  | Sequence 128, App  |
| C 150 | 14 | 1.4 | 282    | 6 | 5218099-8         | Patent No. 5218099 | 223   | 14 | 1.4 | 776 | 2 | US-08-766-605-2    | Sequence 2, Appl1  |
| C 151 | 14 | 1.4 | 297    | 2 | US-08-637-759B-19 | Sequence 19, Appl1 | 224   | 14 | 1.4 | 776 | 2 | US-09-094-212-2    | Sequence 2, Appl1  |
| C 152 | 14 | 1.4 | 297    | 3 | US-08-871-355A-19 | Sequence 19, Appl1 | 225   | 14 | 1.4 | 777 | 3 | US-09-332-934-10   | Sequence 10, Appl1 |
| C 153 | 14 | 1.4 | 298    | 2 | US-08-637-759B-21 | Sequence 21, Appl1 | C 226 | 14 | 1.4 | 810 | 1 | US-08-307-499-51   | Sequence 51, Appl1 |
| C 154 | 14 | 1.4 | 298    | 2 | US-08-871-355A-21 | Sequence 21, Appl1 | C 227 | 14 | 1.4 | 810 | 4 | US-09-299-566-51   | Sequence 51, Appl1 |
| C 155 | 14 | 1.4 | 305    | 4 | US-09-042-575-85  | Sequence 85, Appl1 | C 228 | 14 | 1.4 | 817 | 1 | US-08-672-566-2    | Sequence 2, Appl1  |
| C 156 | 14 | 1.4 | 326    | 4 | US-08-916-576B-16 | Sequence 16, Appl1 | 229   | 14 | 1.4 | 821 | 4 | US-08-990-823-62   | Sequence 62, Appl1 |
| C 157 | 14 | 1.4 | 348    | 4 | US-08-285-440-7   | Sequence 7, Appl1  | 230   | 14 | 1.4 | 937 | 4 | US-08-927-219-48   | Sequence 48, Appl1 |
| C 158 | 14 | 1.4 | 348    | 4 | US-08-630-349-7   | Sequence 7, Appl1  | 231   | 14 | 1.4 | 939 | 1 | US-08-285-440-10   | Sequence 10, Appl1 |
| C 159 | 14 | 1.4 | 357    | 1 | US-08-285-440-8   | Sequence 8, Appl1  | 232   | 14 | 1.4 | 939 | 1 | US-08-630-349-10   | Sequence 10, Appl1 |
| C 160 | 14 | 1.4 | 357    | 1 | US-08-630-349-8   | Sequence 8, Appl1  | C 233 | 14 | 1.4 | 939 | 1 | US-08-420-235B-10  | Sequence 10, Appl1 |
| C 161 | 14 | 1.4 | 369    | 1 | US-08-285-440-9   | Sequence 9, Appl1  | C 234 | 14 | 1.4 | 939 | 3 | US-08-793-62A-12   | Sequence 12, Appl1 |
| C 162 | 14 | 1.4 | 369    | 1 | US-08-630-349-9   | Sequence 9, Appl1  | C 235 | 14 | 1.4 | 939 | 5 | PCr-US95-10194-10  | Sequence 10, Appl1 |
| C 163 | 14 | 1.4 | 399    | 3 | US-08-894-699-18  | Sequence 18, Appl1 | C 236 | 14 | 1.4 | 943 | 3 | US-08-705-875A-1   | Sequence 1, Appl1  |
| C 164 | 14 | 1.4 | 399    | 3 | US-08-894-699-58  | Sequence 58, Appl1 | C 237 | 14 | 1.4 | 943 | 3 | US-08-705-875A-3   | Sequence 3, Appl1  |
| C 165 | 14 | 1.4 | 399    | 3 | US-08-894-699-59  | Sequence 59, Appl1 | C 238 | 14 | 1.4 | 951 | 1 | US-08-671-525B-1   | Sequence 1, Appl1  |
| C 166 | 14 | 1.4 | 399    | 3 | US-08-894-699-61  | Sequence 61, Appl1 | C 239 | 14 | 1.4 | 951 | 1 | US-08-842-045-1    | Sequence 1, Appl1  |
| C 167 | 14 | 1.4 | 421    | 6 | 5196523-22        | Patent No. 5196523 | C 240 | 14 | 1.4 | 951 | 1 | US-08-842-238-1    | Sequence 1, Appl1  |
| C 168 | 14 | 1.4 | 435    | 6 | 5169835-7         | Patent No. 5169835 | C 241 | 14 | 1.4 | 951 | 2 | US-08-629-335B-1   | Sequence 1, Appl1  |
| C 169 | 14 | 1.4 | 444    | 3 | US-08-873-709-1   | Sequence 1, Appl1  | C 242 | 14 | 1.4 | 951 | 3 | US-08-520-550A-44  | Sequence 44, Appl1 |
| C 170 | 14 | 1.4 | 448    | 3 | US-08-520-550A-45 | Sequence 45, Appl1 | C 243 | 14 | 1.4 | 968 | 3 | US-08-705-875A-9   | Sequence 9, Appl1  |
| C 171 | 14 | 1.4 | 483    | 1 | US-08-592-126-118 | Sequence 118, App  | C 244 | 14 | 1.4 | 971 | 1 | US-08-253-155A-11  | Sequence 11, Appl1 |
| C 172 | 14 | 1.4 | 485    | 4 | US-08-905-223-54  | Sequence 54, Appl1 | C 245 | 14 | 1.4 | 981 | 2 | US-08-770-565-1    | Sequence 1, Appl1  |
| C 173 | 14 | 1.4 |        |   |                   |                    | 246   | 14 | 1.4 |     |   |                    |                    |



|       |    |     |      |   |                   |                    |       |    |     |      |   |                    |                    |
|-------|----|-----|------|---|-------------------|--------------------|-------|----|-----|------|---|--------------------|--------------------|
| 247   | 14 | 1.4 | 981  | 2 | US-08-710-249-5   | Sequence 5, Appl1  | 320   | 14 | 1.4 | 1570 | 3 | US-08-468-577B-5   | Sequence 5, Appl1  |
| 248   | 14 | 1.4 | 981  | 2 | US-08-833-377-1   | Sequence 1, Appl1  | c 321 | 14 | 1.4 | 1591 | 2 | US-08-194-981E-3   | Sequence 3, Appl1  |
| 249   | 14 | 1.4 | 981  | 2 | US-08-714-482-2   | Sequence 2, Appl1  | c 322 | 14 | 1.4 | 1599 | 1 | US-08-285-440-11   | Sequence 11, Appl  |
| 250   | 14 | 1.4 | 981  | 3 | US-08-838-545-22  | Sequence 22, Appl  | 323   | 14 | 1.4 | 1599 | 1 | US-08-630-349-11   | Sequence 11, Appl  |
| 251   | 14 | 1.4 | 1083 | 4 | US-09-276-531-30  | Sequence 30, Appl  | c 324 | 14 | 1.4 | 1601 | 3 | US-08-817-188-3    | Sequence 9, Appl1  |
| c 252 | 14 | 1.4 | 1089 | 3 | US-09-195-666A-10 | Sequence 10, Appl  | 325   | 14 | 1.4 | 1602 | 4 | US-09-153-804-9    | Sequence 5, Appl1  |
| c 253 | 14 | 1.4 | 1097 | 2 | US-08-907-492A-1  | Sequence 1, Appl1  | 326   | 14 | 1.4 | 1610 | 4 | US-09-276-531-56   | Sequence 56, Appl  |
| c 254 | 14 | 1.4 | 1110 | 2 | US-08-257-341-4   | Sequence 4, Appl1  | c 327 | 14 | 1.4 | 1633 | 1 | US-07-866-979-5    | Sequence 5, Appl1  |
| c 255 | 14 | 1.4 | 1113 | 2 | US-08-907-492A-3  | Sequence 3, Appl1  | c 328 | 14 | 1.4 | 1633 | 2 | US-08-466-006B-5   | Sequence 5, Appl1  |
| 256   | 14 | 1.4 | 1116 | 1 | US-08-672-569-1   | Sequence 1, Appl1  | c 329 | 14 | 1.4 | 1633 | 2 | US-08-706-281A-5   | Sequence 5, Appl1  |
| 257   | 14 | 1.4 | 1116 | 4 | US-08-776-571-139 | Sequence 139, App  | c 330 | 14 | 1.4 | 1633 | 4 | US-09-201-746-5    | Sequence 5, Appl1  |
| c 258 | 14 | 1.4 | 1170 | 2 | US-08-846-705-1   | Sequence 1, Appl1  | c 331 | 14 | 1.4 | 1640 | 3 | US-09-330-095-2    | Sequence 2, Appl1  |
| c 259 | 14 | 1.4 | 1200 | 3 | US-08-859-167-5   | Sequence 5, Appl1  | 332   | 14 | 1.4 | 1643 | 4 | US-08-827-171B-1   | Sequence 1, Appl1  |
| 260   | 14 | 1.4 | 1200 | 3 | US-09-109-273-5   | Sequence 5, Appl1  | c 333 | 14 | 1.4 | 1669 | 2 | US-08-552-421-1    | Sequence 1, Appl1  |
| 261   | 14 | 1.4 | 1200 | 4 | US-09-276-993-5   | Sequence 5, Appl1  | 334   | 14 | 1.4 | 1677 | 1 | US-08-285-440-12   | Sequence 12, Appl  |
| 262   | 14 | 1.4 | 1203 | 4 | US-08-827-171B-16 | Sequence 16, Appl  | 335   | 14 | 1.4 | 1677 | 1 | US-08-630-349-12   | Sequence 12, Appl  |
| c 263 | 14 | 1.4 | 1205 | 2 | US-09-154-802-2   | Sequence 2, Appl1  | 336   | 14 | 1.4 | 1680 | 2 | US-08-759-581B-3   | Sequence 3, Appl1  |
| c 264 | 14 | 1.4 | 1205 | 3 | US-09-373-029-2   | Sequence 2, Appl1  | c 337 | 14 | 1.4 | 1682 | 4 | US-09-318-443-7    | Sequence 7, Appl1  |
| c 265 | 14 | 1.4 | 1225 | 1 | US-08-286-020-1   | Sequence 1, Appl1  | c 338 | 14 | 1.4 | 1689 | 4 | US-09-311-924-1    | Sequence 3, Appl1  |
| c 266 | 14 | 1.4 | 1225 | 1 | US-08-603-919-1   | Sequence 1, Appl1  | c 339 | 14 | 1.4 | 1695 | 3 | US-09-008-481A-3   | Sequence 3, Appl1  |
| c 267 | 14 | 1.4 | 1258 | 1 | US-08-234-939-6   | Sequence 6, Appl1  | c 340 | 14 | 1.4 | 1695 | 3 | US-09-195-666A-17  | Sequence 17, Appl  |
| c 268 | 14 | 1.4 | 1268 | 1 | US-08-558-865-6   | Sequence 6, Appl1  | c 341 | 14 | 1.4 | 1728 | 1 | US-08-403-866-12   | Sequence 12, Appl  |
| 269   | 14 | 1.4 | 1268 | 1 | US-08-910-973-12  | Sequence 12, Appl  | c 342 | 14 | 1.4 | 1733 | 1 | US-08-470-202-58   | Sequence 58, Appl  |
| c 270 | 14 | 1.4 | 1269 | 5 | PCT-US93-00893-4  | Sequence 4, Appl1  | 343   | 14 | 1.4 | 1733 | 1 | US-08-468-059-58   | Sequence 58, Appl  |
| c 271 | 14 | 1.4 | 1289 | 2 | US-08-344-833-1   | Sequence 1, Appl1  | 344   | 14 | 1.4 | 1733 | 2 | US-08-482-677-9    | Sequence 9, Appl1  |
| c 272 | 14 | 1.4 | 1290 | 6 | 5182195-14        | Patent No. 5182195 | 345   | 14 | 1.4 | 1743 | 3 | US-08-828-922-2    | Sequence 2, Appl1  |
| 273   | 14 | 1.4 | 1317 | 3 | US-08-850-227-1   | Sequence 1, Appl1  | c 346 | 14 | 1.4 | 1820 | 2 | US-09-276-531-26   | Sequence 26, Appl  |
| 274   | 14 | 1.4 | 1317 | 3 | US-08-850-227-5   | Sequence 5, Appl1  | 347   | 14 | 1.4 | 1835 | 4 | US-08-201-118-10   | Sequence 10, Appl  |
| 275   | 14 | 1.4 | 1317 | 3 | US-09-054-985A-1  | Sequence 1, Appl1  | c 348 | 14 | 1.4 | 1852 | 1 | US-08-238-821B-10  | Sequence 10, Appl  |
| c 276 | 14 | 1.4 | 1317 | 3 | US-09-054-985A-5  | Sequence 5, Appl1  | c 349 | 14 | 1.4 | 1852 | 2 | PCT-US95-05744-10  | Sequence 10, Appl  |
| c 277 | 14 | 1.4 | 1353 | 4 | US-09-011-197-3   | Sequence 3, Appl1  | c 350 | 14 | 1.4 | 1852 | 5 | US-08-201-118-4    | Sequence 4, Appl1  |
| c 278 | 14 | 1.4 | 1371 | 1 | US-08-181-271A-43 | Sequence 43, Appl  | c 351 | 14 | 1.4 | 1854 | 2 | US-08-238-821B-4   | Sequence 4, Appl1  |
| c 279 | 14 | 1.4 | 1371 | 1 | US-08-449-315-43  | Sequence 43, Appl  | c 352 | 14 | 1.4 | 1854 | 2 | PCT-US93-05744-4   | Sequence 4, Appl1  |
| c 280 | 14 | 1.4 | 1371 | 1 | US-08-444-803-43  | Sequence 43, Appl  | c 353 | 14 | 1.4 | 1854 | 1 | US-08-234-939-4    | Sequence 4, Appl1  |
| c 281 | 14 | 1.4 | 1371 | 1 | US-08-449-043-43  | Sequence 43, Appl  | c 354 | 14 | 1.4 | 1859 | 1 | US-08-558-865-4    | Sequence 4, Appl1  |
| c 282 | 14 | 1.4 | 1371 | 1 | US-08-456-265A-43 | Sequence 43, Appl  | c 355 | 14 | 1.4 | 1859 | 1 | US-08-455-073A-3   | Sequence 3, Appl1  |
| c 283 | 14 | 1.4 | 1371 | 1 | US-08-455-416-43  | Sequence 43, Appl  | 356   | 14 | 1.4 | 1863 | 2 | US-09-067-351-4    | Sequence 4, Appl1  |
| c 284 | 14 | 1.4 | 1371 | 1 | US-08-455-244-43  | Sequence 43, Appl  | 357   | 14 | 1.4 | 1875 | 2 | US-09-360-490-4    | Sequence 4, Appl1  |
| c 285 | 14 | 1.4 | 1371 | 1 | US-08-454-876-43  | Sequence 43, Appl  | 358   | 14 | 1.4 | 1875 | 4 | US-09-179-966-2    | Sequence 2, Appl1  |
| c 286 | 14 | 1.4 | 1371 | 2 | US-08-457-364-43  | Sequence 43, Appl  | 359   | 14 | 1.4 | 1922 | 3 | US-08-980-994-2    | Sequence 9, Appl1  |
| c 287 | 14 | 1.4 | 1371 | 2 | US-08-456-262-43  | Sequence 43, Appl  | c 360 | 14 | 1.4 | 1922 | 4 | US-09-008-481A-9   | Sequence 9, Appl1  |
| c 288 | 14 | 1.4 | 1371 | 2 | US-08-456-240-43  | Sequence 43, Appl  | c 361 | 14 | 1.4 | 1928 | 3 | US-09-195-666A-15  | Sequence 15, Appl  |
| c 289 | 14 | 1.4 | 1371 | 2 | US-08-455-736-43  | Sequence 43, Appl  | c 362 | 14 | 1.4 | 1928 | 3 | US-08-234-939-3    | Sequence 3, Appl1  |
| c 290 | 14 | 1.4 | 1371 | 2 | US-08-971-217-43  | Sequence 43, Appl  | c 363 | 14 | 1.4 | 1933 | 1 | US-08-558-865-3    | Sequence 3, Appl1  |
| c 291 | 14 | 1.4 | 1380 | 2 | US-08-467-559B-1  | Sequence 1, Appl1  | c 364 | 14 | 1.4 | 1933 | 1 | US-09-313-300-3    | Sequence 3, Appl1  |
| 292   | 14 | 1.4 | 1383 | 3 | US-08-935-263-3   | Sequence 3, Appl1  | c 365 | 14 | 1.4 | 1942 | 4 | 5169835-1          | Patent No. 5169835 |
| c 293 | 14 | 1.4 | 1385 | 1 | US-08-234-939-5   | Sequence 5, Appl1  | 366   | 14 | 1.4 | 1958 | 6 | US-09-311-924-3    | Sequence 3, Appl1  |
| c 294 | 14 | 1.4 | 1385 | 1 | US-08-558-865-5   | Sequence 5, Appl1  | c 367 | 14 | 1.4 | 1973 | 4 | US-09-165-042-2    | Sequence 2, Appl1  |
| c 295 | 14 | 1.4 | 1392 | 3 | US-08-850-227-3   | Sequence 3, Appl1  | 368   | 14 | 1.4 | 1976 | 3 | US-08-483-170-1    | Sequence 1, Appl1  |
| 296   | 14 | 1.4 | 1392 | 3 | US-08-850-227-6   | Sequence 6, Appl1  | 369   | 14 | 1.4 | 2000 | 1 | US-08-867-331-1    | Sequence 1, Appl1  |
| 297   | 14 | 1.4 | 1392 | 3 | US-09-054-985A-3  | Sequence 6, Appl1  | 370   | 14 | 1.4 | 2000 | 3 | US-08-535-276-1    | Sequence 1, Appl1  |
| 298   | 14 | 1.4 | 1392 | 3 | US-08-468-579B-1  | Sequence 1, Appl1  | c 371 | 14 | 1.4 | 2037 | 2 | US-07-973-324A-1   | Sequence 1, Appl1  |
| 299   | 14 | 1.4 | 1397 | 2 | US-08-239-276-1   | Sequence 1, Appl1  | c 372 | 14 | 1.4 | 2042 | 1 | US-08-343-380-1    | Sequence 1, Appl1  |
| 300   | 14 | 1.4 | 1397 | 3 | US-08-468-579B-1  | Sequence 1, Appl1  | c 373 | 14 | 1.4 | 2086 | 1 | US-09-072-435-1    | Sequence 1, Appl1  |
| c 301 | 14 | 1.4 | 1401 | 2 | US-08-812-412-1   | Sequence 1, Appl1  | c 374 | 14 | 1.4 | 2086 | 4 | US-08-796-101-48   | Sequence 48, Appl  |
| c 302 | 14 | 1.4 | 1401 | 4 | US-09-180-371-4   | Sequence 4, Appl1  | c 375 | 14 | 1.4 | 2115 | 4 | 5428012-1          | Patent No. 5428012 |
| c 303 | 14 | 1.4 | 1401 | 4 | US-08-713-828-2   | Sequence 2, Appl1  | c 376 | 14 | 1.4 | 2124 | 6 | US-09-187-124-1    | Sequence 1, Appl1  |
| c 304 | 14 | 1.4 | 1417 | 1 | US-08-919-627-2   | Sequence 2, Appl1  | c 377 | 14 | 1.4 | 2133 | 1 | US-08-285-440-13   | Sequence 13, Appl  |
| c 305 | 14 | 1.4 | 1417 | 2 | US-09-096-245-2   | Sequence 2, Appl1  | c 378 | 14 | 1.4 | 2137 | 1 | US-08-888-077A-18  | Sequence 18, Appl  |
| c 306 | 14 | 1.4 | 1417 | 2 | US-08-875-972-1   | Sequence 1, Appl1  | c 379 | 14 | 1.4 | 2243 | 3 | US-09-084-079-4    | Sequence 4, Appl1  |
| c 307 | 14 | 1.4 | 1417 | 2 | US-08-916-576B-3  | Sequence 3, Appl1  | 380   | 14 | 1.4 | 2215 | 1 | US-08-650-349-14   | Sequence 14, Appl  |
| 308   | 14 | 1.4 | 1437 | 4 | US-08-252-966B-14 | Sequence 14, Appl  | 381   | 14 | 1.4 | 2215 | 1 | US-08-850-227-1    | Sequence 1, Appl1  |
| 309   | 14 | 1.4 | 1437 | 4 | US-09-153-804-7   | Sequence 7, Appl1  | 382   | 14 | 1.4 | 2215 | 1 | US-08-403-866-14   | Sequence 14, Appl  |
| 310   | 14 | 1.4 | 1493 | 4 | US-09-173-581-14  | Sequence 14, Appl  | 383   | 14 | 1.4 | 2223 | 3 | US-08-827-171B-1   | Sequence 1, Appl1  |
| 311   | 14 | 1.4 | 1498 | 3 | US-08-997-362-88  | Sequence 88, Appl  | c 384 | 14 | 1.4 | 2243 | 3 | US-08-875-972-28   | Sequence 28, Appl  |
| 312   | 14 | 1.4 | 1518 | 2 | US-08-997-362-88  | Sequence 88, Appl  | c 385 | 14 | 1.4 | 2285 | 2 | US-08-952-541-136  | Sequence 136, App  |
| 313   | 14 | 1.4 | 1518 | 2 | US-08-873-970-88  | Sequence 88, Appl  | c 386 | 14 | 1.4 | 2285 | 3 | US-09-124-648-136  | Sequence 136, App  |
| 314   | 14 | 1.4 | 1518 | 2 | US-08-873-970-88  | Sequence 88, Appl  | c 387 | 14 | 1.4 | 2285 | 4 | US-09-127-480-136  | Sequence 136, App  |
| 315   | 14 | 1.4 | 1518 | 2 | US-09-095-855-88  | Sequence 88, Appl  | c 388 | 14 | 1.4 | 2296 | 4 | US-08-496-841C-137 | Sequence 137, App  |
| 316   | 14 | 1.4 | 1523 | 4 | US-08-713-636-1   | Sequence 1, Appl1  | c 389 | 14 | 1.4 |      |   |                    |                    |
| c 317 | 14 | 1.4 | 1536 | 4 | US-09-318-443-5   | Sequence 5, Appl1  | c 390 | 14 | 1.4 |      |   |                    |                    |
| 318   | 14 | 1.4 | 1570 | 2 | US-08-239-276-5   | Sequence 5, Appl1  | c 391 | 14 | 1.4 |      |   |                    |                    |
| 319   | 14 | 1.4 | 1570 | 2 | US-08-468-579B-5  | Sequence 5, Appl1  | c 392 | 14 | 1.4 |      |   |                    |                    |

|       |    |      |   |                   |                    |       |    |      |   |                   |                    |
|-------|----|------|---|-------------------|--------------------|-------|----|------|---|-------------------|--------------------|
| 393   | 14 | 2335 | 2 | US-08-300-584-3   | Sequence 3, Appl1  | 466   | 14 | 3627 | 2 | US-09-025-583-7   | Sequence 7, Appl1  |
| 394   | 14 | 2336 | 4 | US-08-476-123-3   | Sequence 3, Appl1  | 467   | 14 | 3630 | 4 | US-09-378-255-5   | Sequence 5, Appl1  |
| 395   | 14 | 2337 | 4 | US-08-796-101-47  | Sequence 47, Appl1 | 468   | 14 | 3630 | 4 | US-09-141-212-1   | Sequence 1, Appl1  |
| C 396 | 14 | 2361 | 4 | US-09-011-197-1   | Sequence 1, Appl1  | 469   | 14 | 3630 | 4 | US-09-141-212-3   | Sequence 3, Appl1  |
| C 397 | 14 | 2409 | 1 | US-08-392-828C-1  | Sequence 1, Appl1  | 470   | 14 | 3630 | 4 | US-09-552-351-3   | Sequence 3, Appl1  |
| C 398 | 14 | 2409 | 3 | US-09-330-945-1   | Sequence 1, Appl1  | 471   | 14 | 3630 | 4 | US-09-251-372-5   | Sequence 5, Appl1  |
| 399   | 14 | 2420 | 1 | US-08-330-123A-3  | Sequence 1, Appl1  | 472   | 14 | 3701 | 4 | US-08-845-258-10  | Sequence 10, Appl1 |
| 400   | 14 | 2425 | 2 | US-08-485-778-1   | Sequence 3, Appl1  | C 473 | 14 | 3701 | 4 | US-08-990-571-10  | Sequence 10, Appl1 |
| 401   | 14 | 2425 | 1 | US-08-520-550A-1  | Sequence 1, Appl1  | 474   | 14 | 3744 | 2 | US-08-348-353-16  | Sequence 16, Appl1 |
| 402   | 14 | 2426 | 3 | US-08-482-115B-3  | Sequence 3, Appl1  | 475   | 14 | 3744 | 2 | US-08-465-965-16  | Sequence 16, Appl1 |
| 403   | 14 | 2426 | 2 | US-08-660-678A-3  | Sequence 3, Appl1  | 476   | 14 | 3744 | 3 | US-08-465-966-16  | Sequence 16, Appl1 |
| 404   | 14 | 2426 | 2 | US-08-472-802C-4  | Sequence 4, Appl1  | 477   | 14 | 3807 | 1 | US-08-357-598-1   | Sequence 16, Appl1 |
| 405   | 14 | 2426 | 2 | US-08-714-482-1   | Sequence 1, Appl1  | 478   | 14 | 3807 | 2 | US-09-003-289-1   | Sequence 1, Appl1  |
| 406   | 14 | 2426 | 3 | US-08-998-443-3   | Sequence 3, Appl1  | 479   | 14 | 4027 | 5 | PCT-US95-16435-1  | Sequence 1, Appl1  |
| C 407 | 14 | 2455 | 3 | US-09-103-429A-1  | Sequence 3, Appl1  | C 480 | 14 | 4027 | 1 | US-08-348-143-3   | Sequence 1, Appl1  |
| C 408 | 14 | 2456 | 3 | US-08-813-150-5   | Sequence 5, Appl1  | C 481 | 14 | 4027 | 1 | US-08-348-143-4   | Sequence 4, Appl1  |
| C 409 | 14 | 2474 | 2 | US-08-666-392A-2  | Sequence 5, Appl1  | C 482 | 14 | 4027 | 1 | US-08-571-788-3   | Sequence 3, Appl1  |
| C 410 | 14 | 2529 | 3 | US-09-051-969A-5  | Sequence 5, Appl1  | C 483 | 14 | 4027 | 1 | US-08-571-788-4   | Sequence 4, Appl1  |
| C 411 | 14 | 2540 | 1 | US-08-446-919A-1  | Sequence 1, Appl1  | 484   | 14 | 4094 | 2 | US-08-841-483-5   | Sequence 5, Appl1  |
| C 412 | 14 | 2550 | 6 | 5258287-23        | Sequence 1, Appl1  | 485   | 14 | 4094 | 2 | US-09-382-912-5   | Sequence 5, Appl1  |
| 413   | 14 | 2609 | 4 | US-09-141-212-7   | Sequence 7, Appl1  | 486   | 14 | 4190 | 4 | US-08-924-345-1   | Sequence 1, Appl1  |
| 414   | 14 | 2625 | 4 | US-09-378-255-1   | Sequence 1, Appl1  | 487   | 14 | 4190 | 3 | US-08-781-891-205 | Sequence 205, App  |
| 415   | 14 | 2669 | 4 | US-09-141-212-9   | Sequence 9, Appl1  | 488   | 14 | 4800 | 4 | US-09-106-638-1   | Sequence 1, Appl1  |
| 416   | 14 | 2693 | 4 | US-09-141-212-5   | Sequence 5, Appl1  | C 489 | 14 | 4849 | 2 | US-08-540-804-13  | Sequence 13, Appl1 |
| 417   | 14 | 2709 | 4 | US-09-251-372-1   | Sequence 1, Appl1  | C 490 | 14 | 4849 | 2 | US-08-218-263-13  | Sequence 13, Appl1 |
| 418   | 14 | 2733 | 4 | US-08-310-271-1   | Sequence 1, Appl1  | C 491 | 14 | 4849 | 2 | US-08-521-872-13  | Sequence 13, Appl1 |
| 419   | 14 | 2733 | 1 | US-09-032-742-9   | Sequence 9, Appl1  | C 492 | 14 | 4849 | 4 | US-08-590-399-13  | Sequence 13, Appl1 |
| 420   | 14 | 2764 | 2 | US-08-465-971B-1  | Sequence 1, Appl1  | C 493 | 14 | 4895 | 3 | US-09-053-866-1   | Sequence 1, Appl1  |
| 421   | 14 | 2816 | 1 | US-08-785-241-1   | Sequence 1, Appl1  | C 494 | 14 | 4906 | 2 | US-09-047-028A-1  | Sequence 1, Appl1  |
| C 422 | 14 | 2821 | 4 | US-09-103-429A-2  | Sequence 2, Appl1  | C 495 | 14 | 4922 | 2 | US-08-330-227-5   | Sequence 5, Appl1  |
| C 423 | 14 | 2887 | 3 | US-09-183-253-1   | Sequence 1, Appl1  | C 496 | 14 | 4922 | 2 | PCT-US93-13663-5  | Sequence 5, Appl1  |
| C 424 | 14 | 2943 | 2 | US-08-788-892-1   | Sequence 1, Appl1  | C 497 | 14 | 5000 | 3 | US-09-104-070-1   | Sequence 1, Appl1  |
| C 425 | 14 | 2982 | 1 | US-08-348-143-2   | Sequence 1, Appl1  | C 498 | 14 | 5135 | 3 | US-08-369-822C-9  | Sequence 9, Appl1  |
| C 426 | 14 | 2982 | 1 | US-08-571-785-2   | Sequence 2, Appl1  | C 499 | 14 | 5135 | 3 | US-08-582-776C-9  | Sequence 9, Appl1  |
| C 427 | 14 | 2984 | 5 | PCT-US93-00893-1  | Sequence 2, Appl1  | C 500 | 14 | 5135 | 3 | US-08-434-831B-9  | Sequence 9, Appl1  |
| C 428 | 14 | 2984 | 5 | PCT-US93-00893-2  | Sequence 2, Appl1  | C 501 | 14 | 5183 | 3 | US-09-039-555B-18 | Sequence 18, Appl1 |
| C 429 | 14 | 2999 | 2 | US-09-014-969-8   | Sequence 8, Appl1  | 502   | 14 | 5275 | 4 | US-08-796-101-49  | Sequence 49, Appl1 |
| C 430 | 14 | 3006 | 4 | US-09-552-351-1   | Sequence 1, Appl1  | C 503 | 14 | 5275 | 4 | US-08-796-101-49  | Sequence 49, Appl1 |
| C 431 | 14 | 3018 | 3 | US-08-942-572-1   | Sequence 1, Appl1  | 504   | 14 | 5470 | 4 | US-08-441-139-12  | Sequence 12, Appl1 |
| 432   | 14 | 3040 | 4 | US-09-378-255-3   | Sequence 3, Appl1  | 505   | 14 | 5470 | 6 | 5196523-5         | Patent No. 5196523 |
| 433   | 14 | 3046 | 1 | US-08-726-725-1   | Sequence 1, Appl1  | C 506 | 14 | 5529 | 3 | US-08-869-696-1   | Sequence 1, Appl1  |
| 434   | 14 | 3057 | 1 | US-08-551-459-3   | Sequence 3, Appl1  | C 507 | 14 | 5559 | 1 | US-08-287-443-3   | Sequence 3, Appl1  |
| 435   | 14 | 3065 | 1 | US-08-156-866-1   | Sequence 1, Appl1  | C 508 | 14 | 5559 | 1 | US-08-459-701-3   | Sequence 3, Appl1  |
| C 436 | 14 | 3133 | 1 | US-08-162-809-1   | Sequence 1, Appl1  | C 509 | 14 | 5559 | 1 | US-08-460-296-3   | Sequence 3, Appl1  |
| C 437 | 14 | 3240 | 4 | US-08-195-152-1   | Sequence 1, Appl1  | C 510 | 14 | 5559 | 1 | US-08-459-174-3   | Sequence 3, Appl1  |
| C 438 | 14 | 3240 | 4 | US-09-262-773-7   | Sequence 7, Appl1  | C 511 | 14 | 5575 | 5 | PCT-US93-06300A-3 | Sequence 3, Appl1  |
| 439   | 14 | 3243 | 2 | US-08-239-276-6   | Sequence 6, Appl1  | C 512 | 14 | 5775 | 5 | US-08-306-691B-15 | Sequence 15, Appl1 |
| 440   | 14 | 3243 | 2 | US-08-468-579B-6  | Sequence 6, Appl1  | C 513 | 14 | 5775 | 5 | PCT-US93-06281-29 | Sequence 29, Appl1 |
| 441   | 14 | 3243 | 4 | US-08-468-577B-6  | Sequence 6, Appl1  | 514   | 14 | 5855 | 1 | US-08-592-218A-20 | Sequence 20, Appl1 |
| C 442 | 14 | 3244 | 4 | US-09-262-773-3   | Sequence 3, Appl1  | 515   | 14 | 5855 | 3 | US-09-149-976-20  | Sequence 20, Appl1 |
| 443   | 14 | 3255 | 2 | US-08-916-917-11  | Sequence 11, Appl1 | 516   | 14 | 6008 | 1 | US-07-789-915A-5  | Sequence 5, Appl1  |
| 444   | 14 | 3255 | 3 | US-09-225-170-11  | Sequence 11, Appl1 | 517   | 14 | 6008 | 1 | US-08-005-002C-5  | Sequence 5, Appl1  |
| C 445 | 14 | 3264 | 4 | US-09-262-773-5   | Sequence 5, Appl1  | 518   | 14 | 6008 | 1 | US-08-487-203A-5  | Sequence 5, Appl1  |
| C 446 | 14 | 3268 | 4 | US-09-262-773-1   | Sequence 1, Appl1  | 519   | 14 | 6306 | 1 | US-08-466-390-3   | Sequence 3, Appl1  |
| C 447 | 14 | 3268 | 2 | US-08-620-694A-1  | Sequence 1, Appl1  | 520   | 14 | 6306 | 1 | US-08-470-950-3   | Sequence 3, Appl1  |
| 448   | 14 | 3288 | 3 | US-09-022-255-1   | Sequence 1, Appl1  | 521   | 14 | 6306 | 1 | US-08-467-781-3   | Sequence 3, Appl1  |
| 449   | 14 | 3288 | 3 | US-09-022-696-1   | Sequence 1, Appl1  | 522   | 14 | 6306 | 1 | US-08-195-487-3   | Sequence 3, Appl1  |
| 450   | 14 | 3288 | 3 | US-08-978-773-1   | Sequence 1, Appl1  | 523   | 14 | 6306 | 2 | US-08-483-924-3   | Sequence 3, Appl1  |
| 451   | 14 | 3288 | 3 | US-09-022-253-1   | Sequence 1, Appl1  | 524   | 14 | 6306 | 5 | PCT-US93-06160-3  | Sequence 3, Appl1  |
| 452   | 14 | 3288 | 3 | US-09-022-260-1   | Sequence 1, Appl1  | 525   | 14 | 6317 | 1 | US-08-920-812-21  | Sequence 21, Appl1 |
| 453   | 14 | 3288 | 4 | US-09-022-259-1   | Sequence 1, Appl1  | 526   | 14 | 6317 | 1 | US-08-920-827-21  | Sequence 21, Appl1 |
| 454   | 14 | 3288 | 4 | US-09-022-257-1   | Sequence 1, Appl1  | 527   | 14 | 6317 | 1 | US-08-921-177-21  | Sequence 21, Appl1 |
| 455   | 14 | 3300 | 2 | US-08-928-692-29  | Sequence 29, Appl1 | 528   | 14 | 6317 | 1 | US-08-362-577C-21 | Sequence 21, Appl1 |
| C 456 | 14 | 3426 | 1 | US-08-234-939-1   | Sequence 1, Appl1  | 529   | 14 | 6317 | 2 | US-08-920-828-21  | Sequence 21, Appl1 |
| C 457 | 14 | 3426 | 1 | US-08-558-865-1   | Sequence 1, Appl1  | 530   | 14 | 6443 | 6 | 5183745-5         | Patent No. 5183745 |
| C 458 | 14 | 3426 | 3 | US-08-654-025-6   | Sequence 5, Appl1  | 531   | 14 | 6443 | 2 | US-09-127-670-5   | Sequence 5, Appl1  |
| C 459 | 14 | 3466 | 1 | US-08-551-429-5   | Sequence 5, Appl1  | 532   | 14 | 7032 | 2 | US-08-149-097D-24 | Sequence 24, Appl1 |
| 460   | 14 | 3546 | 1 | US-08-162-809-9   | Sequence 9, Appl1  | 533   | 14 | 7032 | 3 | US-08-949-386-24  | Sequence 24, Appl1 |
| 461   | 14 | 3591 | 1 | US-08-162-809-13  | Sequence 13, Appl1 | 534   | 14 | 7032 | 3 | US-08-450-562-24  | Sequence 24, Appl1 |
| C 462 | 14 | 3622 | 5 | US-08-306-691B-13 | Sequence 13, Appl1 | 535   | 14 | 7089 | 3 | US-08-949-386-25  | Sequence 25, Appl1 |
| C 463 | 14 | 3622 | 5 | PCT-US93-06251-24 | Sequence 24, Appl1 | 536   | 14 | 7089 | 3 | US-08-450-562-25  | Sequence 25, Appl1 |
| C 464 | 14 | 3627 | 1 | US-08-104-072B-6  | Sequence 6, Appl1  | 537   | 14 | 7881 | 2 | US-08-751-189-1   | Sequence 1, Appl1  |
| 465   | 14 | 3627 | 1 | US-08-351-413-7   | Sequence 7, Appl1  | 538   | 14 | 7881 | 2 | US-09-060-836-1   | Sequence 1, Appl1  |

|       |    |     |        |   |                   |                    |       |    |     |     |   |                     |                    |
|-------|----|-----|--------|---|-------------------|--------------------|-------|----|-----|-----|---|---------------------|--------------------|
| 539   | 14 | 1.4 | 7881   | 4 | US-09-184-445-1   | Sequence 1, Appl   | C 612 | 13 | 1.3 | 17  | 4 | US-07-987-264-46    | Sequence 46, Appl  |
| C 540 | 14 | 1.4 | 8910   | 3 | US-08-369-822C-19 | Sequence 19, Appl  | C 613 | 13 | 1.3 | 19  | 1 | US-08-410-540-5     | Sequence 5, Appl   |
| C 541 | 14 | 1.4 | 8910   | 3 | US-08-779-764A-1  | Sequence 1, Appl   | C 614 | 13 | 1.3 | 20  | 1 | US-08-045-806-15    | Sequence 15, Appl  |
| C 542 | 14 | 1.4 | 8910   | 3 | US-08-582-776C-19 | Sequence 19, Appl  | C 615 | 13 | 1.3 | 20  | 1 | US-08-366-051B-15   | Sequence 15, Appl  |
| C 543 | 14 | 1.4 | 8910   | 3 | US-08-434-831B-19 | Sequence 19, Appl  | C 616 | 13 | 1.3 | 21  | 1 | US-08-372-892-5     | Sequence 5, Appl   |
| C 544 | 14 | 1.4 | 9045   | 3 | US-09-121-321-1   | Sequence 1, Appl   | C 617 | 13 | 1.3 | 21  | 1 | US-08-357-565-31    | Sequence 31, Appl  |
| C 545 | 14 | 1.4 | 9045   | 3 | US-08-933-803A-1  | Sequence 1, Appl   | C 618 | 13 | 1.3 | 21  | 1 | US-08-252-626A-4    | Sequence 4, Appl   |
| C 546 | 14 | 1.4 | 9370   | 4 | US-08-320-559-27  | Sequence 27, Appl  | C 619 | 13 | 1.3 | 21  | 1 | US-08-454-720A-31   | Sequence 31, Appl  |
| 547   | 14 | 1.4 | 9370   | 3 | US-08-545-860D-27 | Sequence 27, Appl  | C 620 | 13 | 1.3 | 21  | 3 | US-08-840-316-48    | Sequence 48, Appl  |
| 548   | 14 | 1.4 | 9370   | 5 | PCT-US94-04496-27 | Sequence 27, Appl  | C 621 | 13 | 1.3 | 21  | 3 | US-08-987-326-21    | Sequence 21, Appl  |
| 549   | 14 | 1.4 | 9391   | 5 | US-08-320-559-25  | Sequence 25, Appl  | C 622 | 13 | 1.3 | 21  | 3 | US-08-353-901-6     | Sequence 6, Appl   |
| 550   | 14 | 1.4 | 9391   | 5 | US-08-545-860D-25 | Sequence 25, Appl  | C 623 | 13 | 1.3 | 21  | 3 | US-09-436-605-17    | Sequence 17, Appl  |
| 551   | 14 | 1.4 | 9391   | 5 | PCT-US94-04496-25 | Sequence 25, Appl  | C 624 | 13 | 1.3 | 21  | 4 | US-09-195-817-6     | Sequence 6, Appl   |
| C 552 | 14 | 1.4 | 9515   | 1 | US-08-920-812-13  | Sequence 13, Appl  | C 625 | 13 | 1.3 | 21  | 4 | US-08-809-523-48    | Sequence 48, Appl  |
| C 553 | 14 | 1.4 | 9515   | 1 | US-08-920-827-13  | Sequence 13, Appl  | C 626 | 13 | 1.3 | 21  | 5 | PCT-US93-08849A-48  | Sequence 48, Appl  |
| C 554 | 14 | 1.4 | 9515   | 1 | US-08-921-177-13  | Sequence 13, Appl  | C 627 | 13 | 1.3 | 21  | 5 | PCT-US93-08849-48   | Sequence 48, Appl  |
| C 555 | 14 | 1.4 | 9515   | 2 | US-08-362-577C-13 | Sequence 13, Appl  | C 628 | 13 | 1.3 | 21  | 6 | 5219727-66          | Patent No. 5219727 |
| C 556 | 14 | 1.4 | 9515   | 2 | US-08-920-828-13  | Sequence 13, Appl  | C 629 | 13 | 1.3 | 22  | 4 | US-08-928-465-3     | Sequence 3, Appl   |
| 557   | 14 | 1.4 | 9775   | 4 | US-08-977-171-1   | Sequence 1, Appl   | C 630 | 13 | 1.3 | 23  | 3 | US-08-911-894-89    | Sequence 89, Appl  |
| 558   | 14 | 1.4 | 9934   | 4 | US-08-977-171-2   | Sequence 2, Appl   | C 631 | 13 | 1.3 | 23  | 3 | US-09-230-222-13    | Sequence 13, Appl  |
| 559   | 14 | 1.4 | 10014  | 4 | US-08-927-219-130 | Sequence 130, App  | C 632 | 13 | 1.3 | 27  | 1 | US-08-221-817-6     | Sequence 6, Appl   |
| 560   | 14 | 1.4 | 10095  | 3 | US-08-822-586-45  | Sequence 45, Appl  | C 633 | 13 | 1.3 | 27  | 1 | US-08-454-439-6     | Sequence 6, Appl   |
| C 561 | 14 | 1.4 | 10095  | 3 | US-08-822-586-45  | Sequence 45, Appl  | C 634 | 13 | 1.3 | 27  | 2 | US-08-859-998-245   | Sequence 245, App  |
| C 562 | 14 | 1.4 | 10627  | 1 | US-08-060-925A-12 | Sequence 12, Appl  | C 635 | 13 | 1.3 | 27  | 5 | PCT-US94-10487-6    | Sequence 6, Appl   |
| C 563 | 14 | 1.4 | 10763  | 1 | US-08-761-258-1   | Sequence 1, Appl   | C 636 | 13 | 1.3 | 28  | 2 | US-08-484-575A-2    | Sequence 2, Appl   |
| C 564 | 14 | 1.4 | 10763  | 2 | US-08-977-306-1   | Sequence 1, Appl   | C 637 | 13 | 1.3 | 28  | 3 | US-08-477-459-2     | Sequence 2, Appl   |
| 565   | 14 | 1.4 | 10862  | 2 | US-09-056-411-1   | Sequence 1, Appl   | C 638 | 13 | 1.3 | 28  | 3 | US-08-479-869-2     | Sequence 2, Appl   |
| 566   | 14 | 1.4 | 10898  | 2 | US-08-481-658B-5  | Sequence 5, Appl   | C 639 | 13 | 1.3 | 28  | 3 | US-08-486-414-2     | Sequence 2, Appl   |
| 567   | 14 | 1.4 | 10898  | 2 | US-08-477-504A-5  | Sequence 5, Appl   | C 640 | 13 | 1.3 | 28  | 5 | PCT-US94-01826A-2   | Sequence 2, Appl   |
| 568   | 14 | 1.4 | 10898  | 2 | US-08-486-756A-5  | Sequence 5, Appl   | C 641 | 13 | 1.3 | 28  | 5 | PCT-US94-02252A-2   | Sequence 2, Appl   |
| 569   | 14 | 1.4 | 10898  | 2 | US-08-485-862B-5  | Sequence 5, Appl   | C 642 | 13 | 1.3 | 30  | 2 | US-08-859-998-186   | Sequence 186, App  |
| 570   | 14 | 1.4 | 10898  | 3 | US-08-787-739-5   | Sequence 5, Appl   | C 643 | 13 | 1.3 | 38  | 1 | US-08-151-391A-7    | Sequence 7, Appl   |
| 571   | 14 | 1.4 | 10898  | 3 | US-08-487-863A-5  | Sequence 5, Appl   | C 644 | 13 | 1.3 | 39  | 1 | US-08-453-588-5     | Sequence 5, Appl   |
| 572   | 14 | 1.4 | 10898  | 3 | US-08-485-863A-5  | Sequence 5, Appl   | C 645 | 13 | 1.3 | 39  | 1 | US-08-644-664B-4    | Sequence 4, Appl   |
| 573   | 14 | 1.4 | 10898  | 3 | US-08-485-863A-5  | Sequence 5, Appl   | C 646 | 13 | 1.3 | 39  | 1 | US-08-644-664B-5    | Sequence 5, Appl   |
| C 574 | 14 | 1.4 | 11225  | 6 | 5182210-9         | Patent No. 5182210 | C 647 | 13 | 1.3 | 39  | 2 | US-08-761-277A-5    | Sequence 4, Appl   |
| C 575 | 14 | 1.4 | 11284  | 3 | US-08-978-741-5   | Sequence 5, Appl   | C 648 | 13 | 1.3 | 39  | 2 | US-08-521-079-5     | Sequence 5, Appl   |
| C 576 | 14 | 1.4 | 12145  | 3 | US-08-968-563-19  | Sequence 19, Appl  | C 649 | 13 | 1.3 | 39  | 3 | US-07-987-264-41    | Sequence 41, Appl  |
| C 577 | 14 | 1.4 | 12145  | 3 | US-08-969-683A-19 | Sequence 19, Appl  | C 650 | 13 | 1.3 | 39  | 4 | US-08-453-588-29    | Sequence 29, Appl  |
| C 578 | 14 | 1.4 | 12720  | 1 | US-08-403-886-11  | Sequence 11, Appl  | C 651 | 13 | 1.3 | 45  | 1 | US-08-475-228A-216  | Sequence 216, App  |
| C 579 | 14 | 1.4 | 13417  | 2 | US-08-637-759B-37 | Sequence 37, Appl  | C 652 | 13 | 1.3 | 45  | 3 | US-08-724-814-20    | Sequence 20, Appl  |
| C 580 | 14 | 1.4 | 13417  | 3 | US-08-871-355A-37 | Sequence 37, Appl  | C 653 | 13 | 1.3 | 45  | 3 | US-08-521-079-29    | Sequence 29, Appl  |
| C 581 | 14 | 1.4 | 14176  | 1 | US-08-307-499-1   | Sequence 1, Appl   | C 654 | 13 | 1.3 | 48  | 1 | US-08-171-389-216   | Sequence 216, App  |
| C 582 | 14 | 1.4 | 14176  | 1 | US-08-307-499-14  | Sequence 14, Appl  | C 655 | 13 | 1.3 | 48  | 1 | US-08-171-389-216   | Sequence 216, App  |
| C 583 | 14 | 1.4 | 14176  | 4 | US-09-299-268-1   | Sequence 1, Appl   | C 656 | 13 | 1.3 | 48  | 1 | US-08-123-936-216   | Sequence 216, App  |
| C 584 | 14 | 1.4 | 14176  | 4 | US-09-299-268-14  | Sequence 14, Appl  | C 657 | 13 | 1.3 | 48  | 1 | US-08-123-936-216   | Sequence 216, App  |
| C 585 | 14 | 1.4 | 20137  | 4 | US-09-262-773-206 | Sequence 206, App  | C 658 | 13 | 1.3 | 48  | 2 | US-08-475-228A-216  | Sequence 216, App  |
| C 586 | 14 | 1.4 | 20138  | 4 | US-09-262-773-9   | Sequence 9, Appl   | C 659 | 13 | 1.3 | 48  | 2 | US-08-475-228A-216  | Sequence 216, App  |
| C 587 | 14 | 1.4 | 20303  | 1 | US-08-370-975B-6  | Sequence 6, Appl   | C 660 | 13 | 1.3 | 48  | 3 | US-08-482-080A-216  | Sequence 216, App  |
| C 588 | 14 | 1.4 | 20710  | 1 | US-08-420-235B-1  | Sequence 1, Appl   | C 661 | 13 | 1.3 | 48  | 3 | US-08-482-080A-216  | Sequence 216, App  |
| C 589 | 14 | 1.4 | 20710  | 3 | US-08-793-624-1   | Sequence 1, Appl   | C 662 | 13 | 1.3 | 48  | 3 | PCT-US93-12388-216  | Sequence 216, App  |
| C 590 | 14 | 1.4 | 20710  | 5 | PCT-US95-10194-1  | Sequence 1, Appl   | C 663 | 13 | 1.3 | 48  | 5 | PCT-US93-12388-216  | Sequence 216, App  |
| C 591 | 14 | 1.4 | 23071  | 4 | US-09-262-773-210 | Sequence 210, App  | C 664 | 13 | 1.3 | 51  | 1 | US-08-126-564A-37   | Sequence 37, Appl  |
| C 592 | 14 | 1.4 | 26700  | 1 | US-08-472-217-1   | Sequence 1, Appl   | C 665 | 13 | 1.3 | 51  | 1 | US-08-453-588-13    | Sequence 13, Appl  |
| C 593 | 14 | 1.4 | 26700  | 2 | US-08-488-199-5   | Sequence 5, Appl   | C 666 | 13 | 1.3 | 51  | 2 | US-08-850-049-37    | Sequence 37, Appl  |
| C 594 | 14 | 1.4 | 26700  | 3 | US-08-760-534A-1  | Sequence 1, Appl   | C 667 | 13 | 1.3 | 51  | 2 | US-08-050-478-37    | Sequence 37, Appl  |
| C 595 | 14 | 1.4 | 26764  | 1 | US-08-370-975B-1  | Sequence 1, Appl   | C 668 | 13 | 1.3 | 51  | 3 | US-08-521-079-13    | Sequence 13, Appl  |
| C 596 | 14 | 1.4 | 28804  | 2 | US-08-592-874-1   | Sequence 2, Appl   | C 669 | 13 | 1.3 | 51  | 5 | PCT-US94-09143-37   | Sequence 37, Appl  |
| C 597 | 14 | 1.4 | 28804  | 2 | US-09-096-942-2   | Sequence 2, Appl   | C 670 | 13 | 1.3 | 54  | 1 | US-08-373-124A-2244 | Sequence 2244, App |
| C 598 | 14 | 1.4 | 28804  | 3 | US-09-096-867-2   | Sequence 2, Appl   | C 671 | 13 | 1.3 | 54  | 1 | US-08-435-628-2244  | Sequence 2244, App |
| C 599 | 14 | 1.4 | 32207  | 2 | US-08-770-379-20  | Sequence 20, Appl  | C 672 | 13 | 1.3 | 60  | 3 | US-08-911-894-53    | Sequence 53, Appl  |
| C 600 | 14 | 1.4 | 32207  | 4 | US-08-757-669A-20 | Sequence 20, Appl  | C 673 | 13 | 1.3 | 69  | 2 | US-08-180-524-4     | Sequence 4, Appl   |
| C 601 | 14 | 1.4 | 35100  | 2 | US-08-770-379-18  | Sequence 18, Appl  | C 674 | 13 | 1.3 | 69  | 2 | US-08-975-166-4     | Sequence 4, Appl   |
| C 602 | 14 | 1.4 | 35100  | 2 | US-08-770-379-19  | Sequence 19, Appl  | C 675 | 13 | 1.3 | 75  | 2 | US-09-073-323-1     | Sequence 1, Appl   |
| C 603 | 14 | 1.4 | 35100  | 4 | US-08-757-669A-18 | Sequence 18, Appl  | C 676 | 13 | 1.3 | 80  | 2 | US-07-733-095B-10   | Sequence 10, Appl  |
| C 604 | 14 | 1.4 | 35100  | 4 | US-08-757-669A-19 | Sequence 19, Appl  | C 677 | 13 | 1.3 | 87  | 2 | US-09-073-323-5     | Sequence 5, Appl   |
| C 605 | 14 | 1.4 | 49272  | 1 | US-08-616-770A-1  | Sequence 1, Appl   | C 678 | 13 | 1.3 | 89  | 2 | US-09-073-323-3     | Sequence 3, Appl   |
| C 606 | 14 | 1.4 | 80161  | 3 | US-09-036-987A-1  | Sequence 1, Appl   | C 679 | 13 | 1.3 | 107 | 1 | US-08-248-474-92    | Sequence 92, Appl  |
| C 607 | 14 | 1.4 | 87350  | 3 | US-08-781-891-79  | Sequence 79, Appl  | C 680 | 13 | 1.3 | 107 | 3 | US-08-736-849-92    | Sequence 92, Appl  |
| C 608 | 14 | 1.4 | 246240 | 2 | US-08-724-394A-20 | Sequence 20, Appl  | C 681 | 13 | 1.3 | 110 | 1 | US-07-666-648-11    | Sequence 11, Appl  |
| C 609 | 14 | 1.4 | 246240 | 2 | US-08-724-394A-21 | Sequence 21, Appl  | C 682 | 13 | 1.3 | 110 | 2 | US-08-429-998-11    | Sequence 11, Appl  |
| C 610 | 14 | 1.4 | 246240 | 2 | US-08-724-394A-22 | Sequence 22, Appl  | C 683 | 13 | 1.3 | 110 | 2 | US-08-431-333-11    | Sequence 11, Appl  |
| C 611 | 13 | 1.3 | 14     | 3 | US-08-882-046-81  | Sequence 81, Appl  | C 684 | 13 | 1.3 | 110 | 5 | PCT-US91-02321-11   | Sequence 11, Appl  |

|       |    |     |     |   |                   |                    |     |    |     |     |   |                    |                    |
|-------|----|-----|-----|---|-------------------|--------------------|-----|----|-----|-----|---|--------------------|--------------------|
| 685   | 13 | 1.3 | 120 | 1 | US-07-666-719-21  | Sequence 21, Appl  | 758 | 13 | 1.3 | 355 | 1 | US-08-398-627-5    | Sequence 5, Appl1  |
| 686   | 13 | 1.3 | 120 | 6 | 5191064-1         | Patent No. 5191064 | 759 | 13 | 1.3 | 355 | 1 | US-08-406-858-5    | Sequence 7, Appl1  |
| C 687 | 13 | 1.3 | 134 | 1 | US-07-998-003A-78 | Sequence 78, Appl  | 760 | 13 | 1.3 | 355 | 1 | US-08-476-519-7    | Sequence 5, Appl1  |
| C 688 | 13 | 1.3 | 134 | 1 | US-08-453-274B-78 | Sequence 78, Appl  | 761 | 13 | 1.3 | 355 | 5 | PCT-US91-04036-5   | Sequence 5, Appl1  |
| C 689 | 13 | 1.3 | 134 | 1 | US-08-453-695A-78 | Sequence 78, Appl  | 762 | 13 | 1.3 | 355 | 5 | PCT-US94-05275-5   | Sequence 5, Appl1  |
| C 690 | 13 | 1.3 | 134 | 1 | US-08-268-161A-78 | Sequence 78, Appl  | 763 | 13 | 1.3 | 355 | 5 | PCT-US95-09323-7   | Sequence 7, Appl1  |
| C 691 | 13 | 1.3 | 134 | 2 | US-08-453-702A-78 | Sequence 78, Appl  | 764 | 13 | 1.3 | 357 | 2 | US-08-318-157B-1   | Sequence 1, Appl1  |
| C 692 | 13 | 1.3 | 134 | 5 | PCT-US93-12588-78 | Sequence 78, Appl  | 765 | 13 | 1.3 | 357 | 6 | 5405942-9          | Sequence 1, Appl1  |
| C 693 | 13 | 1.3 | 134 | 5 | PCT-US95-08071-78 | Sequence 78, Appl  | 766 | 13 | 1.3 | 357 | 6 | 5405942-13         | Patent No. 5405942 |
| C 694 | 13 | 1.3 | 142 | 1 | US-08-488-144-29  | Sequence 29, Appl  | 767 | 13 | 1.3 | 360 | 3 | US-08-680-726A-61  | Sequence 61, Appl  |
| C 695 | 13 | 1.3 | 146 | 2 | US-08-180-524-3   | Sequence 3, Appl1  | 768 | 13 | 1.3 | 360 | 3 | US-09-092-409-61   | Sequence 61, Appl  |
| C 696 | 13 | 1.3 | 155 | 2 | US-08-975-166-3   | Sequence 3, Appl1  | 769 | 13 | 1.3 | 363 | 5 | US-08-599-252-100  | Sequence 100, App  |
| C 697 | 13 | 1.3 | 155 | 2 | US-07-733-095B-12 | Sequence 12, Appl1 | 770 | 13 | 1.3 | 363 | 5 | PCT-US96-06352-100 | Sequence 100, App  |
| C 698 | 13 | 1.3 | 171 | 6 | 5466585-4         | Patent No. 5466585 | 771 | 13 | 1.3 | 364 | 5 | PCT-US96-06583-100 | Sequence 100, App  |
| C 699 | 13 | 1.3 | 179 | 6 | US-08-621-018B-36 | Sequence 36, Appl  | 772 | 13 | 1.3 | 368 | 2 | US-08-905-223-162  | Sequence 162, App  |
| C 700 | 13 | 1.3 | 180 | 6 | 5437990-1         | Patent No. 5437990 | 773 | 13 | 1.3 | 368 | 2 | US-08-443-530B-21  | Sequence 21, Appl  |
| C 701 | 13 | 1.3 | 186 | 4 | US-08-905-223-43  | Sequence 43, Appl  | 774 | 13 | 1.3 | 371 | 1 | US-08-335-573-5    | Sequence 5, Appl1  |
| C 702 | 13 | 1.3 | 190 | 4 | US-07-987-264-40  | Sequence 40, Appl  | 775 | 13 | 1.3 | 371 | 2 | US-08-822-841-6    | Sequence 6, Appl1  |
| C 703 | 13 | 1.3 | 196 | 5 | PCT-US93-06251-15 | Sequence 15, Appl  | 776 | 13 | 1.3 | 399 | 4 | US-09-369-494-12   | Sequence 12, Appl  |
| C 704 | 13 | 1.3 | 198 | 2 | US-08-588-258B-16 | Sequence 16, Appl  | 777 | 13 | 1.3 | 403 | 4 | US-09-060-756-391  | Sequence 391, App  |
| C 705 | 13 | 1.3 | 198 | 3 | US-08-460-505-16  | Sequence 16, Appl  | 778 | 13 | 1.3 | 417 | 4 | US-09-136-315-1    | Sequence 1, Appl1  |
| C 706 | 13 | 1.3 | 198 | 5 | PCT-US96-08295-16 | Sequence 16, Appl  | 779 | 13 | 1.3 | 417 | 4 | US-09-136-315-5    | Sequence 5, Appl1  |
| C 707 | 13 | 1.3 | 207 | 1 | US-08-435-684A-40 | Sequence 40, Appl  | 780 | 13 | 1.3 | 420 | 1 | US-08-149-099C-9   | Sequence 9, Appl1  |
| C 708 | 13 | 1.3 | 207 | 2 | US-08-934-877A-40 | Sequence 40, Appl  | 781 | 13 | 1.3 | 420 | 1 | US-08-476-275-5    | Sequence 5, Appl1  |
| C 709 | 13 | 1.3 | 207 | 6 | US-08-871-678C-40 | Sequence 40, Appl  | 782 | 13 | 1.3 | 420 | 2 | US-08-478-967A-9   | Sequence 9, Appl1  |
| C 710 | 13 | 1.3 | 210 | 6 | 5405942-7         | Sequence 40, Appl  | 783 | 13 | 1.3 | 420 | 4 | US-09-120-663-3    | Sequence 3, Appl1  |
| C 711 | 13 | 1.3 | 210 | 6 | 5405942-11        | Patent No. 5405942 | 784 | 13 | 1.3 | 420 | 4 | US-09-120-663-3    | Sequence 3, Appl1  |
| C 712 | 13 | 1.3 | 210 | 6 | 5405942-15        | Patent No. 5405942 | 785 | 13 | 1.3 | 428 | 2 | US-09-036-089-5    | Sequence 5, Appl1  |
| C 713 | 13 | 1.3 | 211 | 6 | US-08-905-223-213 | Sequence 213, App  | 786 | 13 | 1.3 | 429 | 4 | US-08-905-223-61   | Sequence 61, Appl  |
| C 714 | 13 | 1.3 | 227 | 3 | US-08-621-018B-38 | Sequence 38, Appl  | 787 | 13 | 1.3 | 442 | 4 | US-09-060-756-293  | Sequence 293, App  |
| C 715 | 13 | 1.3 | 228 | 3 | US-08-621-018B-40 | Sequence 40, Appl  | 788 | 13 | 1.3 | 450 | 1 | US-08-602-010A-20  | Sequence 20, Appl  |
| C 716 | 13 | 1.3 | 236 | 3 | US-08-621-018B-34 | Sequence 34, Appl  | 789 | 13 | 1.3 | 450 | 1 | US-08-680-726A-20  | Sequence 20, Appl  |
| C 717 | 13 | 1.3 | 239 | 1 | US-08-337-268A-44 | Sequence 44, Appl  | 790 | 13 | 1.3 | 450 | 3 | US-09-092-409-20   | Sequence 20, Appl  |
| C 718 | 13 | 1.3 | 239 | 1 | US-08-484-570A-44 | Sequence 44, Appl  | 791 | 13 | 1.3 | 456 | 1 | US-08-450-945-70   | Sequence 70, Appl  |
| C 719 | 13 | 1.3 | 240 | 1 | US-08-700-575-13  | Sequence 44, Appl  | 792 | 13 | 1.3 | 456 | 4 | US-08-976-161-70   | Sequence 70, Appl  |
| C 720 | 13 | 1.3 | 243 | 2 | US-08-747-121-6   | Sequence 6, Appl1  | 793 | 13 | 1.3 | 457 | 4 | US-09-060-756-591  | Sequence 591, App  |
| C 721 | 13 | 1.3 | 243 | 4 | US-09-060-756-177 | Sequence 177, App  | 794 | 13 | 1.3 | 461 | 3 | US-09-087-232A-11  | Sequence 11, Appl  |
| C 722 | 13 | 1.3 | 249 | 1 | US-08-729-447-19  | Sequence 19, Appl  | 795 | 13 | 1.3 | 467 | 4 | US-09-060-756-662  | Sequence 662, App  |
| C 723 | 13 | 1.3 | 253 | 6 | 5466585-5         | Patent No. 5466585 | 796 | 13 | 1.3 | 480 | 1 | US-08-375-186-2    | Sequence 2, Appl1  |
| C 724 | 13 | 1.3 | 254 | 4 | US-09-318-978-6   | Sequence 6, Appl1  | 797 | 13 | 1.3 | 480 | 1 | US-08-457-797A-6   | Sequence 6, Appl1  |
| C 725 | 13 | 1.3 | 259 | 2 | US-09-036-089-3   | Sequence 3, Appl1  | 798 | 13 | 1.3 | 480 | 1 | US-08-812-025-6    | Sequence 6, Appl1  |
| C 726 | 13 | 1.3 | 285 | 1 | US-08-202-389-3   | Sequence 3, Appl1  | 799 | 13 | 1.3 | 480 | 3 | US-08-814-052-14   | Sequence 14, Appl  |
| C 727 | 13 | 1.3 | 285 | 4 | US-09-060-756-135 | Sequence 135, App  | 800 | 13 | 1.3 | 480 | 3 | US-08-814-052-15   | Sequence 15, Appl  |
| C 728 | 13 | 1.3 | 286 | 1 | US-07-977-630-24  | Sequence 24, Appl  | 801 | 13 | 1.3 | 480 | 3 | US-08-814-052-16   | Sequence 16, Appl  |
| C 729 | 13 | 1.3 | 288 | 3 | US-08-621-018B-35 | Sequence 35, Appl  | 802 | 13 | 1.3 | 511 | 3 | US-09-188-930-216  | Sequence 16, App   |
| C 730 | 13 | 1.3 | 292 | 2 | US-08-245-511-15  | Sequence 15, Appl  | 803 | 13 | 1.3 | 512 | 1 | US-08-722-001-10   | Sequence 10, Appl  |
| C 731 | 13 | 1.3 | 292 | 2 | US-08-600-993A-15 | Sequence 15, Appl  | 804 | 13 | 1.3 | 531 | 2 | US-08-631-097-2    | Sequence 2, Appl1  |
| C 732 | 13 | 1.3 | 297 | 2 | US-08-468-819-89  | Sequence 89, Appl  | 805 | 13 | 1.3 | 531 | 2 | US-08-810-712-2    | Sequence 2, Appl1  |
| C 733 | 13 | 1.3 | 298 | 2 | US-09-036-089-4   | Sequence 4, Appl1  | 806 | 13 | 1.3 | 545 | 4 | US-08-446-935-5    | Sequence 5, Appl1  |
| C 734 | 13 | 1.3 | 327 | 3 | US-08-959-212-9   | Sequence 9, Appl1  | 807 | 13 | 1.3 | 554 | 4 | US-08-975-762-3    | Sequence 3, Appl1  |
| C 735 | 13 | 1.3 | 327 | 4 | US-09-240-274-127 | Sequence 127, App  | 808 | 13 | 1.3 | 554 | 4 | US-08-821-324-3    | Sequence 3, Appl1  |
| C 736 | 13 | 1.3 | 329 | 1 | US-08-148-910-2   | Sequence 2, Appl1  | 809 | 13 | 1.3 | 559 | 4 | US-08-975-762-4    | Sequence 4, Appl1  |
| C 737 | 13 | 1.3 | 329 | 1 | US-08-148-910-2   | Sequence 2, Appl1  | 810 | 13 | 1.3 | 559 | 4 | US-08-821-324-4    | Sequence 4, Appl1  |
| C 738 | 13 | 1.3 | 329 | 1 | US-08-148-910-13  | Sequence 13, Appl  | 811 | 13 | 1.3 | 561 | 2 | US-08-655-821-1    | Sequence 1, Appl1  |
| C 739 | 13 | 1.3 | 329 | 1 | US-08-148-910-13  | Sequence 13, Appl  | 812 | 13 | 1.3 | 568 | 3 | US-09-188-930-253  | Sequence 253, App  |
| C 740 | 13 | 1.3 | 329 | 1 | US-08-448-937A-2  | Sequence 2, Appl1  | 813 | 13 | 1.3 | 578 | 4 | US-08-991-789A-222 | Sequence 222, App  |
| C 741 | 13 | 1.3 | 329 | 1 | US-08-448-937A-2  | Sequence 2, Appl1  | 814 | 13 | 1.3 | 579 | 1 | US-08-602-010A-17  | Sequence 17, Appl  |
| C 742 | 13 | 1.3 | 329 | 1 | US-08-448-937A-13 | Sequence 13, Appl  | 815 | 13 | 1.3 | 579 | 1 | US-08-602-010A-19  | Sequence 19, Appl  |
| C 743 | 13 | 1.3 | 329 | 1 | US-08-448-937A-13 | Sequence 13, Appl  | 816 | 13 | 1.3 | 579 | 1 | US-08-680-726A-17  | Sequence 17, Appl  |
| C 744 | 13 | 1.3 | 329 | 1 | US-08-358-171-20  | Sequence 20, Appl  | 817 | 13 | 1.3 | 579 | 1 | US-08-680-726A-19  | Sequence 19, Appl  |
| C 745 | 13 | 1.3 | 329 | 3 | US-09-090-947-20  | Sequence 20, Appl  | 818 | 13 | 1.3 | 579 | 3 | US-09-092-409-17   | Sequence 17, Appl  |
| C 746 | 13 | 1.3 | 332 | 2 | US-08-469-412A-8  | Sequence 8, Appl1  | 819 | 13 | 1.3 | 584 | 4 | US-09-092-409-19   | Sequence 19, Appl  |
| C 747 | 13 | 1.3 | 332 | 4 | US-09-021-715-8   | Sequence 8, Appl1  | 820 | 13 | 1.3 | 584 | 4 | US-09-347-819-3    | Sequence 3, Appl1  |
| C 748 | 13 | 1.3 | 335 | 4 | US-09-060-756-715 | Sequence 715, App  | 821 | 13 | 1.3 | 585 | 3 | US-08-938-548B-5   | Sequence 5, Appl1  |
| C 749 | 13 | 1.3 | 336 | 4 | US-09-060-756-174 | Sequence 174, App  | 822 | 13 | 1.3 | 588 | 1 | US-08-808-303-1    | Sequence 1, Appl1  |
| C 750 | 13 | 1.3 | 342 | 5 | US-08-475-844-15  | Sequence 15, Appl  | 823 | 13 | 1.3 | 609 | 1 | US-08-808-303-2    | Sequence 2, Appl1  |
| C 751 | 13 | 1.3 | 342 | 5 | PCT-US95-08429-15 | Sequence 15, Appl  | 824 | 13 | 1.3 | 609 | 1 | US-08-087-772A-6   | Sequence 6, Appl1  |
| C 752 | 13 | 1.3 | 347 | 2 | US-08-546-117-7   | Sequence 7, Appl1  | 825 | 13 | 1.3 | 620 | 2 | US-08-522-841-4    | Sequence 4, Appl1  |
| C 753 | 13 | 1.3 | 348 | 2 | US-08-483-749A-17 | Sequence 17, Appl1 | 826 | 13 | 1.3 | 621 | 2 | US-08-522-841-4    | Sequence 4, Appl1  |
| C 754 | 13 | 1.3 | 350 | 2 | US-09-036-089-1   | Sequence 1, Appl1  | 827 | 13 | 1.3 | 622 | 6 | 5405942-2          | Patent No. 5405942 |
| C 755 | 13 | 1.3 | 350 | 2 | US-09-036-089-2   | Sequence 2, Appl1  | 828 | 13 | 1.3 | 627 | 1 | US-08-284-784-26   | Sequence 26, Appl  |
| C 756 | 13 | 1.3 | 351 | 3 | US-08-621-018B-3  | Sequence 3, Appl1  | 829 | 13 | 1.3 | 637 | 2 | US-08-854-811-26   | Sequence 26, Appl  |
| C 757 | 13 | 1.3 | 355 | 1 | US-08-090-523-5   | Sequence 5, Appl1  | 830 | 13 | 1.3 | 638 | 3 | US-08-705-771-11   | Sequence 11, Appl  |

|       |    |     |     |   |                     |                    |       |    |     |      |   |                   |                    |
|-------|----|-----|-----|---|---------------------|--------------------|-------|----|-----|------|---|-------------------|--------------------|
| 831   | 13 | 1.3 | 641 | 6 | 546585-6            | Patent No. 546585  | 904   | 13 | 1.3 | 840  | 3 | US-09-248-335-45  | Sequence 45, Appl  |
| C 832 | 13 | 1.3 | 660 | 0 | US-08-990-791-1     | Sequence 1, Appl1  | 905   | 13 | 1.3 | 846  | 1 | US-07-901-707-12  | Sequence 12, Appl  |
| C 833 | 13 | 1.3 | 681 | 6 | 5187078-24          | Patent No. 5187078 | 906   | 13 | 1.3 | 846  | 1 | US-07-988-430-12  | Sequence 12, Appl  |
| C 834 | 13 | 1.3 | 686 | 4 | US-08-998-416-715   | Sequence 715, App  | 907   | 13 | 1.3 | 846  | 1 | US-08-425-336-12  | Sequence 12, Appl  |
| C 835 | 13 | 1.3 | 686 | 4 | US-08-998-416-715   | Sequence 715, App  | 908   | 13 | 1.3 | 846  | 1 | US-08-488-1138-12 | Sequence 12, Appl  |
| C 836 | 13 | 1.3 | 703 | 4 | US-09-276-531-31    | Sequence 31, Appl  | 909   | 13 | 1.3 | 846  | 1 | US-08-477-484B-12 | Sequence 12, Appl  |
| C 837 | 13 | 1.3 | 707 | 2 | US-08-850-910A-40   | Sequence 40, Appl  | 910   | 13 | 1.3 | 846  | 2 | US-08-646-360-12  | Sequence 12, Appl  |
| C 838 | 13 | 1.3 | 716 | 4 | US-08-850-910A-40   | Sequence 40, Appl  | 911   | 13 | 1.3 | 846  | 3 | US-08-839-765-12  | Sequence 12, Appl  |
| C 839 | 13 | 1.3 | 716 | 4 | US-08-998-416-963   | Sequence 963, App  | 912   | 13 | 1.3 | 846  | 5 | US-09-136-389-12  | Sequence 12, Appl  |
| C 840 | 13 | 1.3 | 719 | 4 | US-08-998-416-1129  | Sequence 1129, App | 913   | 13 | 1.3 | 846  | 3 | PCT-US92-09487-12 | Sequence 12, Appl  |
| C 841 | 13 | 1.3 | 720 | 1 | US-09-411-578-39    | Sequence 39, Appl  | C 914 | 13 | 1.3 | 849  | 3 | US-08-807-300-2   | Sequence 2, Appl1  |
| C 842 | 13 | 1.3 | 720 | 2 | US-08-284-784-22    | Sequence 22, Appl  | 915   | 13 | 1.3 | 853  | 3 | US-08-963-409-2   | Sequence 2, Appl1  |
| C 843 | 13 | 1.3 | 720 | 2 | US-08-854-811-22    | Sequence 22, Appl  | 916   | 13 | 1.3 | 854  | 4 | US-09-064-693A-24 | Sequence 24, Appl  |
| C 844 | 13 | 1.3 | 720 | 4 | US-08-998-416-957   | Sequence 957, App  | 917   | 13 | 1.3 | 856  | 1 | US-08-117-373-10  | Sequence 10, Appl  |
| C 845 | 13 | 1.3 | 732 | 4 | US-08-361-395-2     | Sequence 2, Appl1  | 918   | 13 | 1.3 | 861  | 4 | US-08-953-326-8   | Sequence 8, Appl1  |
| C 846 | 13 | 1.3 | 732 | 4 | US-08-998-416-927   | Sequence 927, App  | 919   | 13 | 1.3 | 863  | 4 | US-08-998-416-489 | Sequence 489, App  |
| C 847 | 13 | 1.3 | 736 | 1 | US-08-808-303-7     | Sequence 7, Appl1  | C 920 | 13 | 1.3 | 867  | 4 | US-08-869-696-6   | Sequence 6, Appl1  |
| C 848 | 13 | 1.3 | 744 | 4 | US-09-163-285-3     | Sequence 3, Appl1  | 921   | 13 | 1.3 | 867  | 4 | US-09-475-316A-22 | Sequence 22, Appl  |
| C 849 | 13 | 1.3 | 745 | 1 | US-08-036-555B-163  | Sequence 163, App  | 922   | 13 | 1.3 | 869  | 4 | US-08-998-416-518 | Sequence 518, App  |
| C 850 | 13 | 1.3 | 745 | 1 | US-08-469-569-163   | Sequence 163, App  | C 923 | 13 | 1.3 | 870  | 2 | US-08-403-853-15  | Sequence 15, Appl  |
| C 851 | 13 | 1.3 | 745 | 1 | US-08-249-322A-163  | Sequence 163, App  | 924   | 13 | 1.3 | 885  | 3 | US-08-651-136C-23 | Sequence 23, Appl  |
| C 852 | 13 | 1.3 | 745 | 1 | US-08-469-526A-163  | Sequence 163, App  | 925   | 13 | 1.3 | 894  | 3 | US-08-651-136C-3  | Sequence 3, Appl1  |
| C 853 | 13 | 1.3 | 745 | 2 | US-08-734-591A-163  | Sequence 163, App  | 926   | 13 | 1.3 | 898  | 2 | US-08-966-316-4   | Sequence 4, Appl1  |
| C 854 | 13 | 1.3 | 745 | 2 | US-08-469-660-163   | Sequence 163, App  | 927   | 13 | 1.3 | 903  | 4 | US-08-944-604-15  | Sequence 15, Appl  |
| C 855 | 13 | 1.3 | 745 | 3 | US-08-341-018-51    | Sequence 51, App   | C 928 | 13 | 1.3 | 921  | 1 | US-08-420-235B-30 | Sequence 30, Appl  |
| C 856 | 13 | 1.3 | 745 | 3 | US-08-470-335-163   | Sequence 163, App  | C 929 | 13 | 1.3 | 921  | 5 | US-08-793-624-30  | Sequence 30, Appl  |
| C 857 | 13 | 1.3 | 745 | 4 | US-08-735-021-163   | Sequence 163, App  | C 930 | 13 | 1.3 | 921  | 5 | PCT-US95-10194-30 | Sequence 30, Appl  |
| C 858 | 13 | 1.3 | 745 | 4 | US-08-470-339-163   | Sequence 163, App  | C 931 | 13 | 1.3 | 925  | 3 | US-08-858-003-1   | Sequence 3, Appl   |
| C 859 | 13 | 1.3 | 745 | 4 | US-08-470-339-163   | Sequence 163, App  | C 932 | 13 | 1.3 | 925  | 3 | US-08-078-186-1   | Sequence 1, Appl1  |
| C 860 | 13 | 1.3 | 745 | 5 | PCT-US94-05083C-159 | Sequence 159, App  | C 933 | 13 | 1.3 | 925  | 4 | US-08-997-467-1   | Sequence 1, Appl1  |
| C 861 | 13 | 1.3 | 745 | 5 | PCT-US95-06846A-163 | Sequence 163, App  | C 934 | 13 | 1.3 | 927  | 2 | US-08-997-080-116 | Sequence 116, App  |
| C 862 | 13 | 1.3 | 747 | 4 | US-08-998-416-246   | Sequence 246, App  | C 935 | 13 | 1.3 | 927  | 2 | US-08-997-362-121 | Sequence 121, App  |
| C 863 | 13 | 1.3 | 753 | 5 | US-08-376-157B-1    | Sequence 1, Appl1  | C 936 | 13 | 1.3 | 927  | 3 | US-08-651-136C-5  | Sequence 5, Appl   |
| C 864 | 13 | 1.3 | 753 | 5 | PCT-US96-00845-1    | Sequence 1, Appl1  | C 937 | 13 | 1.3 | 927  | 4 | US-09-095-855-116 | Sequence 116, App  |
| C 865 | 13 | 1.3 | 754 | 1 | US-07-958-140-1     | Sequence 1, Appl1  | C 938 | 13 | 1.3 | 934  | 6 | 5258283-5         | Patent No. 5258283 |
| C 866 | 13 | 1.3 | 754 | 5 | PCT-US93-09166-1    | Sequence 1, Appl1  | C 939 | 13 | 1.3 | 946  | 2 | US-08-816-605-1   | Sequence 1, Appl1  |
| C 867 | 13 | 1.3 | 754 | 5 | US-08-998-416-435   | Sequence 435, App  | C 940 | 13 | 1.3 | 957  | 2 | US-08-544-822-2   | Sequence 2, Appl1  |
| C 868 | 13 | 1.3 | 777 | 4 | US-09-142-583A-10   | Sequence 10, Appl  | C 941 | 13 | 1.3 | 957  | 3 | US-09-070-964-2   | Sequence 2, Appl1  |
| C 869 | 13 | 1.3 | 780 | 1 | US-08-325-553-27    | Sequence 27, Appl  | C 942 | 13 | 1.3 | 965  | 1 | US-08-736-361A-3  | Sequence 3, Appl1  |
| C 870 | 13 | 1.3 | 780 | 2 | US-08-394-152A-27   | Sequence 27, Appl  | C 943 | 13 | 1.3 | 967  | 3 | US-09-248-335-21  | Sequence 51, Appl  |
| C 871 | 13 | 1.3 | 783 | 1 | US-08-455-001-3     | Sequence 3, Appl1  | C 944 | 13 | 1.3 | 970  | 1 | US-08-148-910-3   | Sequence 3, Appl1  |
| C 872 | 13 | 1.3 | 783 | 5 | PCT-US95-11869-3    | Sequence 3, Appl1  | C 945 | 13 | 1.3 | 970  | 1 | US-08-448-937A-3  | Sequence 3, Appl1  |
| C 873 | 13 | 1.3 | 787 | 4 | US-08-998-416-340   | Sequence 340, App  | C 946 | 13 | 1.3 | 970  | 1 | US-08-448-937A-3  | Sequence 3, Appl1  |
| C 874 | 13 | 1.3 | 798 | 1 | US-08-461-731-1     | Sequence 1, Appl1  | C 947 | 13 | 1.3 | 983  | 1 | US-08-886-765-1   | Sequence 1, Appl1  |
| C 875 | 13 | 1.3 | 798 | 2 | US-09-002-072B-1    | Sequence 1, Appl1  | C 948 | 13 | 1.3 | 983  | 4 | US-08-115-660-1   | Sequence 1, Appl1  |
| C 876 | 13 | 1.3 | 798 | 5 | PCT-US94-10465-2    | Sequence 2, Appl1  | C 949 | 13 | 1.3 | 985  | 2 | US-08-997-080-161 | Sequence 161, App  |
| C 877 | 13 | 1.3 | 798 | 5 | US-08-998-416-420   | Sequence 16, App   | C 950 | 13 | 1.3 | 985  | 2 | US-08-997-362-161 | Sequence 161, App  |
| C 878 | 13 | 1.3 | 801 | 2 | US-08-770-379-16    | Sequence 16, App   | C 951 | 13 | 1.3 | 985  | 4 | US-09-095-855-161 | Sequence 161, App  |
| C 879 | 13 | 1.3 | 801 | 4 | US-08-757-669A-16   | Sequence 16, App   | C 952 | 13 | 1.3 | 996  | 1 | US-07-975-526-2   | Sequence 2, Appl1  |
| C 880 | 13 | 1.3 | 802 | 3 | US-08-984-295-2     | Sequence 2, Appl1  | C 953 | 13 | 1.3 | 996  | 5 | PCT-US95-15353-38 | Sequence 38, Appl  |
| C 881 | 13 | 1.3 | 807 | 1 | US-08-566-369-1     | Sequence 1, Appl1  | C 954 | 13 | 1.3 | 996  | 5 | PCT-US95-15353-40 | Sequence 40, Appl  |
| C 882 | 13 | 1.3 | 807 | 1 | US-08-566-369-1     | Sequence 1, Appl1  | C 955 | 13 | 1.3 | 996  | 5 | US-09-018-584A-41 | Sequence 41, Appl  |
| C 883 | 13 | 1.3 | 807 | 4 | US-09-074-331-1     | Sequence 4, Appl1  | C 956 | 13 | 1.3 | 1000 | 4 | US-08-657-866-10  | Sequence 10, Appl  |
| C 884 | 13 | 1.3 | 807 | 4 | US-09-074-331-1     | Sequence 4, Appl1  | C 957 | 13 | 1.3 | 1005 | 2 | US-08-665-647-2   | Sequence 2, Appl1  |
| C 885 | 13 | 1.3 | 807 | 5 | PCT-US95-01937-1    | Sequence 1, Appl1  | C 958 | 13 | 1.3 | 1007 | 2 | US-09-084-120-17  | Sequence 17, Appl  |
| C 886 | 13 | 1.3 | 807 | 5 | PCT-US95-01937-1    | Sequence 4, Appl1  | C 959 | 13 | 1.3 | 1013 | 4 | US-07-648-796A-9  | Sequence 9, Appl1  |
| C 887 | 13 | 1.3 | 812 | 5 | PCT-US95-01937-1    | Sequence 4, Appl1  | C 960 | 13 | 1.3 | 1014 | 1 | US-08-444-083-6   | Sequence 6, Appl1  |
| C 888 | 13 | 1.3 | 812 | 5 | US-08-998-416-410   | Sequence 410, App  | 961   | 13 | 1.3 | 1018 | 1 | US-08-286-304-6   | Sequence 6, Appl1  |
| C 889 | 13 | 1.3 | 813 | 1 | US-08-425-336-11    | Sequence 11, Appl  | 962   | 13 | 1.3 | 1018 | 1 | US-08-442-745-6   | Sequence 6, Appl1  |
| C 890 | 13 | 1.3 | 813 | 1 | US-08-488-113B-11   | Sequence 11, Appl  | 963   | 13 | 1.3 | 1018 | 1 | US-08-442-745-6   | Sequence 6, Appl1  |
| C 891 | 13 | 1.3 | 813 | 1 | US-08-477-484B-11   | Sequence 11, Appl  | 964   | 13 | 1.3 | 1018 | 1 | US-08-443-129-6   | Sequence 6, Appl1  |
| C 892 | 13 | 1.3 | 813 | 2 | US-08-646-360-11    | Sequence 11, Appl  | 965   | 13 | 1.3 | 1018 | 1 | US-08-443-129-6   | Sequence 6, Appl1  |
| C 893 | 13 | 1.3 | 813 | 2 | US-08-621-803-246   | Sequence 246, App  | 966   | 13 | 1.3 | 1018 | 1 | US-08-443-130-6   | Sequence 6, Appl1  |
| C 894 | 13 | 1.3 | 813 | 3 | US-08-839-765-11    | Sequence 11, Appl  | C 967 | 13 | 1.3 | 1018 | 3 | US-08-866-095-2   | Sequence 2, Appl1  |
| C 895 | 13 | 1.3 | 813 | 3 | US-09-136-389-11    | Sequence 11, Appl  | C 968 | 13 | 1.3 | 1018 | 3 | US-08-896-911-6   | Sequence 6, Appl1  |
| C 896 | 13 | 1.3 | 817 | 4 | US-08-998-416-374   | Sequence 374, App  | 969   | 13 | 1.3 | 1018 | 5 | PCT-US95-04467-6  | Sequence 6, Appl1  |
| C 897 | 13 | 1.3 | 832 | 2 | US-08-340-539A-6    | Sequence 6, Appl1  | 970   | 13 | 1.3 | 1021 | 4 | US-09-095-117-5   | Sequence 5, Appl1  |
| C 898 | 13 | 1.3 | 832 | 2 | US-08-461-592B-6    | Sequence 6, Appl1  | 971   | 13 | 1.3 | 1028 | 4 | US-08-990-823-69  | Sequence 69, Appl  |
| C 899 | 13 | 1.3 | 836 | 4 | US-08-971-090-6     | Sequence 6, Appl1  | C 972 | 13 | 1.3 | 1029 | 1 | US-07-809-457A-15 | Sequence 15, Appl  |
| C 900 | 13 | 1.3 | 836 | 4 | US-08-971-090-7     | Sequence 7, Appl1  | C 973 | 13 | 1.3 | 1029 | 1 | US-08-553-943-15  | Sequence 15, Appl  |
| C 901 | 13 | 1.3 | 836 | 4 | US-09-187-946-5     | Sequence 5, Appl1  | C 974 | 13 | 1.3 | 1029 | 5 | PCT-US91-09437-15 | Sequence 15, Appl  |
| C 902 | 13 | 1.3 | 838 | 5 | PCT-US94-10457-1    | Sequence 7, Appl1  | C 975 | 13 | 1.3 | 1030 | 4 | US-09-095-117-7   | Sequence 7, Appl1  |
| C 903 | 13 | 1.3 | 838 | 5 | PCT-US96-03965-7    | Sequence 7, Appl1  | 976   | 13 | 1.3 | 1031 | 3 | US-08-651-136C-19 | Sequence 19, Appl  |



```
RESULT 2
US-08-480-917-9
; Sequence 9, Application US/08480917
; Patent No. 5820864
; GENERAL INFORMATION:
; APPLICANT: PARANHOS-BACCALA, Glaucia
; APPLICANT: LESENECHAL, Mylene
; APPLICANT: JOLIVET, Michel
; TITLE OF INVENTION: NEW TRYPAOSOMA CRUZI ANTIGEN, AND GENE
; TITLE OF INVENTION: ENCODING THE LATTER; THEIR APPLICATION TO THE DETECTION OF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oliff & Berridge
; STREET: 700 South Washington Street, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,917
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 36400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6400
; TELEFAX: 703-836-2787
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-480-917-9

Query Match 2.3%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 35 cagccgacgtagctgctct 56
Db 1 CAGCGACGCTAGCTGCTCT 22

RESULT 3
US-08-480-917-10/c
; Sequence 10, Application US/08480917
; Patent No. 5820864
; GENERAL INFORMATION:
; APPLICANT: PARANHOS-BACCALA, Glaucia
; APPLICANT: LESENECHAL, Mylene
; APPLICANT: JOLIVET, Michel
; TITLE OF INVENTION: NEW TRYPAOSOMA CRUZI ANTIGEN, AND GENE
; TITLE OF INVENTION: ENCODING THE LATTER; THEIR APPLICATION TO THE DETECTION OF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oliff & Berridge
; STREET: 700 South Washington Street, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.A.
```

```
ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,917
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 36400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6400
; TELEFAX: 703-836-2787
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-480-917-10

Query Match 2.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 956 gtgtgaacgagccattatgt 976
Db 21 GTGTGACGAGCCATTATGT 1

RESULT 4
US-08-480-917-12
; Sequence 12, Application US/08480917
; Patent No. 5820864
; GENERAL INFORMATION:
; APPLICANT: PARANHOS-BACCALA, Glaucia
; APPLICANT: LESENECHAL, Mylene
; APPLICANT: JOLIVET, Michel
; TITLE OF INVENTION: NEW TRYPAOSOMA CRUZI ANTIGEN, AND GENE
; TITLE OF INVENTION: ENCODING THE LATTER; THEIR APPLICATION TO THE DETECTION OF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oliff & Berridge
; STREET: 700 South Washington Street, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,917
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 36400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6400
; TELEFAX: 703-836-2787
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
```





MEDIUM TYPE: Floppy disk  
COMPUTER: Apple  
OPERATING SYSTEM: Macintosh  
SOFTWARE: Microsoft Word for Macintosh  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/970,269A  
FILING DATE: No. 5976803ember 14, 1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Adler Ph.D., Benjamin A.  
REGISTRATION NUMBER: 35,423  
REFERENCE/DOCKET NUMBER: D5860  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713-777-2321  
TELEFAX: 713-777-6908  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11883 bp  
TYPE: nucleic acid  
STRANDEDNESS: double stranded  
TOPOLOGY: linear  
MOLECULE TYPE: linear  
DESCRIPTION: other nucleic acid  
HYPOTHETICAL: no  
ANTI-SENSE: no  
ORIGINAL SOURCE:  
US-08-970-269A-28

Query Match 1.9%; Score 19; DB 2; Length 11883;  
Best Local Similarity 100.0%; Pred. No. 1.6;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 211 actctgcgcgtctgcatt 229  
|||||  
Db 6449 ACTTCTGCCGCTGCGCAT 6431

RESULT 8  
US-08-480-917-5  
Sequence 5, Application US/08480917  
Patent No. 5820864  
GENERAL INFORMATION:  
APPLICANT: PARANHOS-BACCALA, Glaucia  
APPLICANT: LESENECHAL, Mylene  
APPLICANT: JOLIVET, Michel  
TITLE OF INVENTION: NEW TRYPAOSOMA CRUZI ANTIGEN, AND GENE  
TITLE OF INVENTION: ENCODING THE LATTER; THEIR APPLICATION TO THE DETECTION OF  
TITLE OF INVENTION: CHAGAS DISEASE  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Oliff & Berridge  
STREET: 700 South Washington Street, Suite 300  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22314  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,917  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Berridge, William P.  
REGISTRATION NUMBER: 30,024  
REFERENCE/DOCKET NUMBER: WPB 36400  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6400  
TELEFAX: 703-836-2787

INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-480-917-5

Query Match 1.8%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.1;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 172 tcgggactgacggcgccg 189  
|||||  
Db 1 TCGGGCACTGACGGCGCG 18

RESULT 9  
US-08-480-917-8/C  
Sequence 8, Application US/08480917  
Patent No. 5820864  
GENERAL INFORMATION:  
APPLICANT: PARANHOS-BACCALA, Glaucia  
APPLICANT: LESENECHAL, Mylene  
APPLICANT: JOLIVET, Michel  
TITLE OF INVENTION: NEW TRYPAOSOMA CRUZI ANTIGEN, AND GENE  
TITLE OF INVENTION: ENCODING THE LATTER; THEIR APPLICATION TO THE DETECTION OF  
TITLE OF INVENTION: CHAGAS DISEASE  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Oliff & Berridge  
STREET: 700 South Washington Street, Suite 300  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22314  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,917  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Berridge, William P.  
REGISTRATION NUMBER: 30,024  
REFERENCE/DOCKET NUMBER: WPB 36400  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6400  
TELEFAX: 703-836-2787  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-480-917-8

Query Match 1.8%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.1;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 211 actctgcgcgtctgcatt 228  
|||||  
Db 18 ACTTCTGCCGCTGCGCA 1

RESULT 10  
US-08-454-557C-50  
Sequence 50, Application US/08454557C  
Patent No. 5830670  
GENERAL INFORMATION:  
APPLICANT: de la Monte, Suzanne  
TITLE OF INVENTION: Neutral Thread Protein Gene Expression and Detection  
NUMBER OF SEQUENCES: 121  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Avenue, Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/454,557C  
FILING DATE: 30-MAY-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Ludwig, Steven R.  
REGISTRATION NUMBER: 36,203  
REFERENCE/DOCKET NUMBER: 0609.3840003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2520 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
US-08-454-557C-50

Query Match 1.8%; Score 18; DB 2; Length 2520;  
Best Local Similarity 100.0%; Pred. No. 5.2;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 230 cccctgcatcaccctg 247  
|||||  
Db 298 cccctgcatcaccctg 315

RESULT 11  
US-08-340-426D-50  
Sequence 50, Application US/08340426D  
Patent No. 5948634  
GENERAL INFORMATION:  
APPLICANT: de la Monte, Suzanne  
TITLE OF INVENTION: Neutral Thread Protein Gene Expression and Detection  
NUMBER OF SEQUENCES: 121  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Avenue, Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/340,426D  
FILING DATE: 14-NOV-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ludwig, Steven R.  
REGISTRATION NUMBER: 36,203  
REFERENCE/DOCKET NUMBER: 0609.3840002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2520 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
US-08-340-426D-50

Query Match 1.8%; Score 18; DB 2; Length 2520;  
Best Local Similarity 100.0%; Pred. No. 5.2;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 230 cccctgcatcaccctg 247  
|||||  
Db 298 cccctgcatcaccctg 315

RESULT 12  
US-08-450-673C-50  
Sequence 50, Application US/08450673C  
Patent No. 5948888  
GENERAL INFORMATION:  
APPLICANT: de la Monte, Suzanne  
TITLE OF INVENTION: Neutral Thread Protein Gene Expression and Detection  
NUMBER OF SEQUENCES: 121  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Avenue, Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,673C  
FILING DATE: 30-MAY-1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Ludwig, Steven R.  
REGISTRATION NUMBER: 36,203  
REFERENCE/DOCKET NUMBER: 0609.3840004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2520 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
US-08-450-673C-50

Query Match 1.8%; Score 18; DB 2; Length 2520;  
Best Local Similarity 100.0%; Pred. No. 5.2;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 230 cccctgcatcacccctg 247  
|||||  
Db 298 CCCTGCATCACCCCTG 315

RESULT 13  
PCT-US95-17111A-50

; Sequence 50, Application PC/TUS9517111A  
; GENERAL INFORMATION:  
; APPLICANT: de la Monte, Suzanne  
; APPLICANT: Mands, Jack R.  
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and  
; TITLE OF INVENTION: Detection of Alzheimer's Disease  
; NUMBER OF SEQUENCES: 121  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentln Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/17111A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/340,426  
; FILING DATE: 14-NOV-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ludwig, Steven R.  
; REGISTRATION NUMBER: 36,203  
; REFERENCE/DOCKET NUMBER: 0609.3840002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 50:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2520 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; PCT-US95-17111A-50

Query Match 1.8%; Score 18; DB 5; Length 2520;  
Best Local Similarity 100.0%; Pred. No. 5.2;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 230 cccctgcatcacccctg 247  
|||||  
Db 298 CCCTGCATCACCCCTG 315

RESULT 14  
US-09-335-409-1/c  
; Sequence 1, Application US/09335409  
; Patent No. 6121029  
; GENERAL INFORMATION:  
; APPLICANT: Schupp, Thomas  
; APPLICANT: Ligon, James  
; APPLICANT: Molnar, Istvan  
; APPLICANT: Zirkle, Ross  
; APPLICANT: Cyr, Devon  
; APPLICANT: Goelach, Joern  
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES  
; FILE REFERENCE: 4-30582A

; CURRENT APPLICATION NUMBER: US/09/335,409  
; CURRENT FILING DATE: 1999-06-17  
; NUMBER OF SEQ. ID NOS: 30  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 68750  
; TYPE: DNA  
; ORGANISM: Sorangium cellulosum  
US-09-335-409-1

Query Match 1.8%; Score 18; DB 3; Length 68750;  
Best Local Similarity 100.0%; Pred. No. 5.2;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 517 tcgtctccacagccgcg 534  
|||||  
Db 19020 TCGTCTCCACAGCGCGC 19003

RESULT 15  
US-07-624-742-4/c

; Sequence 4, Application US/07624742  
; Patent No. 5236829  
; GENERAL INFORMATION:  
; APPLICANT: Farber, Joshua M.  
; TITLE OF INVENTION: MONOKINE MIG INDUCED BY IFN-GAMMA  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Banner, Birch, McKie and Beckett  
; STREET: 1001 G Street N.W.  
; CITY: Washington, D.C.  
; COUNTRY: USA  
; ZIP: 20001

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentln Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/624,742  
; FILING DATE: 19901210  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kagan, Sarah A.  
; REGISTRATION NUMBER: 32,141  
; REFERENCE/DOCKET NUMBER: 1107.29102  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 2025089100  
; TELEFAX: 2025089299  
; TELEX: 197430BBMB UT

; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 417 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 40..414  
US-07-624-742-4

Query Match 1.7%; Score 17; DB 1; Length 417;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 787 ctgaatcgggttaga 803

DB 277 CTGAATCTGGTTAGA 261

## RESULT 16

US-08-692-787-4  
Sequence 4, Application US/08692787  
Patent No. 5882864  
GENERAL INFORMATION:  
APPLICANT: An, Gang  
APPLICANT: O'Hara, S. Mark  
APPLICANT: Ralph, David  
APPLICANT: Veltri, Robert  
TITLE OF INVENTION: BIOMARKERS AND TARGETS FOR DIAGNOSIS,  
TITLE OF INVENTION: PROGNOSIS AND MANAGEMENT OF PROSTATE  
NUMBER OF SEQUENCES: 82  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: United States of America  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/692,787  
FILING DATE: Concurrently Herewith  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Corder, Timothy S.  
REGISTRATION NUMBER: 38,414  
REFERENCE/DOCKET NUMBER: UROC:012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 673 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-692-787-4

Query Match 1.7%; Score 17; DB 2; Length 673;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 537 gaacacacagaggaag 553  
DB 542 GAACCAACAGAGGAG 558

RESULT 17  
US-09-097-199-4  
Sequence 4, Application US/09097199  
Patent No. 6218529  
GENERAL INFORMATION:  
APPLICANT: An, Gang  
APPLICANT: O'Hara, S. Mark  
APPLICANT: Ralph, David  
APPLICANT: Veltri, Robert  
TITLE OF INVENTION: BIOMARKERS AND TARGETS FOR DIAGNOSIS,  
TITLE OF INVENTION: PROGNOSIS AND MANAGEMENT OF PROSTATE DISEASE  
NUMBER OF SEQUENCES: 87  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433

CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/097,199  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/692,787  
FILING DATE: 31-JUL-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Nakashima, Richard A.  
REGISTRATION NUMBER: P-42,023  
REFERENCE/DOCKET NUMBER: UROC:018  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 673 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-097-199-4

Query Match 1.7%; Score 17; DB 4; Length 673;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 537 gaacacacagaggaag 553  
DB 542 GAACCAACAGAGGAG 558

## RESULT 18

US-08-468-819-72/C  
Sequence 72, Application US/08468819  
Patent No. 5871723  
GENERAL INFORMATION:  
APPLICANT: Strieter, Robert M.  
APPLICANT: Kunkel, Steven L.  
TITLE OF INVENTION: CXc Chemokines as Regulators of  
TITLE OF INVENTION: Angiogenesis  
NUMBER OF SEQUENCES: 93  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: TX  
COUNTRY: US  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,819  
FILING DATE: Concurrently herewith  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L.  
REGISTRATION NUMBER: 37,642  
REFERENCE/DOCKET NUMBER: UMIC:003/HYL  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/418-3000  
TELEFAX: 512/474-7477  
TELEX: N/A  
INFORMATION FOR SEQ ID NO: 72:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2545 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-468-819-72

Query Match 1.7%; Score 17; DB 2; Length 2545;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 787 ctgaatctgggttaga 803  
|||||  
DB 277 CTGAATCTGGGTTAGA 261

RESULT 19  
US-08-072-610-1  
Sequence 1, Application US/08072610  
Patent No. 5532133  
GENERAL INFORMATION:  
APPLICANT: Barnwell, John  
TITLE OF INVENTION: Plasmodium vivax Blood Stage Antigens,  
TITLE OF INVENTION: Monoclonal Antibodies, and Diagnostic Assays  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Darby and Darby  
STREET: 805 Third Ave.  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022-7513  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/072,610  
FILING DATE: 19930602  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Gogoris, Adda  
REGISTRATION NUMBER: 29,714  
REFERENCE/DOCKET NUMBER: 5986/07686  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)527-7700  
TELEFAX: (212)753-6237  
TELEX: 236687  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3337 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Plasmodium vivax  
IMMEDIATE SOURCE:  
CLONE: PwMB3.3.1  
US-08-072-610-1

Query Match 1.7%; Score 17; DB 1; Length 3337;

Best Local Similarity 100.0%; Pred. No. 17;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 539 aaccaacagagaaga 555  
|||||  
DB 2029 AACCAACAGAGAGAAGA 2045

RESULT 20  
US-08-719-822B-1  
Sequence 1, Application US/08719822B  
Patent No. 5874527  
GENERAL INFORMATION:  
APPLICANT: Barnwell, John  
TITLE OF INVENTION: Plasmodium vivax Blood Stage Antigens  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Darby and Darby  
STREET: 805 Third Ave.  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022-7513  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/719,822B  
FILING DATE: 09/30/96  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Gogoris, Adda  
REGISTRATION NUMBER: 29,714  
REFERENCE/DOCKET NUMBER: 5986/17686US2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)527-7700  
TELEFAX: (212)753-6237  
TELEX: 236687  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3337 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Plasmodium vivax  
IMMEDIATE SOURCE:  
CLONE: PwMB3.3.1  
US-08-719-822B-1

Query Match 1.7%; Score 17; DB 2; Length 3337;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 539 aaccaacagagaaga 555  
|||||  
DB 2029 AACCAACAGAGAGAAGA 2045

RESULT 21  
US-09-092-458-1  
Sequence 1, Application US/09092458  
Patent No. 6231861  
GENERAL INFORMATION:  
APPLICANT: Barnwell, John  
TITLE OF INVENTION: Plasmodium vivax Blood Stage Antigens,  
TITLE OF INVENTION: Monoclonal Antibodies, and Diagnostic Assays

NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Darryl and Darryl  
STREET: 805 Third Ave.  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022-7513  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/092,458  
CLASSIFICATION:  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/719,821  
FILING DATE: 09/30/96  
ATTORNEY/AGENT INFORMATION:  
NAME: Gogoris, Adda  
REGISTRATION NUMBER: 29,714  
REFERENCE/DOCKET NUMBER: 5986/17686US3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)527-7700  
TELEFAX: (212)753-6237  
TELEX: 236687  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3337 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Plasmodium vivax  
IMMEDIATE SOURCE:  
CLONE: pVMB3.3.1  
US-09-092-458-1

Query Match 1.7%; Score 17; DB 4; Length 3337;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 539 aaccacagagagaaga 555  
|||||  
DB 2029 AACCAACAGGACAGAGA 2045

RESULT 22  
US-08-142-897-1/C  
Sequence 1, Application US/08142897  
Patent No. 5447852  
GENERAL INFORMATION:  
APPLICANT: Friedman, Jeffrey S.  
APPLICANT: Weissman, Irving L.  
TITLE OF INVENTION: No. 5447852el Cyclophilins, Associating Proteins  
TITLE OF INVENTION: and Uses  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Tracy J. Dunn  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/142,897  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/005,917  
FILING DATE: 15-JAN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/740,375  
FILING DATE: 05-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Dunn, Tracy D.  
REGISTRATION NUMBER: 34,587  
REFERENCE/DOCKET NUMBER: 5490A-92-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 41 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Primer  
FEATURE:  
NAME/KEY: misc-feature  
LOCATION: 1..41  
OTHER INFORMATION: /note="Adaptor-Primer"  
US-08-142-897-1

Query Match 1.6%; Score 16; DB 1; Length 41;  
Best Local Similarity 100.0%; Pred. No. 56;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 554 aaaggcttcgcgcgcg 569  
|||||  
DB 27 AAAAGCCTCCGCGGC 12

RESULT 23  
US-08-998-416-1039  
Sequence 1039, Application US/08998416  
Patent No. 6239264  
GENERAL INFORMATION:  
APPLICANT: Philippson, Peter  
APPLICANT: Pohlmann, Rainer  
APPLICANT: Steiner, Sabine  
APPLICANT: Mohr, Christine  
APPLICANT: Wendland, Jurgen  
APPLICANT: Knechtle, Philipp  
APPLICANT: Reibischung, Corinne  
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSTYPTI  
TITLE OF INVENTION: AND USES THEREOF  
NUMBER OF SEQUENCES: 1152  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6239264artis Corporation  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: No. 6239264th Carolina  
COUNTRY: USA  
ZIP: 27709  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/998,416  
FILING DATE: 24-DEC-1997  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: CH 0016/97  
FILING DATE: 31-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-541-8587  
TELEFAX: 919-541-8689  
INFORMATION FOR SEQ ID NO: 1039:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 737 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
ORGANISM: 1635RP  
US-08-998-416-1039

Query Match 1.6%; Score 16; DB 4; Length 737;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 696 gtgcgtgagcgctg 711  
|||||  
DB 85 GTCGCTGAGCGCTG 100

RESULT 24  
US-08-628-039-9/C  
Sequence 9, Application US/08628039  
Patent No. 5942660  
GENERAL INFORMATION:  
APPLICANT: Gruys, Kenneth J.  
APPLICANT: Mitsky, Timothy A.  
APPLICANT: Kishore, Ganesh M.  
APPLICANT: Slater, Steven C.  
APPLICANT: Padgett, Stephen R.  
APPLICANT: Stark, David M.  
APPLICANT: Hincbee, Maud A. W.  
APPLICANT: Clemente, Thomas E.  
APPLICANT: Connor-Ward, Dannelte V.  
APPLICANT: Fedele, Mary J.  
APPLICANT: Fry, Joyce E.  
APPLICANT: Howe, Arlene R.  
APPLICANT: Rozman, Renee J.  
TITLE OF INVENTION: Methods of Optimizing Substrate Pools and  
TITLE OF INVENTION: Biosynthesis of poly-B-hydroxybutyrate-co-poly-B-hydroxyvalerate  
TITLE OF INVENTION: In Bacteria and Plants  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Gary M. Bond, Monsanto Company, A35B  
STREET: 800 No. 5942660th Lindbergh Boulevard  
CITY: St. Louis  
STATE: Missouri  
COUNTRY: USA  
ZIP: 63167  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/628,039  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE: 13-MAR-1996  
ATTORNEY/AGENT INFORMATION:

NAME: Bond, Gary  
REGISTRATION NUMBER: 29,283  
REFERENCE/DOCKET NUMBER: 38-21(13585)A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314)694-3412  
TELEFAX: (314)695-5435  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1185 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-628-039-9

Query Match 1.6%; Score 16; DB 2; Length 1185;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 506 ccagcgcgctgctg 521  
|||||  
DB 544 CCAGCGCGGCGCTG 529

RESULT 25  
US-08-912-205-9/C  
Sequence 9, Application US/08912205  
Patent No. 6091002  
GENERAL INFORMATION:  
APPLICANT: Asrar, Jawed  
APPLICANT: Mitsky, Timothy A.  
APPLICANT: Shah, Devang T.  
TITLE OF INVENTION: Polyhydroxyalkanoates of narrow molecular  
TITLE OF INVENTION: Weight distribution prepared in transgenic plants  
NUMBER OF SEQUENCES: 11  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/912,205  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/673,388  
FILING DATE: 28-JUN-1996  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1185 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-912-205-9

Query Match 1.6%; Score 16; DB 3; Length 1185;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 506 ccagcgcgctgctg 521  
|||||  
DB 544 CCAGCGCGGCGCTG 529

RESULT 26  
US-09-440-400-9/C  
Sequence 9, Application US/09440400  
Patent No. 6228623  
GENERAL INFORMATION:  
APPLICANT: Asrar, Jawed

APPLICANT: Mitsky, Timothy A.  
APPLICANT: Shah, Devang T.  
TITLE OF INVENTION: Polyhydroxyalkanoates of narrow molecular  
TITLE OF INVENTION: weight distribution prepared in transgenic plants  
NUMBER OF SEQUENCES: 11  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/440,400  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/912,205  
FILING DATE:  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1185 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-440-400-9

Query Match 1.6%; Score 16; DB 4; Length 1185;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 506 ccagcgagcctcgtc 521  
|||||  
DB 544 CCAGCGGCGCTCGTC 529

RESULT 27  
US-09-031-059-2  
Sequence 2, Application US/09031059  
Patent No. 5948659  
GENERAL INFORMATION:  
APPLICANT: KATO, NOBUO  
APPLICANT: SAKAI, YASUYOSHI  
APPLICANT: TANI, YOSHIKI  
APPLICANT: FUKUYA, HIROSHI  
TITLE OF INVENTION: RECOMBINANT FRUCTOSYL AMINO ACID  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH  
STREET: PO BOX 747  
CITY: FALLS CHURCH  
STATE: VA  
COUNTRY: USA  
ZIP: 22040-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/031,059  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/899,172  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: WEINER, MARC S  
REGISTRATION NUMBER: 32,181  
REFERENCE/DOCKET NUMBER: 0020-4253P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 205-8000  
TELEFAX: (703) 205-8050

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1314 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA to mRNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1311  
US-09-031-059-2

Query Match 1.6%; Score 16; DB 2; Length 1314;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 351 taatgtaccacaag 366  
|||||  
DB 1281 TAATGTACCAAG 1296

RESULT 28  
US-07-952-817-10  
Sequence 10, Application US/07952817  
Patent No. 5356796

GENERAL INFORMATION:  
APPLICANT: Keller, John W.  
TITLE OF INVENTION: A Repressor Protein and Gene for Regulating  
TITLE OF INVENTION: Expression of Polypeptides and Its Use in the Preparation o  
TITLE OF INVENTION: 2,2-Dialkylglycine Decarboxylase of Pseudomonas Cepacia  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finegan, Henderson, Farabow, Garrett &  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
COUNTRY: US  
ZIP: 20005-3315

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/952,817  
FILING DATE: 19920928  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 01120,0002-01000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4400  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1411 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-07-952-817-10

Query Match 1.6%; Score 16; DB 1; Length 1411;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 459 caatggcgcactgtg 474  
|||||  
DB 372 CAATGCCGCGCTCGTC 387



RESULT 29  
5210025-3  
; Patent No. 5210025  
; APPLICANT: KELLER, JOHN W.  
; TITLE OF INVENTION: REPRESSOR PROTEIN GENE FOR REGULATING  
; EXPRESSION OF POLYPEPTIDES AND ITS USE IN THE PREPARATION OF  
; 2,2-DIALKYLGLYCINE DECARBOXYLASE OF PSEUDOMONAS CEPACIA  
; NUMBER OF SEQUENCES: 18  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/501,814  
; FILING DATE: 30-MAR-1990  
; SEQ ID NO:3:  
; LENGTH: 1411  
5210025-3

Query Match 1.6%; Score 16; DB 6; Length 1411;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 459 caatgcccgcactgtg 474  
|||||  
DB 372 caatgcccgcactgtg 387

RESULT 30  
US-08-360-606B-29/c  
; Sequence 29, Application US/08360606B  
; Patent No. 5919617  
; GENERAL INFORMATION:  
; APPLICANT: Jnanendra K. Bhattacharjee  
; APPLICANT: Richard C. Garrad  
; APPLICANT: Paul L. Skatrud  
; APPLICANT: Robert P. Peery  
; TITLE OF INVENTION: Methods and Reagents for  
; TITLE OF INVENTION: Detecting Fungal Pathogens in a  
; TITLE OF INVENTION: Biological Sample  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
; STREET: 300 S. Wacker Drive Suite 3200  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: U.S.A.  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: MS Word 7.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/360,606B  
; FILING DATE: December 21, 1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Berghoff, Paul H.  
; REGISTRATION NUMBER: 30,243  
; REFERENCE/DOCKET NUMBER: 94,319  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312)913-0001  
; TELEFAX: (312)913-0002  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1856 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; HYPOHETICAL: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Saccharomyces cerevisiae  
US-08-360-606B-29

Query Match 1.6%; Score 16; DB 2; Length 1856;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 gtaatggcgcgcgcga 154  
|||||  
DB 167 gtaatggcgcgcgcga 152

RESULT 31  
US-08-673-388-9/c  
; Sequence 9, Application US/08673388  
; Patent No. 5958745  
; GENERAL INFORMATION:  
; APPLICANT: Gruys, Kenneth J.  
; APPLICANT: Mitsky, Timothy A.  
; APPLICANT: Kishore, Ganesh M.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Padgett, Stephen R.  
; APPLICANT: Stark, David M.  
; APPLICANT: Hincbee, Maud A. W.  
; APPLICANT: Clemente, Thomas E.  
; APPLICANT: Connor-Ward, Dannelte V.  
; APPLICANT: Fedele, Mary J.  
; APPLICANT: Fry, Joyce E.  
; APPLICANT: Howe, Arlene R.  
; APPLICANT: Rozman, Renee J.  
; TITLE OF INVENTION: Methods of Optimizing Substrate Pools and  
; TITLE OF INVENTION: Biosynthesis of Poly-B-hydroxybutyrate-co-poly-B-hydroxyval  
; TITLE OF INVENTION: in Bacteria and Plants  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BR4F  
; STREET: 700 Chesterfield Parkway No. 5958745th  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/673,388  
; FILING DATE: 13-MAR-1996  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cohen, Charles E.  
; REGISTRATION NUMBER: 34,565  
; REFERENCE/DOCKET NUMBER: 38-21(13618)A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)537-6224  
; TELEFAX: (314)537-6047  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1864 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-673-388-9

Query Match 1.6%; Score 16; DB 2; Length 1864;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 506 ccagcgcgcgcctcgtc 521  
|||||  
DB 1073 CCAGCGCGGCCTCGTC 1058

RESULT 32  
US-08-614-877-9/c  
Sequence 9, Application US/08614877  
Patent No. 5959179  
GENERAL INFORMATION:  
APPLICANT: Gruys, Kenneth J.  
APPLICANT: Mitsky, Timothy A.  
APPLICANT: Kishore, Ganesh M.  
APPLICANT: Slater, Steven C.  
APPLICANT: Padgett, Stephen R.  
APPLICANT: Stark, David M.  
APPLICANT: Hinchey, Maud A. W.  
APPLICANT: Clemente, Thomas E.  
APPLICANT: Connor-Ward, Dannelle V.  
APPLICANT: Fedele, Mary J.  
APPLICANT: Fry, Joyce E.  
APPLICANT: Howe, Arlene R.  
APPLICANT: Rozman, Renee J.  
TITLE OF INVENTION: Methods of Optimizing Substrate Pools and  
TITLE OF INVENTION: Biosynthesis of Poly-B-hydroxybutyrate-co-poly-B-hydroxyvalerate  
TITLE OF INVENTION: in Bacteria and Plants  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Charles E. Cohen, Monsanto Company, B44F  
STREET: 700 Chesterfield Parkway No. 5959179th  
CITY: St. Louis  
STATE: Missouri  
COUNTRY: USA  
ZIP: 63198  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/614,877  
FILING DATE: 13-MAR-1996  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Cohen, Charles E.  
REGISTRATION NUMBER: 34,565  
REFERENCE/DOCKET NUMBER: 38-21(10695)A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314)537-6224  
TELEFAX: (314)537-6047  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1864 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-614-877-9

Query Match 1.6%; Score 16; DB 2; Length 1864;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 506 ccagcgcgagcctgcgc 521  
|||||  
DB 1073 CCAGCGCGCGCTGTC 1058

RESULT 33  
US-08-508-761B-5  
Sequence 5, Application US/08508761B  
Patent No. 6027920  
GENERAL INFORMATION:  
APPLICANT: Joliff, Gwennael  
APPLICANT: Guyonvarch, Arnel

APPLICANT: Purification, Relano  
APPLICANT: Duchiron, Francis  
APPLICANT: Renaud, Michel  
TITLE OF INVENTION: System for Protein Expression and  
TITLE OF INVENTION: Secretion Especially in Corynebacteria  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jacobson, Price, Holman & Stern, PLLC  
STREET: 400 Seventh St. N.W.  
CITY: Washington D.C.  
COUNTRY: U.S.A.  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/508,761B  
FILING DATE: 31-JUL-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 91/09652  
FILING DATE: 29-JUL-1991  
APPLICATION NUMBER: FR 91/09870  
FILING DATE: 02-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Player, William E.  
REGISTRATION NUMBER: 31,409  
REFERENCE/DOCKET NUMBER: P58525NA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 638-6666  
TELEFAX: (202) 393-5350  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2190 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Corynebacterium Melassecola  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 573..1913  
US-08-508-761B-5

Query Match 1.6%; Score 16; DB 3; Length 2190;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 864 aagctcgcgcaatca 879  
|||||  
DB 1407 AAGCTCCGCGCAATCA 1422

RESULT 34  
US-08-864-038A-1  
Sequence 1, Application US/08864038A  
Patent No. 6001592  
GENERAL INFORMATION:  
APPLICANT: Kunio NAKASHIMA et al.  
TITLE OF INVENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR  
TITLE OF INVENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID  
VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING  
TITLE OF INVENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBOD  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: 812-5 Hirano

STREET: Isshinden  
CITY: Tsu-city  
STATE: Mie-prefecture  
COUNTRY: JAPAN  
ZIP: 514-01  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Microsoft Windows 95  
SOFTWARE: Word Perfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/864,038A  
FILING DATE: May 28, 1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-184459  
FILING DATE: 15-July-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: C. Bruce Hamburg  
REGISTRATION NUMBER: 22,389  
REFERENCE/DOCKET NUMBER: F-5610  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)986-2340  
TELEFAX: (212)953-7733  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2214  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
ORIGINAL SOURCE:  
ORGANISM: Pinctada fucata  
CELL TYPE: mantle epithelial cell  
US-08-864-038A-1

Query Match 1.6%; Score 16; DB 3; Length 2214;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 215 ctgcgcgtctgcac 230  
|||||  
Db 1544 CTGCgcgtctgcac 1559

RESULT 35  
US-09-036-987A-25  
Sequence 25, Application US/09036987A  
Patent No. 6143526  
GENERAL INFORMATION:  
APPLICANT: Baltz, Richard H.  
APPLICANT: Broughton, Mary C.  
APPLICANT: Crawford, Kathryn P.  
APPLICANT: Madduri, Krishnamurthy  
APPLICANT: Merlo, Donald J.  
APPLICANT: Treadway, Patti J.  
APPLICANT: Turner, Jan R.  
TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide  
TITLE OF INVENTION: Production  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Dow Agrosciences LLC Patent Department  
STREET: 9330 Zionsville Road  
CITY: Indianapolis  
STATE: Indiana  
COUNTRY: USA  
ZIP: 46268  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/036,987A  
FILING-DATE: 09-MAR-1998  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Stuart, Donald R.  
REGISTRATION NUMBER: 28,479  
REFERENCE/DOCKET NUMBER: 50,608  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (317)337-4816  
TELEFAX: (317)337-4847  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2310 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 88..1077  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1165..1992  
US-09-036-987A-25

Query Match 1.6%; Score 16; DB 3; Length 2310;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 395 cgacgaggtctacgac 410  
|||||  
Db 468 CGACGAGGCTTACGCG 483

RESULT 36  
US-08-864-038A-2  
Sequence 2, Application US/08864038A  
Patent No. 6001592  
GENERAL INFORMATION:  
APPLICANT: Kunio NAKASHIMA et al.  
TITLE OF INVENTION: NOVEL POLYPEPTIDE GENE cDNA, VECTOR  
TITLE OF INVENTION: CONTAINING SAID cDNA, HOST CELLS TRANSFORMED WITH SAID  
TITLE OF INVENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING  
TITLE OF INVENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBOD  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: 812-5 Hirano  
STREET: Isshinden  
CITY: Tsu-city  
STATE: Mie-prefecture  
COUNTRY: JAPAN  
ZIP: 514-01  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Microsoft Windows 95  
SOFTWARE: Word Perfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/864,038A  
FILING DATE: May 28, 1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-184459  
FILING-DATE: 15-July-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: C. Bruce Hamburg  
REGISTRATION NUMBER: 22,389  
REFERENCE/DOCKET NUMBER: F-5610  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)986-2340  
TELEFAX: (212)953-7733  
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:  
LENGTH: 3331  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
ORGANISM: Pinctada fucata  
CELL TYPE: mantle epithelial cell  
FEATURE: mRNA  
LOCATION: from 1 to 3331  
IDENTIFICATION METHOD: E (by experiment)  
US-08-864-038A-2

Query Match 1.6%; Score 16; DB 3; Length 3331;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 215 ctgccgctgctgcatc 230  
|||||  
DB 1593 CTGCCGCTGCTGCATC 1608

RESULT 37  
US-08-864-038A-4  
Sequence 4, Application US/08864038A  
Patent No. 6001592  
GENERAL INFORMATION:  
APPLICANT: Kunio NAKASHIMA et al.  
TITLE OF INVENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR  
TITLE OF INVENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID  
TITLE OF INVENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING  
TITLE OF INVENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: 812-5 Hirano  
STREET: Ieshinden  
CITY: Tsu-city  
STATE: Mie-prefecture  
COUNTRY: JAPAN  
ZIP: 514-01  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Microsoft Windows 95  
SOFTWARE: Word Perfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/864,038A  
FILING DATE: May 28, 1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-184459  
FILING DATE: 15-July-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: C. Bruce Hamburg  
REGISTRATION NUMBER: 22,389  
REFERENCE/DOCKET NUMBER: F-5610  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)986-2340  
TELEFAX: (212)953-7733  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3331  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
ORIGINAL SOURCE: Pinctada fucata  
CELL TYPE: mantle epithelial cell  
FEATURE:  
NAME/KEY: CDS

LOCATION: from 50 to 2263  
IDENTIFICATION METHOD: P (by similarity to some other pattern)  
US-08-864-038A-4

Query Match 1.6%; Score 16; DB 3; Length 3331;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 215 ctgccgctgctgcatc 230  
|||||  
DB 1593 CTGCCGCTGCTGCATC 1608

RESULT 38  
US-08-750-152A-1/C  
Sequence 1, Application US/08750152A  
Patent No. 5977331  
GENERAL INFORMATION:  
APPLICANT: ASAKURA, YOKO  
APPLICANT: KIMURA, EIICHIRO  
APPLICANT: ABE, CHIZU  
APPLICANT: KAWAHARA, YOSHIO  
APPLICANT: NAKAMATSU, TSUYOSHI  
TITLE OF INVENTION: ALPHA-KETOGLUTARATE DEHYDROGENASE GENE  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22152  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/750,152A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: NORMAN F. OBLON  
REGISTRATION NUMBER: 24,618  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4394 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: genomic DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Brevibacterium lactofermentum  
STRAIN: ATCC13869  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 443..4213  
FEATURE:  
NAME/KEY: -35 signal  
LOCATION: 281..287  
FEATURE:  
NAME/KEY: -10 signal  
LOCATION: 307..312  
FEATURE:

NAME/KEY: RBS  
LOCATION: 421..428  
FEATURE:  
NAME/KEY: terminator  
LOCATION: 4243..4281  
US-08-750-152A-1

Query Match 1.6%; Score 16; DB 2; Length 4394;

Best Local Similarity 100.0%; Pred. No. 57;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 701 tggagcgcgtgagtc 716  
|||||  
Db 2624 TGGAGCGCGCTGAGTC 2609

RESULT 39

US-08-854-585-1/c  
Sequence 1, Application US/08854585  
Patent No. 6114140

GENERAL INFORMATION:

APPLICANT: Tonks, Nicholas K. and stman, Arne

TITLE OF INVENTION: Density Enhanced Protein Tyrosine Phosphatase

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 233 South Wacker Drive, Suite 6300

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/854,585

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/237,940

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Borun, Michael F.

REGISTRATION NUMBER: 25,447

REFERENCE/DOCKET NUMBER: 27866/31954

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-474-6300

TELEFAX: 312-474-0448

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 5117 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 350..4364

US-08-854-585-1

Query Match 1.6%; Score 16; DB 3; Length 5117;

Best Local Similarity 100.0%; Pred. No. 57;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 263 aggcagccgcgcctcc 278  
|||||  
Db 382 AGGCAGCGCGCCTCC 367

RESULT 40

PCT-US95-05512-1/c

Sequence 1, Application PC/TUS9505512

GENERAL INFORMATION:

APPLICANT: Tonks, Nicholas K. and stman, Arne

TITLE OF INVENTION: Density Enhanced Protein Tyrosine

Phosphatase

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

ADDRESS: Borun

STREET: 233 South Wacker Drive, Suite 6300

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/05512

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Borun, Michael F.

REGISTRATION NUMBER: 25,447

REFERENCE/DOCKET NUMBER: 27866/31954

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-474-6300

TELEFAX: 312-474-0448

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 5117 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 350..4364

PCT-US95-05512-1

Query Match 1.6%; Score 16; DB 5; Length 5117;

Best Local Similarity 100.0%; Pred. No. 57;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 263 aggcagccgcgcctcc 278  
|||||  
Db 382 AGGCAGCGCGCCTCC 367

RESULT 41

PCT-US95-13749-3

Sequence 3, Application PC/TUS9513749

GENERAL INFORMATION:

APPLICANT: Amgen Inc.

TITLE OF INVENTION: COMPOSITIONS FOR INCREASED

BIOAVAILABILITY OF ORALLY DELIVERED THERAPEUTIC AGENTS

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Amgen Inc.

STREET: 1840 Dehavilland Drive

CITY: Thousand Oaks

STATE: California

COUNTRY: USA

ZIP: 91320-1789

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:



NAME/KEY: CDS  
LOCATION: 2512..8070  
US-08-800-644-93

Query Match 1.6%; Score 16; DB 2; Length 9551;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 106 aggaagacagcagc 121  
|||||  
Db 6658 AGGAGAGACAGCAGC 6673

RESULT 44  
US-09-009-913-1/C

Sequence 1, Application US/09009913  
Patent No. 6087485  
GENERAL INFORMATION:  
APPLICANT: Axy's Pharmaceuticals, Inc.  
TITLE OF INVENTION: Asthma Related Genes  
NUMBER OF SEQUENCES: 339  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Bozicevic & Reed, LLP  
STREET: 285 Hamilton Ave, Suite 200  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/009,913  
FILING DATE: 21-JAN-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Sherwood, Pamela J  
REGISTRATION NUMBER: 36,677  
REFERENCE/DOCKET NUMBER: SEQ-4P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-327-3231  
TELEFAX: 650-327-3231  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 72928 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
US-09-009-913-1

Query Match 1.6%; Score 16; DB 3; Length 72928;  
Best Local Similarity 100.0%; Pred. No. 56;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 809 agatgacagactgca 824  
|||||  
Db 2985 AGATGACAGACTGCA 2970

RESULT 45  
US-08-633-779-2/C  
Sequence 2, Application US/08633779  
Patent No. 5723332  
GENERAL INFORMATION:

APPLICANT:  
TITLE OF INVENTION: TRANSLATIONAL ENHANCER DNA  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon & Vanderhye  
STREET: 1100 No. 5723332th Glebe Road, 8th Floor  
CITY: Arlington  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (ERO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/633,779  
FILING DATE: 19-APR-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Leonard C. Mitchard  
REGISTRATION NUMBER: 29,009  
REFERENCE/DOCKET NUMBER: 604-381  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 60 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-633-779-2

Query Match 1.5%; Score 15; DB 1; Length 60;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 425 ctaccgccccgcagc 439  
|||||  
Db 29 CTACGCCCCGCAGC 15

RESULT 46  
US-08-238-863-14  
Sequence 14, Application US/08238863  
Patent No. 5503978  
GENERAL INFORMATION:  
APPLICANT: SCHNEIDER, D. J., GOLD, L., AND FEIGON, J.  
TITLE OF INVENTION: HIGH-AFFINITY ssDNA LIGANDS OF HIV-1  
NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Beaton & Swanson, P.C.  
STREET: 4582 South Uister Street Parkway, Suite  
STREET: #403  
CITY: Denver  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80237  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/238,863  
FILING DATE: 6-MAY-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/714,131  
FILING DATE: 10-JUNE-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/536,428  
FILING DATE: 11-JUNE-1990

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/964,624
; FILING DATE: 21-OCTOBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 850-9900
; TELEFAX: (303) 850-9401
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 81
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-238-863-14

Query Match          1.5%; Score 15; DB 1; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 cccctgttcagcgc 256
Db 30 CCCCTGTTTCAGCGC 44

RESULT 47
US-08-443-407-14
; Sequence 14, Application US/08443407
; Patent No. 5786462
; GENERAL INFORMATION:
; APPLICANT: SCHNEIDER, D. J., GOLD, L., AND FELIGON, J.
; TITLE OF INVENTION: HIGH-AFFINITY sSDNA
; TITLE OF INVENTION: LIGANDS OF HIV-1 REVERSE
; TITLE OF INVENTION: TRANSCRIPTASE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,407
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/238,863
; FILING DATE: 6-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/964,624
; FILING DATE: 21-OCTOBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX17/C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
```

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; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 81
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-443-407-14

Query Match          1.5%; Score 15; DB 1; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 cccctgttcagcgc 256
Db 30 CCCCTGTTTCAGCGC 44

PCT-US95-05600-158
; Sequence 158, Application PC/TUS9505600
; GENERAL INFORMATION:
; APPLICANT: GOLD, LARRY
; APPLICANT: NIEUWLANDT, DAN
; APPLICANT: WECKER, MATTHEW
; APPLICANT: SCHNEIDER, DANIEL J.
; APPLICANT: FEIGON, JULI
; APPLICANT: ALLEN, PATRICK
; APPLICANT: SULENGER, BRUCE A.
; APPLICANT: DOUDNA, JENNIFER, A.
; TITLE OF INVENTION: HIGH-AFFINITY LIGANDS OF
; TITLE OF INVENTION: INSULIN RECEPTOR ANTIBODIES, TACHYKININ SUBSTANCE
; TITLE OF INVENTION: P, HIV INTEGRASE AND HIV-1 REVERSE TRANSCRIPTASE
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG
; MEDIUM TYPE: Storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05600
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/238,863
; FILING DATE: 06-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/248,632
; FILING DATE: 24-MAY-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/303,362
; FILING DATE: 09-SEPTEMBER-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/361,795
; FILING DATE: 21-DECEMBER-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/117,991
; FILING DATE: 08-SEPTEMBER-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/931,473
; FILING DATE: 17-AUGUST-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/964,624
; FILING DATE: 21-OCTOBER-1992
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE//DOCKET NUMBER: NEX17/PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 158:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 81 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; PCT-US95-05600-158

Query Match          1.5%; Score 15; DB 5; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 cccctgttcagcgc 256
Db 30 CCCCTGTTTCAGCGC 44

RESULT 49
US-08-994-946A-1
; Sequence 1, Application US/0894946A
; Patent No. 6046317
; GENERAL INFORMATION:
; APPLICANT: Koulou, Markku
; APPLICANT: Karvonen, Matti
; APPLICANT: Pesonen, Ullamari
; APPLICANT: Uusitupa, Matti
; TITLE OF INVENTION: A DNA Molecule Encoding a Mutant
; TITLE OF INVENTION: Prepro-Neuropeptide Y, a Mutant Signal Peptide, and Uses
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 13th Street NW, Suite 701-E
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/994,946A
; FILING DATE: 19-DEC-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE//DOCKET NUMBER: 2328-110
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-783-6040
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 base pairs
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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-994-946A-1
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Query Match          1.5%; Score 15; DB 3; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 274 cctcctgcgcgcgcg 288
Db 155 CCTCCTGCCGCGCGC 169
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RESULT 50
US-09-383-586-2/C
; Sequence 2, Application US/09383586
; Patent No. 6242419
; GENERAL INFORMATION:
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Mathew
; APPLICANT: Abernethy, Nevlin
; APPLICANT: Orunust, Rene
; APPLICANT: Kumble, Anand
; APPLICANT: Kurison, Greg
; TITLE OF INVENTION: Compounds isolated from stromal cells
; TITLE OF INVENTION: and methods for their use
; FILE REFERENCE: 11000.1037c1
; CURRENT APPLICATION NUMBER: US/09/383,586
; CURRENT FILING DATE: 1999-08-26
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 689
; TYPE: DNA
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (35) ... (556)
; US-09-383-586-2
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Query Match          1.5%; Score 15; DB 4; Length 689;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 900 cctgttcattgc 914
Db 218 CTTGTTCATTGC 204
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Search completed: September 21, 2001, 16:27:14
Job time: 9005 sec
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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 21, 2001, 16:15:12 : Search time 2753.51 Seconds  
(without alignments)  
5237.739 Million cell updates/sec

Title: US-09-138-735-1\_COPY\_1232\_2207

Perfect score: 976

Sequence: 1 caggtacaggtacgctt.....tgtaacagagccattatgt 976

Scoring table:

OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 14155048 seqs, 7388405095 residues

Word size : 0

Total number of hits satisfying chosen parameters: 28310096

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

Pending\_Patents\_NA\_Main:\*

1: /cgnl\_7/ptodata/1/pna/PCrUS.COMB.seq:\*  
2: /cgnl\_7/ptodata/1/pna/US06.COMB.seq:\*  
3: /cgnl\_7/ptodata/1/pna/US07.COMB.seq:\*  
4: /cgnl\_7/ptodata/1/pna/US08.COMB.seq:\*  
5: /cgnl\_7/ptodata/1/pna/US081.COMB.seq:\*  
6: /cgnl\_7/ptodata/1/pna/US082.COMB.seq:\*  
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33: /cgnl\_7/ptodata/1/pna/US109.COMB.seq:\*  
34: /cgnl\_7/ptodata/1/pna/US110.COMB.seq:\*  
35: /cgnl\_7/ptodata/1/pna/US111.COMB.seq:\*  
36: /cgnl\_7/ptodata/1/pna/US112.COMB.seq:\*  
37: /cgnl\_7/ptodata/1/pna/US113.COMB.seq:\*  
38: /cgnl\_7/ptodata/1/pna/US114.COMB.seq:\*  
39: /cgnl\_7/ptodata/1/pna/US115.COMB.seq:\*  
40: /cgnl\_7/ptodata/1/pna/US116.COMB.seq:\*  
41: /cgnl\_7/ptodata/1/pna/US117.COMB.seq:\*  
42: /cgnl\_7/ptodata/1/pna/US118.COMB.seq:\*  
43: /cgnl\_7/ptodata/1/pna/US119.COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID                   | Description         |
|------------|-------|-------------|--------|----|----------------------|---------------------|
| 1          | 976   | 100.0       | 3402   | 13 | US-08-988-242-1      | Sequence 1, Appli   |
| 2          | 976   | 100.0       | 3402   | 13 | US-09-138-736-1      | Sequence 1, Appli   |
| 3          | 22    | 2.3         | 22     | 15 | US-08-988-242-5      | Sequence 5, Appli   |
| 4          | 22    | 2.3         | 22     | 15 | US-09-138-736-9      | Sequence 9, Appli   |
| 5          | 22    | 2.3         | 366    | 23 | US-09-606-977-3519   | Sequence 3519, Ap   |
| 6          | 21    | 2.2         | 21     | 13 | US-08-988-242-6      | Sequence 6, Appli   |
| 7          | 21    | 2.2         | 21     | 13 | US-08-988-242-7      | Sequence 7, Appli   |
| 8          | 21    | 2.2         | 21     | 15 | US-09-138-736-10     | Sequence 10, Appli  |
| 9          | 21    | 2.2         | 21     | 15 | US-09-138-736-11     | Sequence 11, Appli  |
| 10         | 20    | 2.0         | 391    | 17 | US-09-332-782-18690  | Sequence 18690, A   |
| 11         | 20    | 2.0         | 391    | 19 | US-09-515-694-18690  | Sequence 18690, A   |
| 12         | 20    | 2.0         | 403    | 17 | US-09-332-782-12269  | Sequence 12269, A   |
| 13         | 20    | 2.0         | 403    | 17 | US-09-515-694-12269  | Sequence 12269, A   |
| 14         | 20    | 2.0         | 408    | 17 | US-09-332-782-12260  | Sequence 12260, A   |
| 15         | 20    | 2.0         | 408    | 17 | US-09-515-694-12260  | Sequence 12260, A   |
| 16         | 20    | 2.0         | 718    | 27 | US-09-654-617-126156 | Sequence 126156, A  |
| 17         | 20    | 2.0         | 718    | 27 | US-09-684-016-126156 | Sequence 126156, A  |
| 18         | 20    | 2.0         | 5679   | 24 | US-09-620-392-64793  | Sequence 64793, A   |
| 19         | 20    | 2.0         | 5679   | 24 | US-09-702-134-21010  | Sequence 21010, A   |
| 20         | 20    | 2.0         | 11335  | 49 | US-60-173-464-11335  | Sequence 11335, A   |
| 21         | 20    | 2.0         | 11335  | 51 | US-60-191-637-13953  | Sequence 13953, A   |
| 22         | 20    | 2.0         | 11335  | 51 | US-60-191-637-13953  | Sequence 13953, A   |
| 23         | 20    | 2.0         | 11338  | 48 | US-60-167-217-13998  | Sequence 13998, A   |
| 24         | 20    | 2.0         | 91470  | 20 | US-09-534-859-19     | Sequence 19, Appli  |
| 25         | 20    | 2.0         | 226706 | 19 | US-09-528-237A-1285  | Sequence 1285, Ap   |
| 26         | 19    | 1.9         | 718    | 50 | US-60-182-316-2055   | Sequence 2055, Ap   |
| 27         | 19    | 1.9         | 9895   | 24 | US-09-620-392-32691  | Sequence 32691, A   |
| 28         | 19    | 1.9         | 9895   | 24 | US-09-620-392-67713  | Sequence 67713, A   |
| 29         | 19    | 1.9         | 11873  | 18 | US-09-407-562-32     | Sequence 32, Appli  |
| 30         | 19    | 1.9         | 11878  | 18 | US-09-407-562-31     | Sequence 31, Appli  |
| 31         | 19    | 1.9         | 11883  | 18 | US-09-407-562-28     | Sequence 28, Appli  |
| 32         | 19    | 1.9         | 19505  | 24 | US-09-620-392-10632  | Sequence 10632, A   |
| 33         | 19    | 1.9         | 25670  | 24 | US-09-620-392-4251   | Sequence 4251, Ap   |
| 34         | 19    | 1.9         | 31556  | 28 | US-09-702-134-5295   | Sequence 5295, Ap   |
| 35         | 19    | 1.9         | 159989 | 28 | US-09-702-134-5301   | Sequence 5301, Ap   |
| 36         | 18    | 1.8         | 18     | 13 | US-08-988-242-4      | Sequence 4, Appli   |
| 37         | 18    | 1.8         | 18     | 13 | US-09-138-736-5      | Sequence 5, Appli   |
| 38         | 18    | 1.8         | 18     | 15 | US-09-138-736-8      | Sequence 8, Appli   |
| 39         | 18    | 1.8         | 70     | 17 | US-09-366-691A-1504  | Sequence 1504, Ap   |
| 40         | 18    | 1.8         | 85     | 21 | US-09-076-667-928    | Sequence 928, App   |
| 41         | 18    | 1.8         | 85     | 21 | US-09-540-229-15688  | Sequence 15688, A   |
| 42         | 18    | 1.8         | 85     | 36 | US-60-048-002-928    | Sequence 928, App   |
| 43         | 18    | 1.8         | 180    | 25 | US-09-513-991-2039   | Sequence 2039, Ap   |
| 44         | 18    | 1.8         | 194    | 29 | US-09-654-617-141143 | Sequence 141143, Ap |
| 45         | 18    | 1.8         | 194    | 27 | US-09-684-016-141143 | Sequence 141143, Ap |
| 46         | 18    | 1.8         | 196    | 25 | US-09-654-617-16258  | Sequence 16258, Ap  |

|       |    |     |     |    |                      |                    |       |    |     |     |    |                      |                    |
|-------|----|-----|-----|----|----------------------|--------------------|-------|----|-----|-----|----|----------------------|--------------------|
| C 47  | 18 | 1.8 | 196 | 27 | US-09-684-016-162528 | Sequence 162528,   | C 120 | 18 | 1.8 | 381 | 25 | US-09-654-617-165099 | Sequence 165099,   |
| C 48  | 18 | 1.8 | 217 | 27 | US-09-654-617-141154 | Sequence 141154,   | C 121 | 18 | 1.8 | 381 | 27 | US-09-684-016-165099 | Sequence 165099,   |
| C 49  | 18 | 1.8 | 217 | 27 | US-09-684-016-141154 | Sequence 141154,   | C 122 | 18 | 1.8 | 386 | 51 | US-60-197-872-6873   | Sequence 6873, Ap  |
| C 50  | 18 | 1.8 | 234 | 12 | US-08-810-326-2151   | Sequence 2151, Ap  | C 123 | 18 | 1.8 | 387 | 25 | US-09-654-617-164148 | Sequence 164148,   |
| C 51  | 18 | 1.8 | 234 | 21 | US-09-540-212A-11685 | Sequence 11685, A  | C 124 | 18 | 1.8 | 387 | 27 | US-09-684-016-164148 | Sequence 164148,   |
| C 52  | 18 | 1.8 | 237 | 12 | US-08-878-507-222    | Sequence 222, App  | C 125 | 18 | 1.8 | 388 | 25 | US-09-654-617-118824 | Sequence 118824,   |
| C 53  | 18 | 1.8 | 237 | 21 | US-09-540-212A-16821 | Sequence 16821, A  | C 126 | 18 | 1.8 | 388 | 27 | US-09-684-016-118824 | Sequence 118824,   |
| C 54  | 18 | 1.8 | 237 | 33 | US-60-016-092-222    | Sequence 222, App  | C 127 | 18 | 1.8 | 389 | 25 | US-09-654-617-155731 | Sequence 155731,   |
| C 55  | 18 | 1.8 | 248 | 15 | US-09-100-454-2483   | Sequence 2483, Ap  | C 128 | 18 | 1.8 | 389 | 27 | US-09-684-016-155731 | Sequence 155731,   |
| C 56  | 18 | 1.8 | 248 | 21 | US-09-540-212A-35497 | Sequence 35497, A  | C 129 | 18 | 1.8 | 391 | 25 | US-09-654-617-164091 | Sequence 164091,   |
| C 57  | 18 | 1.8 | 248 | 37 | US-60-051-749-2483   | Sequence 2483, Ap  | C 130 | 18 | 1.8 | 391 | 27 | US-09-684-016-164091 | Sequence 164091,   |
| C 58  | 18 | 1.8 | 249 | 36 | US-60-048-722-3053   | Sequence 3053, Ap  | C 131 | 18 | 1.8 | 393 | 51 | US-60-197-872-2599   | Sequence 2599, Ap  |
| C 59  | 18 | 1.8 | 253 | 13 | US-08-992-623-352    | Sequence 3252, Ap  | C 132 | 18 | 1.8 | 397 | 23 | US-09-605-699-13414  | Sequence 13414, A  |
| C 60  | 18 | 1.8 | 253 | 21 | US-09-540-764-10498  | Sequence 10498, A  | C 133 | 18 | 1.8 | 398 | 25 | US-09-654-617-149519 | Sequence 149519,   |
| C 61  | 18 | 1.8 | 259 | 19 | US-09-521-640-167970 | Sequence 167970, A | C 134 | 18 | 1.8 | 398 | 27 | US-09-684-016-149519 | Sequence 149519,   |
| C 62  | 18 | 1.8 | 259 | 46 | US-60-140-769-5670   | Sequence 5670, Ap  | C 135 | 18 | 1.8 | 401 | 25 | US-09-654-617-152001 | Sequence 152001,   |
| C 63  | 18 | 1.8 | 260 | 51 | US-60-197-872-21718  | Sequence 21718, A  | C 136 | 18 | 1.8 | 401 | 25 | US-09-654-617-160733 | Sequence 160733,   |
| C 64  | 18 | 1.8 | 261 | 5  | US-08-104-507A-4311  | Sequence 4311, Ap  | C 137 | 18 | 1.8 | 401 | 27 | US-09-684-016-152001 | Sequence 152001,   |
| C 65  | 18 | 1.8 | 261 | 5  | US-08-104-507C-4311  | Sequence 4311, Ap  | C 138 | 18 | 1.8 | 401 | 27 | US-09-684-016-160733 | Sequence 160733,   |
| C 66  | 18 | 1.8 | 269 | 16 | US-09-270-849B-53924 | Sequence 53924, A  | C 139 | 18 | 1.8 | 402 | 25 | US-09-654-617-164566 | Sequence 164566,   |
| C 67  | 18 | 1.8 | 271 | 16 | US-09-298-329A-4053  | Sequence 4053, Ap  | C 140 | 18 | 1.8 | 402 | 25 | US-09-654-617-165842 | Sequence 165842,   |
| C 68  | 18 | 1.8 | 271 | 40 | US-60-087-762-211    | Sequence 211, App  | C 141 | 18 | 1.8 | 402 | 27 | US-09-684-016-164566 | Sequence 164566,   |
| C 69  | 18 | 1.8 | 271 | 41 | US-60-093-036-941    | Sequence 941, App  | C 142 | 18 | 1.8 | 402 | 27 | US-09-684-016-165842 | Sequence 165842,   |
| C 70  | 18 | 1.8 | 273 | 25 | US-09-654-617-139099 | Sequence 139099,   | C 143 | 18 | 1.8 | 404 | 25 | US-09-654-617-149119 | Sequence 149119,   |
| C 71  | 18 | 1.8 | 273 | 27 | US-09-684-016-139099 | Sequence 139099,   | C 144 | 18 | 1.8 | 404 | 27 | US-09-684-016-19119  | Sequence 19119,    |
| C 72  | 18 | 1.8 | 284 | 48 | US-60-164-443-401    | Sequence 401, App  | C 145 | 18 | 1.8 | 406 | 25 | US-09-654-617-18666  | Sequence 18666,    |
| C 73  | 18 | 1.8 | 290 | 12 | US-08-826-438-125    | Sequence 125, App  | C 146 | 18 | 1.8 | 406 | 25 | US-09-654-617-151406 | Sequence 151406,   |
| C 74  | 18 | 1.8 | 290 | 13 | US-08-951-197-125    | Sequence 125, App  | C 147 | 18 | 1.8 | 406 | 27 | US-09-684-016-18666  | Sequence 18666,    |
| C 75  | 18 | 1.8 | 290 | 20 | US-09-521-640-21607  | Sequence 21607, A  | C 148 | 18 | 1.8 | 406 | 27 | US-09-684-016-151406 | Sequence 151406,   |
| C 76  | 18 | 1.8 | 290 | 33 | US-60-013-696-4335   | Sequence 4335, Ap  | C 149 | 18 | 1.8 | 410 | 25 | US-09-654-617-137067 | Sequence 137067,   |
| C 77  | 18 | 1.8 | 297 | 16 | US-09-266-640A-3874  | Sequence 3874, Ap  | C 150 | 18 | 1.8 | 410 | 27 | US-09-684-016-137067 | Sequence 137067,   |
| C 78  | 18 | 1.8 | 297 | 16 | US-09-266-640B-3874  | Sequence 3874, Ap  | C 151 | 18 | 1.8 | 412 | 25 | US-09-654-617-162774 | Sequence 162774,   |
| C 79  | 18 | 1.8 | 297 | 17 | US-09-313-294A-6114  | Sequence 6114, Ap  | C 152 | 18 | 1.8 | 412 | 27 | US-09-684-016-162774 | Sequence 162774,   |
| C 80  | 18 | 1.8 | 297 | 40 | US-60-086-722-6114   | Sequence 6114, Ap  | C 153 | 18 | 1.8 | 414 | 22 | US-09-654-617-14931  | Sequence 14931, A  |
| C 81  | 18 | 1.8 | 297 | 40 | US-60-087-762-208    | Sequence 208, App  | C 154 | 18 | 1.8 | 420 | 25 | US-09-654-617-155861 | Sequence 155861,   |
| C 82  | 18 | 1.8 | 297 | 41 | US-60-093-036-939    | Sequence 939, App  | C 155 | 18 | 1.8 | 420 | 25 | US-09-654-617-162566 | Sequence 162566,   |
| C 83  | 18 | 1.8 | 298 | 17 | US-09-304-517A-5225  | Sequence 5225, Ap  | C 156 | 18 | 1.8 | 420 | 27 | US-09-684-016-155861 | Sequence 155861,   |
| C 84  | 18 | 1.8 | 298 | 17 | US-09-371-146A-5225  | Sequence 5225, Ap  | C 157 | 18 | 1.8 | 420 | 27 | US-09-684-016-162566 | Sequence 162566,   |
| C 85  | 18 | 1.8 | 298 | 25 | US-09-654-617-301849 | Sequence 301849,   | C 158 | 18 | 1.8 | 430 | 25 | US-09-654-617-162522 | Sequence 162522,   |
| C 86  | 18 | 1.8 | 298 | 27 | US-09-684-016-301849 | Sequence 301849,   | C 159 | 18 | 1.8 | 430 | 27 | US-09-684-016-162522 | Sequence 162522,   |
| C 87  | 18 | 1.8 | 307 | 25 | US-09-654-617-156718 | Sequence 156718,   | C 160 | 18 | 1.8 | 431 | 25 | US-09-654-617-154959 | Sequence 154959,   |
| C 88  | 18 | 1.8 | 307 | 27 | US-09-684-016-156718 | Sequence 156718,   | C 161 | 18 | 1.8 | 431 | 27 | US-09-684-016-154959 | Sequence 154959,   |
| C 89  | 18 | 1.8 | 316 | 19 | US-09-521-640-172725 | Sequence 172725,   | C 162 | 18 | 1.8 | 432 | 25 | US-09-654-617-151302 | Sequence 151302,   |
| C 90  | 18 | 1.8 | 316 | 46 | US-60-140-769-8191   | Sequence 8191, Ap  | C 163 | 18 | 1.8 | 432 | 25 | US-09-654-617-164311 | Sequence 164311,   |
| C 91  | 18 | 1.8 | 320 | 52 | US-60-202-214-5107   | Sequence 5107, Ap  | C 164 | 18 | 1.8 | 432 | 27 | US-09-684-016-151302 | Sequence 151302,   |
| C 92  | 18 | 1.8 | 320 | 26 | US-09-663-779-4257   | Sequence 4257, Ap  | C 165 | 18 | 1.8 | 432 | 27 | US-09-684-016-164311 | Sequence 164311,   |
| C 93  | 18 | 1.8 | 328 | 1  | PCT-US01-01329-161   | Sequence 161, App  | C 166 | 18 | 1.8 | 438 | 19 | US-09-519-705-2501   | Sequence 2501, App |
| C 94  | 18 | 1.8 | 328 | 1  | PCT-US01-01339-1027  | Sequence 1027, Ap  | C 167 | 18 | 1.8 | 438 | 19 | US-09-519-705-2501   | Sequence 2501, App |
| C 95  | 18 | 1.8 | 332 | 25 | US-09-654-617-165118 | Sequence 165118,   | C 168 | 18 | 1.8 | 442 | 19 | US-09-574-454-2801   | Sequence 2801, Ap  |
| C 96  | 18 | 1.8 | 332 | 25 | US-09-684-016-165118 | Sequence 165118,   | C 169 | 18 | 1.8 | 442 | 19 | US-09-515-126-5771   | Sequence 5771, Ap  |
| C 97  | 18 | 1.8 | 333 | 25 | US-09-654-617-165673 | Sequence 165673,   | C 170 | 18 | 1.8 | 442 | 22 | US-09-577-409-5771   | Sequence 5771, Ap  |
| C 98  | 18 | 1.8 | 333 | 27 | US-09-684-016-165673 | Sequence 165673,   | C 171 | 18 | 1.8 | 443 | 25 | US-09-654-617-149512 | Sequence 149512,   |
| C 99  | 18 | 1.8 | 339 | 21 | US-09-540-229-178511 | Sequence 178511,   | C 172 | 18 | 1.8 | 443 | 27 | US-09-684-016-149512 | Sequence 149512,   |
| C 100 | 18 | 1.8 | 342 | 25 | US-09-654-617-141437 | Sequence 141437,   | C 173 | 18 | 1.8 | 444 | 25 | US-09-654-617-180110 | Sequence 180110,   |
| C 101 | 18 | 1.8 | 342 | 27 | US-09-684-016-141437 | Sequence 141437,   | C 174 | 18 | 1.8 | 444 | 27 | US-09-684-016-180110 | Sequence 180110,   |
| C 102 | 18 | 1.8 | 348 | 11 | US-08-727-898-198    | Sequence 198, App  | C 175 | 18 | 1.8 | 444 | 30 | US-09-770-175-4591   | Sequence 4591, Ap  |
| C 103 | 18 | 1.8 | 348 | 32 | US-60-005-018-198    | Sequence 198, App  | C 176 | 18 | 1.8 | 446 | 25 | US-09-654-617-161266 | Sequence 161266,   |
| C 110 | 18 | 1.8 | 367 | 17 | US-09-304-517A-82813 | Sequence 82813, A  | C 177 | 18 | 1.8 | 446 | 27 | US-09-684-016-161266 | Sequence 161266,   |
| C 111 | 18 | 1.8 | 367 | 17 | US-09-371-146A-82813 | Sequence 82813, A  | C 178 | 18 | 1.8 | 449 | 25 | US-09-654-617-166103 | Sequence 166103,   |
| C 112 | 18 | 1.8 | 367 | 17 | US-09-394-745-7320   | Sequence 7320, Ap  | C 179 | 18 | 1.8 | 449 | 27 | US-09-684-016-166103 | Sequence 166103,   |
| C 113 | 18 | 1.8 | 367 | 22 | US-09-565-306-17581  | Sequence 17581, A  | C 180 | 18 | 1.8 | 451 | 25 | US-09-654-617-170814 | Sequence 170814,   |
| C 114 | 18 | 1.8 | 368 | 25 | US-09-654-617-118825 | Sequence 118825,   | C 181 | 18 | 1.8 | 451 | 27 | US-09-684-016-170814 | Sequence 170814,   |
| C 115 | 18 | 1.8 | 368 | 25 | US-09-684-016-118825 | Sequence 118825,   | C 182 | 18 | 1.8 | 452 | 25 | US-09-654-617-144460 | Sequence 144460,   |
| C 116 | 18 | 1.8 | 375 | 25 | US-60-155-006-4578   | Sequence 4578, Ap  | C 183 | 18 | 1.8 | 452 | 25 | US-09-654-617-164505 | Sequence 164505,   |
| C 117 | 18 | 1.8 | 375 | 25 | US-09-654-617-165400 | Sequence 165400,   | C 184 | 18 | 1.8 | 452 | 27 | US-09-684-016-164505 | Sequence 164505,   |
| C 118 | 18 | 1.8 | 378 | 25 | US-09-684-016-152146 | Sequence 152146,   | C 185 | 18 | 1.8 | 453 | 25 | US-09-684-016-164505 | Sequence 164505,   |
| C 119 | 18 | 1.8 | 378 | 25 | US-09-654-617-161175 | Sequence 161175,   | C 186 | 18 | 1.8 | 453 | 25 | US-09-654-617-165659 | Sequence 165659,   |
| C 120 | 18 | 1.8 | 378 | 25 | US-09-654-617-163270 | Sequence 163270,   | C 187 | 18 | 1.8 | 453 | 27 | US-09-684-016-165659 | Sequence 165659,   |
| C 121 | 18 | 1.8 | 378 | 27 | US-09-684-016-161175 | Sequence 161175,   | C 188 | 18 | 1.8 | 454 | 20 | US-09-533-559-1832   | Sequence 1832, Ap  |
| C 122 | 18 | 1.8 | 378 | 27 | US-09-684-016-161175 | Sequence 161175,   | C 189 | 18 | 1.8 | 456 | 25 | US-09-654-617-170771 | Sequence 170771,   |
| C 123 | 18 | 1.8 | 378 | 27 | US-09-684-016-161175 | Sequence 161175,   | C 190 | 18 | 1.8 | 456 | 27 | US-09-684-016-170771 | Sequence 170771,   |
| C 124 | 18 | 1.8 | 378 | 27 | US-09-684-016-161175 | Sequence 161175,   | C 191 | 18 | 1.8 | 458 | 18 | US-09-401-645-3387   | Sequence 3387, Ap  |
| C 125 | 18 | 1.8 | 378 | 27 | US-09-684-016-161175 | Sequence 161175,   | C 192 | 18 | 1.8 | 459 | 19 | US-09-528-409-105673 | Sequence 105673,   |

|       |    |     |      |    |                       |                     |       |    |     |         |    |                      |                    |
|-------|----|-----|------|----|-----------------------|---------------------|-------|----|-----|---------|----|----------------------|--------------------|
| C 193 | 18 | 1.8 | 459  | 25 | US-09-654-617-151304  | Sequence 151304,    | 266   | 18 | 1.8 | 1707    | 25 | US-09-652-914-7995   | Sequence 7995, Ap  |
| C 194 | 18 | 1.8 | 459  | 25 | US-09-654-617-164138  | Sequence 164138,    | C 267 | 18 | 1.8 | 1896    | 22 | US-09-586-939-130    | Sequence 130, App  |
| C 195 | 18 | 1.8 | 459  | 25 | US-09-654-617-164173  | Sequence 164173,    | C 268 | 18 | 1.8 | 2218    | 49 | US-60-172-723602     | Sequence 22602, A  |
| C 196 | 18 | 1.8 | 459  | 27 | US-09-684-016-151304  | Sequence 151304,    | C 269 | 18 | 1.8 | 2263    | 28 | US-09-702-134-21931  | Sequence 21931, A  |
| C 197 | 18 | 1.8 | 459  | 27 | US-09-684-016-164138  | Sequence 164138,    | C 270 | 18 | 1.8 | 2520    | 7  | US-08-340-4268-50    | Sequence 50, Appl  |
| C 198 | 18 | 1.8 | 459  | 27 | US-09-684-016-164173  | Sequence 164173,    | C 271 | 18 | 1.8 | 2520    | 8  | US-08-450-6733A-50   | Sequence 50, Appl  |
| C 199 | 18 | 1.8 | 462  | 25 | US-09-654-617-156296  | Sequence 156296,    | C 272 | 18 | 1.8 | 2520    | 8  | US-08-454-555A-50    | Sequence 50, Appl  |
| C 200 | 18 | 1.8 | 462  | 25 | US-09-654-617-157269  | Sequence 157269,    | C 273 | 18 | 1.8 | 2762    | 60 | US-60-281-593-39     | Sequence 39, Appl  |
| C 201 | 18 | 1.8 | 462  | 27 | US-09-684-016-156296  | Sequence 156296,    | C 274 | 18 | 1.8 | 2803    | 25 | US-09-652-814-1769   | Sequence 769, Ap   |
| C 202 | 18 | 1.8 | 462  | 27 | US-09-684-016-157269  | Sequence 157269,    | C 275 | 18 | 1.8 | 2803    | 25 | US-09-726-171-1733   | Sequence 1733, Ap  |
| C 203 | 18 | 1.8 | 464  | 25 | US-09-654-617-164178  | Sequence 164178,    | C 276 | 18 | 1.8 | 2803    | 29 | US-09-726-172-1860   | Sequence 1860, Ap  |
| C 204 | 18 | 1.8 | 464  | 27 | US-09-684-016-164178  | Sequence 164178,    | C 277 | 18 | 1.8 | 2810    | 17 | US-09-397-424-5114   | Sequence 5114, Ap  |
| C 205 | 18 | 1.8 | 468  | 22 | PCT-US01-00663-60     | Sequence 60, Appl   | C 278 | 18 | 1.8 | 2817    | 17 | US-09-397-424-5114   | Sequence 5114, Ap  |
| C 206 | 18 | 1.8 | 468  | 22 | US-09-565-309A-180    | Sequence 60, Appl   | C 279 | 18 | 1.8 | 2817    | 15 | US-09-338-663-1298   | Sequence 1298, Ap  |
| C 207 | 18 | 1.8 | 473  | 18 | US-09-654-617-118818  | Sequence 926, App   | C 280 | 18 | 1.8 | 2817    | 25 | US-09-652-915-9199   | Sequence 9199, Ap  |
| C 208 | 18 | 1.8 | 473  | 18 | US-09-489-036-926     | Sequence 926, App   | C 281 | 18 | 1.8 | 2817    | 25 | US-09-652-915-9199   | Sequence 9199, Ap  |
| C 209 | 18 | 1.8 | 473  | 27 | US-09-684-016-118818  | Sequence 118818,    | C 282 | 18 | 1.8 | 3053    | 53 | US-60-212-659-815    | Sequence 815, App  |
| C 210 | 18 | 1.8 | 473  | 27 | US-09-684-016-118818  | Sequence 118818,    | C 283 | 18 | 1.8 | 3078    | 18 | US-09-703-708-635    | Sequence 635, App  |
| C 211 | 18 | 1.8 | 475  | 16 | US-09-240-371-7431    | Sequence 7431, Ap   | C 284 | 18 | 1.8 | 3083    | 19 | US-60-164-320-635    | Sequence 635, App  |
| C 212 | 18 | 1.8 | 475  | 16 | US-09-293-972-5995    | Sequence 5995, Ap   | C 285 | 18 | 1.8 | 3143    | 25 | US-09-428-151A-8869  | Sequence 8869, Ap  |
| C 213 | 18 | 1.8 | 476  | 16 | US-09-234-611-19378   | Sequence 19378, A   | C 286 | 18 | 1.8 | 3175    | 53 | US-09-532-305-1419   | Sequence 1419, Ap  |
| C 214 | 18 | 1.8 | 476  | 16 | US-09-277-227-11623   | Sequence 11623, A   | C 287 | 18 | 1.8 | 3175    | 53 | US-60-212-659-815    | Sequence 27, App   |
| C 215 | 18 | 1.8 | 478  | 1  | PCT-US01-00663-13298  | Sequence 13298, A   | C 288 | 18 | 1.8 | 7959    | 53 | US-60-212-659-815    | Sequence 714, App  |
| C 216 | 18 | 1.8 | 478  | 55 | US-60-236-359-7474    | Sequence 7474, Ap   | C 289 | 18 | 1.8 | 7959    | 48 | US-09-703-708-635    | Sequence 635, App  |
| C 217 | 18 | 1.8 | 484  | 23 | US-09-606-776-3048    | Sequence 3048, Ap   | C 290 | 18 | 1.8 | 7959    | 50 | US-60-164-320-635    | Sequence 635, App  |
| C 218 | 18 | 1.8 | 484  | 25 | US-09-644-867-3664    | Sequence 3664, Ap   | C 291 | 18 | 1.8 | 9227    | 56 | US-60-183-791-635    | Sequence 635, App  |
| C 219 | 18 | 1.8 | 486  | 22 | US-09-565-309A-40135  | Sequence 40135, A   | C 292 | 18 | 1.8 | 10637   | 28 | US-60-248-798-120    | Sequence 120, App  |
| C 220 | 18 | 1.8 | 486  | 22 | US-09-565-309A-45223  | Sequence 45223, A   | C 293 | 18 | 1.8 | 10964   | 24 | US-09-702-134-23597  | Sequence 23597, A  |
| C 221 | 18 | 1.8 | 487  | 22 | US-09-565-309A-223435 | Sequence 223435, A  | C 294 | 18 | 1.8 | 10964   | 24 | US-09-620-392-2862   | Sequence 2862, Ap  |
| C 222 | 18 | 1.8 | 506  | 6  | US-08-276-163A-13709  | Sequence 13709, A   | C 295 | 18 | 1.8 | 11714   | 24 | US-09-620-392-2862   | Sequence 40688, A  |
| C 223 | 18 | 1.8 | 506  | 6  | US-08-276-163B-13709  | Sequence 13709, A   | C 296 | 18 | 1.8 | 11714   | 24 | US-09-702-134-25413  | Sequence 25413, A  |
| C 224 | 18 | 1.8 | 506  | 6  | US-08-276-163D-13709  | Sequence 13709, A   | C 297 | 18 | 1.8 | 15270   | 56 | US-60-248-505-93     | Sequence 93, App   |
| C 225 | 18 | 1.8 | 508  | 25 | US-09-652-914-2822    | Sequence 2822, Ap   | C 298 | 18 | 1.8 | 15270   | 5  | PCT-US01-01354-40566 | Sequence 28829, A  |
| C 226 | 18 | 1.8 | 508  | 25 | US-09-654-617-118823  | Sequence 118823,    | C 299 | 18 | 1.8 | 17108   | 55 | US-60-230-435-291    | Sequence 40566, A  |
| C 227 | 18 | 1.8 | 508  | 27 | US-09-684-016-118823  | Sequence 118823,    | C 300 | 18 | 1.8 | 20671   | 53 | US-60-212-656-217    | Sequence 217, App  |
| C 228 | 18 | 1.8 | 513  | 25 | US-09-654-617-118821  | Sequence 118821,    | C 301 | 18 | 1.8 | 27620   | 55 | US-60-230-435-291    | Sequence 217, App  |
| C 229 | 18 | 1.8 | 513  | 27 | US-09-684-016-118821  | Sequence 118821,    | C 302 | 18 | 1.8 | 27062   | 56 | US-60-242-679-249    | Sequence 249, Appl |
| C 230 | 18 | 1.8 | 538  | 19 | US-09-532-305-313     | Sequence 313, App   | C 303 | 18 | 1.8 | 33085   | 40 | US-60-082-302-1225   | Sequence 725, App  |
| C 231 | 18 | 1.8 | 538  | 25 | US-09-649-165A-3885   | Sequence 3885, Ap   | C 304 | 18 | 1.8 | 33768   | 54 | US-60-229-515-90     | Sequence 89, Appl  |
| C 232 | 18 | 1.8 | 547  | 22 | US-09-565-309A-23436  | Sequence 23436, A   | C 305 | 18 | 1.8 | 33768   | 54 | US-60-229-515-90     | Sequence 90, Appl  |
| C 233 | 18 | 1.8 | 565  | 22 | US-09-565-309A-182    | Sequence 182, App   | C 306 | 18 | 1.8 | 33768   | 54 | US-60-229-515-91     | Sequence 91, Appl  |
| C 234 | 18 | 1.8 | 580  | 25 | US-09-654-617-387081  | Sequence 387081, A  | C 307 | 18 | 1.8 | 33768   | 54 | US-60-229-515-92     | Sequence 92, Appl  |
| C 235 | 18 | 1.8 | 580  | 27 | US-09-684-016-387081  | Sequence 387081, A  | C 308 | 18 | 1.8 | 33768   | 55 | US-60-230-435-115    | Sequence 415, Appl |
| C 236 | 18 | 1.8 | 605  | 25 | US-09-652-915-1811    | Sequence 1811, Ap   | C 309 | 18 | 1.8 | 33042   | 55 | US-60-245-221-47     | Sequence 47, Appl  |
| C 237 | 18 | 1.8 | 614  | 22 | US-09-565-309A-181    | Sequence 181, App   | C 310 | 18 | 1.8 | 34117   | 56 | US-60-245-225-193    | Sequence 193, App  |
| C 238 | 18 | 1.8 | 634  | 22 | US-09-565-309A-49383  | Sequence 49383, App | C 311 | 18 | 1.8 | 44405   | 28 | US-09-703-708-728    | Sequence 728, App  |
| C 239 | 18 | 1.8 | 634  | 22 | US-09-565-309A-49383  | Sequence 49383, A   | C 312 | 18 | 1.8 | 44405   | 48 | US-60-164-320-728    | Sequence 728, App  |
| C 240 | 18 | 1.8 | 664  | 25 | US-09-654-617-274884  | Sequence 274884, A  | C 313 | 18 | 1.8 | 46405   | 50 | US-60-183-791-728    | Sequence 1, Appl   |
| C 241 | 18 | 1.8 | 664  | 25 | US-09-654-617-274884  | Sequence 274884, A  | C 314 | 18 | 1.8 | 66750   | 22 | US-09-567-999-1      | Sequence 1, Appl   |
| C 242 | 18 | 1.8 | 691  | 25 | US-09-684-016-118819  | Sequence 118819,    | C 315 | 18 | 1.8 | 66750   | 22 | US-09-567-999-1      | Sequence 1, Appl   |
| C 243 | 18 | 1.8 | 691  | 25 | US-09-684-016-118819  | Sequence 118819,    | C 316 | 18 | 1.8 | 66750   | 22 | US-09-568-472-1      | Sequence 1, Appl   |
| C 244 | 18 | 1.8 | 696  | 16 | US-09-252-991A-9311   | Sequence 9311, Ap   | C 317 | 18 | 1.8 | 66750   | 22 | US-09-568-480-1      | Sequence 1, Appl   |
| C 245 | 18 | 1.8 | 720  | 40 | US-09-417-507-119997  | Sequence 119997, A  | C 318 | 18 | 1.8 | 66750   | 22 | US-09-568-480-1      | Sequence 1, Appl   |
| C 246 | 18 | 1.8 | 720  | 40 | US-09-417-507-119997  | Sequence 119997, A  | C 319 | 18 | 1.8 | 66750   | 22 | US-09-568-480-1      | Sequence 1, Appl   |
| C 247 | 18 | 1.8 | 771  | 25 | US-09-654-617-118820  | Sequence 118820, Ap | C 320 | 18 | 1.8 | 66750   | 43 | US-60-118-906-1      | Sequence 1, Appl   |
| C 248 | 18 | 1.8 | 771  | 25 | US-09-654-617-118820  | Sequence 118820, Ap | C 321 | 18 | 1.8 | 71989   | 18 | US-09-443-501-2      | Sequence 2, Appl   |
| C 249 | 18 | 1.8 | 779  | 27 | US-09-684-016-118820  | Sequence 118820, Ap | C 322 | 18 | 1.8 | 71989   | 18 | US-09-443-501-2      | Sequence 2, Appl   |
| C 250 | 18 | 1.8 | 891  | 18 | US-09-417-507-438     | Sequence 438, App   | C 323 | 18 | 1.8 | 78596   | 20 | US-09-534-859-896    | Sequence 896, App  |
| C 251 | 18 | 1.8 | 915  | 30 | US-09-770-445-436     | Sequence 436, App   | C 324 | 18 | 1.8 | 91470   | 20 | US-09-534-859-896    | Sequence 896, App  |
| C 252 | 18 | 1.8 | 936  | 25 | US-09-654-617-118809  | Sequence 118809,    | C 325 | 18 | 1.8 | 110684  | 57 | US-09-652-912-120    | Sequence 120, App  |
| C 253 | 18 | 1.8 | 936  | 27 | US-09-684-016-118809  | Sequence 118809,    | C 326 | 18 | 1.8 | 1129110 | 56 | US-60-245-221-24     | Sequence 24, Appl  |
| C 254 | 18 | 1.8 | 940  | 23 | US-09-606-776-5253    | Sequence 5253, Ap   | C 327 | 18 | 1.8 | 164677  | 54 | US-60-226-176-201    | Sequence 201, App  |
| C 255 | 18 | 1.8 | 940  | 23 | US-09-770-175-8299    | Sequence 8299, Ap   | C 328 | 18 | 1.8 | 164677  | 55 | US-60-233-168-201    | Sequence 201, App  |
| C 256 | 18 | 1.8 | 955  | 22 | US-09-565-309A-50543  | Sequence 50543, A   | C 329 | 18 | 1.8 | 164677  | 29 | US-09-724-389-1448   | Sequence 1448, App |
| C 257 | 18 | 1.8 | 955  | 22 | US-09-565-309A-57468  | Sequence 57468, A   | C 330 | 18 | 1.8 | 176888  | 56 | US-60-248-798-28     | Sequence 28, Appl  |
| C 258 | 18 | 1.8 | 1005 | 18 | US-09-489-039A-2199   | Sequence 2199, Ap   | C 331 | 17 | 1.7 | 97      | 13 | US-08-971-401-2749   | Sequence 2749, Ap  |
| C 259 | 18 | 1.8 | 1135 | 1  | US-09-417-507-119997  | Sequence 119997, A  | C 332 | 17 | 1.7 | 97      | 21 | US-09-540-764-7479   | Sequence 7479, Ap  |
| C 260 | 18 | 1.8 | 1302 | 1  | PCT-US00-06823-54     | Sequence 54, Appl   | C 333 | 17 | 1.7 | 115     | 14 | US-09-078-617-1204   | Sequence 1204, Ap  |
| C 261 | 18 | 1.8 | 1353 | 18 | US-09-471-275-9469    | Sequence 9469, Ap   | C 334 | 17 | 1.7 | 133     | 12 | US-08-856-624-1479   | Sequence 1479, Ap  |
| C 262 | 18 | 1.8 | 1380 | 16 | US-09-252-991A-9268   | Sequence 9268, Ap   | C 335 | 17 | 1.7 | 133     | 21 | US-09-540-766-32917  | Sequence 32917, A  |
| C 263 | 18 | 1.8 | 1390 | 27 | US-09-698-010-14005   | Sequence 14005, A   | C 336 | 17 | 1.7 | 154     | 14 | US-09-016-884-1388   | Sequence 1388, Ap  |
| C 264 | 18 | 1.8 | 1589 | 25 | US-09-641-377-783     | Sequence 783, App   | C 337 | 17 | 1.7 | 154     | 16 | US-60-037-043-1388   | Sequence 1388, Ap  |
| C 265 | 18 | 1.8 | 1707 | 25 | US-09-644-867-5948    | Sequence 5948, App  | C 338 | 17 | 1.7 | 155     | 35 | US-09-298-328A-2194  | Sequence 2194, Ap  |

|     |    |     |     |    |                      |                                   |     |    |     |     |    |                       |                     |
|-----|----|-----|-----|----|----------------------|-----------------------------------|-----|----|-----|-----|----|-----------------------|---------------------|
| 339 | 17 | 1.7 | 155 | 40 | US-60-085-147-2194   | Sequence 2194, Ap                 | 412 | 17 | 1.7 | 238 | 32 | US-60-004-674-2116    | Sequence 2116, Ap   |
| 340 | 17 | 1.7 | 158 | 16 | US-09-231-925-1568   | Sequence 1568, Ap                 | 413 | 17 | 1.7 | 238 | 34 | US-60-021-275-35      | Sequence 35, Appl   |
| 341 | 17 | 1.7 | 158 | 21 | US-09-540-229-142669 | Sequence 142669, Ap               | 414 | 17 | 1.7 | 240 | 11 | US-08-731-034-104     | Sequence 104, Appl  |
| 342 | 17 | 1.7 | 163 | 16 | US-09-288-778A-4508  | Sequence 4508, Ap                 | 415 | 17 | 1.7 | 240 | 13 | US-08-986-669-768     | Sequence 768, Appl  |
| 343 | 17 | 1.7 | 163 | 40 | US-60-089-763-4508   | Sequence 4508, Ap                 | 416 | 17 | 1.7 | 240 | 13 | US-08-986-669A-768    | Sequence 768, Appl  |
| 344 | 17 | 1.7 | 166 | 12 | US-08-867-019-190    | Sequence 190, Appl                | 417 | 17 | 1.7 | 240 | 21 | US-09-540-228-54519   | Sequence 54519, Ap  |
| 345 | 17 | 1.7 | 166 | 21 | US-09-540-499-4930   | Sequence 4930, Ap                 | 418 | 17 | 1.7 | 240 | 21 | US-09-540-733-3800    | Sequence 3800, Ap   |
| 346 | 17 | 1.7 | 176 | 18 | US-09-452-747-574    | Sequence 574, Appl                | 419 | 17 | 1.7 | 240 | 32 | US-60-004-674-104     | Sequence 104, Appl  |
| 347 | 17 | 1.7 | 176 | 20 | US-09-539-800-19370  | Sequence 19370, A                 | 420 | 17 | 1.7 | 241 | 14 | US-09-015-080-2355    | Sequence 2355, Ap   |
| 348 | 17 | 1.7 | 176 | 43 | US-60-111-910-574    | Sequence 574, Appl                | 421 | 17 | 1.7 | 241 | 14 | US-09-035-171-51      | Sequence 51, Appl   |
| 349 | 17 | 1.7 | 178 | 13 | US-09-901-904-4790   | Sequence 4790, Ap                 | 422 | 17 | 1.7 | 241 | 15 | US-09-114-065-559     | Sequence 559, Appl  |
| 350 | 17 | 1.7 | 178 | 21 | US-09-540-208-11694  | Sequence 11694, A                 | 423 | 17 | 1.7 | 241 | 18 | US-09-420-691-3732    | Sequence 3732, Ap   |
| 351 | 17 | 1.7 | 197 | 24 | US-09-637-086A-44437 | Sequence 44437, A                 | 424 | 17 | 1.7 | 241 | 21 | US-09-540-212A-6342   | Sequence 6342, Ap   |
| 352 | 17 | 1.7 | 197 | 25 | US-09-654-617-228211 | Sequence 228211, Sequence 228211, | 425 | 17 | 1.7 | 241 | 21 | US-09-540-212A-7553   | Sequence 7553, Ap   |
| 353 | 17 | 1.7 | 197 | 27 | US-09-684-016-228211 | Sequence 228211,                  | 426 | 17 | 1.7 | 241 | 23 | US-09-605-669-18447   | Sequence 18447, A   |
| 354 | 17 | 1.7 | 198 | 14 | US-09-181-708-348    | Sequence 348, Appl                | 427 | 17 | 1.7 | 241 | 35 | US-60-039-416-51      | Sequence 51, Appl   |
| 355 | 17 | 1.7 | 198 | 15 | US-09-181-375-87     | Sequence 87, Appl                 | 428 | 17 | 1.7 | 242 | 13 | US-09-901-904-5784    | Sequence 5784, Ap   |
| 356 | 17 | 1.7 | 198 | 34 | US-60-021-275-239    | Sequence 239, Appl                | 429 | 17 | 1.7 | 242 | 21 | US-09-540-208-6288    | Sequence 6288, Ap   |
| 357 | 17 | 1.7 | 200 | 12 | US-08-883-626-607    | Sequence 607, Appl                | 430 | 17 | 1.7 | 244 | 11 | US-08-731-034-1013    | Sequence 1013, Ap   |
| 358 | 17 | 1.7 | 200 | 21 | US-09-540-499-4241   | Sequence 4241, Appl               | 431 | 17 | 1.7 | 244 | 13 | US-08-917-047-677     | Sequence 677, Appl  |
| 359 | 17 | 1.7 | 200 | 34 | US-60-021-995-607    | Sequence 607, Appl                | 432 | 17 | 1.7 | 244 | 17 | US-09-304-517A-18155  | Sequence 18155, A   |
| 360 | 17 | 1.7 | 206 | 12 | US-08-878-504-1667   | Sequence 1667, Appl               | 433 | 17 | 1.7 | 244 | 17 | US-09-371-146A-18155  | Sequence 18155, A   |
| 361 | 17 | 1.7 | 206 | 34 | US-09-540-229-64908  | Sequence 64908, A                 | 434 | 17 | 1.7 | 244 | 21 | US-09-540-733-2542    | Sequence 2542, Ap   |
| 362 | 17 | 1.7 | 206 | 34 | US-60-020-310-1667   | Sequence 1667, Ap                 | 435 | 17 | 1.7 | 244 | 32 | US-60-004-674-1013    | Sequence 1013, Ap   |
| 363 | 17 | 1.7 | 209 | 18 | US-09-411-999-33638  | Sequence 33638, Ap                | 436 | 17 | 1.7 | 244 | 34 | US-60-025-203-677     | Sequence 677, Appl  |
| 364 | 17 | 1.7 | 210 | 12 | US-08-878-669-1858   | Sequence 1858, Ap                 | 437 | 17 | 1.7 | 245 | 11 | US-08-722-922-29      | Sequence 29, Appl   |
| 365 | 17 | 1.7 | 211 | 13 | US-08-903-802-480    | Sequence 480, Appl                | 438 | 17 | 1.7 | 245 | 11 | US-08-731-034-1670    | Sequence 1670, Appl |
| 366 | 17 | 1.7 | 212 | 13 | US-08-903-469-4342   | Sequence 4342, A                  | 439 | 17 | 1.7 | 245 | 18 | US-09-478-829-4957    | Sequence 4957, Ap   |
| 367 | 17 | 1.7 | 212 | 21 | US-09-540-208-31268  | Sequence 31268, A                 | 440 | 17 | 1.7 | 245 | 21 | US-09-540-229-154330  | Sequence 154330, A  |
| 368 | 17 | 1.7 | 212 | 34 | US-60-023-339-1972   | Sequence 1972, Ap                 | 441 | 17 | 1.7 | 245 | 21 | US-09-540-733-2287    | Sequence 2287, Ap   |
| 369 | 17 | 1.7 | 215 | 21 | US-09-540-764-3722   | Sequence 3722, Ap                 | 442 | 17 | 1.7 | 245 | 32 | US-60-004-674-1670    | Sequence 1670, Ap   |
| 370 | 17 | 1.7 | 216 | 13 | US-08-999-861-2372   | Sequence 2372, Ap                 | 443 | 17 | 1.7 | 245 | 43 | US-60-115-695-559     | Sequence 559, Appl  |
| 371 | 17 | 1.7 | 216 | 16 | US-09-275-082A-3951  | Sequence 3951, Ap                 | 444 | 17 | 1.7 | 246 | 11 | US-08-731-034-614     | Sequence 614, Appl  |
| 372 | 17 | 1.7 | 216 | 17 | US-09-394-745-53715  | Sequence 53715, A                 | 445 | 17 | 1.7 | 246 | 13 | US-08-905-885-2902    | Sequence 2902, Ap   |
| 373 | 17 | 1.7 | 216 | 39 | US-60-079-234-3951   | Sequence 3951, Ap                 | 446 | 17 | 1.7 | 246 | 14 | US-09-035-171-48      | Sequence 48, Appl   |
| 374 | 17 | 1.7 | 216 | 41 | US-60-085-533-783    | Sequence 783, Appl                | 447 | 17 | 1.7 | 246 | 21 | US-09-540-212A-9617   | Sequence 9617, Ap   |
| 375 | 17 | 1.7 | 216 | 41 | US-60-093-036-1116   | Sequence 1116, Ap                 | 448 | 17 | 1.7 | 246 | 21 | US-09-540-733-2706    | Sequence 2706, Ap   |
| 376 | 17 | 1.7 | 218 | 16 | US-09-294-086A-5439  | Sequence 5439, Ap                 | 449 | 17 | 1.7 | 246 | 32 | US-60-004-674-614     | Sequence 614, Appl  |
| 377 | 17 | 1.7 | 218 | 40 | US-60-084-492-5364   | Sequence 5364, Ap                 | 450 | 17 | 1.7 | 246 | 35 | US-60-039-416-48      | Sequence 48, Appl   |
| 378 | 17 | 1.7 | 222 | 14 | US-09-021-702-8      | Sequence 8, Appl1                 | 451 | 17 | 1.7 | 247 | 13 | US-08-903-556-324     | Sequence 324, Appl  |
| 379 | 17 | 1.7 | 222 | 21 | US-09-540-766-6330   | Sequence 6330, Ap                 | 452 | 17 | 1.7 | 247 | 21 | US-09-540-764-10605   | Sequence 10605, A   |
| 380 | 17 | 1.7 | 222 | 36 | US-60-041-220-8      | Sequence 8, Appl1                 | 453 | 17 | 1.7 | 247 | 36 | US-60-040-957-83      | Sequence 83, Appl   |
| 381 | 17 | 1.7 | 223 | 13 | US-08-922-314-1076   | Sequence 1076, Ap                 | 454 | 17 | 1.7 | 248 | 20 | US-09-539-806-36947   | Sequence 36947, A   |
| 382 | 17 | 1.7 | 223 | 13 | US-08-922-314A-1076  | Sequence 1076, Ap                 | 455 | 17 | 1.7 | 248 | 14 | US-09-016-884-1232    | Sequence 1232, Ap   |
| 383 | 17 | 1.7 | 223 | 22 | US-09-565-306-78209  | Sequence 78209, A                 | 456 | 17 | 1.7 | 249 | 20 | US-09-534-083-1652    | Sequence 1652, Ap   |
| 384 | 17 | 1.7 | 224 | 13 | US-08-903-469-3395   | Sequence 3395, Ap                 | 457 | 17 | 1.7 | 249 | 35 | US-60-037-043-1232    | Sequence 1232, Ap   |
| 385 | 17 | 1.7 | 224 | 14 | US-09-015-080-1958   | Sequence 1958, Ap                 | 458 | 17 | 1.7 | 250 | 14 | US-09-010-765-731     | Sequence 731, Appl  |
| 386 | 17 | 1.7 | 224 | 21 | US-09-540-208-41542  | Sequence 41542, A                 | 459 | 17 | 1.7 | 250 | 18 | US-09-436-711-4823    | Sequence 4823, Ap   |
| 387 | 17 | 1.7 | 224 | 21 | US-09-540-212A-40039 | Sequence 40039, A                 | 460 | 17 | 1.7 | 250 | 21 | US-09-540-766-36329   | Sequence 36329, A   |
| 388 | 17 | 1.7 | 224 | 34 | US-60-023-339-1025   | Sequence 1025, Ap                 | 461 | 17 | 1.7 | 250 | 35 | US-60-036-145-731     | Sequence 731, Appl  |
| 389 | 17 | 1.7 | 224 | 34 | US-60-023-143-1472   | Sequence 1472, Ap                 | 462 | 17 | 1.7 | 251 | 14 | US-09-035-171-21      | Sequence 21, Appl   |
| 390 | 17 | 1.7 | 226 | 13 | US-08-917-045-77     | Sequence 77, Appl1                | 463 | 17 | 1.7 | 251 | 17 | US-09-304-517A-136266 | Sequence 136266, A  |
| 391 | 17 | 1.7 | 226 | 13 | US-08-922-314-1188   | Sequence 1188, Ap                 | 464 | 17 | 1.7 | 251 | 17 | US-09-371-146A-136266 | Sequence 136266, A  |
| 392 | 17 | 1.7 | 226 | 13 | US-08-922-314A-1188  | Sequence 1188, Ap                 | 465 | 17 | 1.7 | 251 | 21 | US-09-540-212A-11572  | Sequence 11572, A   |
| 393 | 17 | 1.7 | 226 | 34 | US-60-025-216-77     | Sequence 77, Appl1                | 466 | 17 | 1.7 | 251 | 23 | US-09-605-701-11766   | Sequence 11766, A   |
| 394 | 17 | 1.7 | 227 | 11 | US-08-768-900-365    | Sequence 365, Appl                | 467 | 17 | 1.7 | 251 | 35 | US-60-039-416-21      | Sequence 21, Appl1  |
| 395 | 17 | 1.7 | 228 | 13 | US-08-922-315-3101   | Sequence 3101, Ap                 | 468 | 17 | 1.7 | 252 | 17 | US-09-329-021-5640    | Sequence 5640, Ap   |
| 396 | 17 | 1.7 | 230 | 21 | US-09-540-499-23732  | Sequence 23732, A                 | 469 | 17 | 1.7 | 252 | 40 | US-60-089-805-5640    | Sequence 5640, Ap   |
| 397 | 17 | 1.7 | 230 | 42 | US-60-108-396-2048   | Sequence 2048, Ap                 | 470 | 17 | 1.7 | 253 | 14 | US-09-022-335-1796    | Sequence 1796, Ap   |
| 398 | 17 | 1.7 | 232 | 11 | US-08-731-034-390    | Sequence 390, Appl                | 471 | 17 | 1.7 | 253 | 14 | US-09-022-335-1803    | Sequence 1803, Ap   |
| 399 | 17 | 1.7 | 232 | 21 | US-09-540-733-2131   | Sequence 2131, Ap                 | 472 | 17 | 1.7 | 253 | 14 | US-09-036-589-1307    | Sequence 1307, Ap   |
| 400 | 17 | 1.7 | 232 | 32 | US-60-004-674-390    | Sequence 390, Appl                | 473 | 17 | 1.7 | 253 | 20 | US-09-539-806-14216   | Sequence 14216, A   |
| 401 | 17 | 1.7 | 233 | 15 | US-09-187-860-819    | Sequence 819, Appl                | 474 | 17 | 1.7 | 253 | 21 | US-09-540-208-16509   | Sequence 16509, A   |
| 402 | 17 | 1.7 | 233 | 12 | US-08-859-945-3184   | Sequence 3184, Ap                 | 475 | 17 | 1.7 | 253 | 35 | US-09-540-212A-7313   | Sequence 7313, Ap   |
| 403 | 17 | 1.7 | 234 | 17 | US-09-390-960A-2212  | Sequence 2212, Ap                 | 476 | 17 | 1.7 | 253 | 31 | US-60-039-128-1307    | Sequence 1307, Ap   |
| 404 | 17 | 1.7 | 236 | 21 | US-09-540-229-15848  | Sequence 15848, A                 | 477 | 17 | 1.7 | 253 | 36 | US-60-044-847-1796    | Sequence 1796, Ap   |
| 405 | 17 | 1.7 | 236 | 41 | US-60-099-523-2212   | Sequence 2212, Ap                 | 478 | 17 | 1.7 | 253 | 36 | US-60-044-847-1803    | Sequence 1803, Ap   |
| 406 | 17 | 1.7 | 237 | 12 | US-08-859-945-4119   | Sequence 4119, Ap                 | 479 | 17 | 1.7 | 255 | 14 | US-09-015-080-1921    | Sequence 1921, Ap   |
| 407 | 17 | 1.7 | 238 | 11 | US-08-731-034-2116   | Sequence 2116, Ap                 | 480 | 17 | 1.7 | 255 | 16 | US-09-252-691-4939    | Sequence 4939, Ap   |
| 408 | 17 | 1.7 | 238 | 21 | US-09-540-733-1091   | Sequence 1091, Ap                 | 481 | 17 | 1.7 | 255 | 16 | US-09-252-691C-4939   | Sequence 4939, Ap   |
| 409 | 17 | 1.7 | 238 | 22 | US-09-594-596-2285   | Sequence 2285, Ap                 | 482 | 17 | 1.7 | 255 | 21 | US-09-540-212A-20606  | Sequence 20606, A   |
| 410 | 17 | 1.7 | 238 | 25 | US-09-654-617-44888  | Sequence 44888, A                 | 483 | 17 | 1.7 | 256 | 19 | US-09-522-304-3687    | Sequence 3687, Ap   |
| 411 | 17 | 1.7 | 238 | 27 | US-09-684-016-44888  | Sequence 44888, A                 | 484 | 17 | 1.7 | 257 | 8  | US-08-435-761-1431    | Sequence 1431, Ap   |

|     |    |     |     |    |                      |                     |     |    |     |     |    |                      |                     |
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| 485 | 17 | 1.7 | 257 | 13 | US-08-903-469-1121   | Sequence 1121, Ap   | 558 | 17 | 1.7 | 284 | 22 | US-09-577-410-4954   | Sequence 4954, Ap   |
| 486 | 17 | 1.7 | 257 | 21 | US-09-540-208-10133  | Sequence 10133, A   | 559 | 17 | 1.7 | 284 | 33 | US-60-010-158-56     | Sequence 56, Appl   |
| 487 | 17 | 1.7 | 257 | 23 | US-09-619-643-29916  | Sequence 29916, A   | 560 | 17 | 1.7 | 284 | 40 | US-60-089-804-111    | Sequence 11, Appl   |
| 488 | 17 | 1.7 | 257 | 25 | US-09-654-617-350120 | Sequence 350120, A  | 561 | 17 | 1.7 | 285 | 15 | US-09-149-716B-42    | Sequence 42, Appl   |
| 489 | 17 | 1.7 | 257 | 27 | US-09-684-016-350120 | Sequence 350120, A  | 562 | 17 | 1.7 | 285 | 21 | US-09-540-229-142795 | Sequence 142795, A  |
| 490 | 17 | 1.7 | 257 | 46 | US-60-145-146-3690   | Sequence 3690, Ap   | 563 | 17 | 1.7 | 285 | 21 | US-09-540-499-22079  | Sequence 22079, A   |
| 491 | 17 | 1.7 | 258 | 12 | US-08-865-291-1612   | Sequence 1612, Ap   | 564 | 17 | 1.7 | 286 | 21 | US-09-540-208-69920  | Sequence 69920, A   |
| 492 | 17 | 1.7 | 258 | 13 | US-08-992-868-2604   | Sequence 2604, Ap   | 565 | 17 | 1.7 | 287 | 18 | US-09-411-999-95118  | Sequence 35118, A   |
| 493 | 17 | 1.7 | 258 | 14 | US-09-056-942-1059   | Sequence 1059, Ap   | 566 | 17 | 1.7 | 287 | 18 | US-09-442-384-171    | Sequence 171, Appl  |
| 494 | 17 | 1.7 | 258 | 15 | US-09-100-454-1399   | Sequence 1399, Ap   | 567 | 17 | 1.7 | 287 | 21 | US-09-540-499-21348  | Sequence 21348, Ap  |
| 495 | 17 | 1.7 | 258 | 16 | US-09-231-925-74     | Sequence 74, Appl   | 568 | 17 | 1.7 | 287 | 24 | US-09-637-886-2609   | Sequence 2609, Ap   |
| 496 | 17 | 1.7 | 258 | 20 | US-09-539-801-274    | Sequence 274, Appl  | 569 | 17 | 1.7 | 289 | 14 | US-09-056-942-310    | Sequence 310, Appl  |
| 497 | 17 | 1.7 | 258 | 21 | US-09-540-212A-15521 | Sequence 15521, A   | 570 | 17 | 1.7 | 289 | 16 | US-09-266-640A-1238  | Sequence 1238, Ap   |
| 498 | 17 | 1.7 | 258 | 21 | US-09-540-229-155027 | Sequence 155027, A  | 571 | 17 | 1.7 | 289 | 16 | US-09-266-640B-1238  | Sequence 1238, Ap   |
| 499 | 17 | 1.7 | 258 | 36 | US-60-044-082-1059   | Sequence 1059, Ap   | 572 | 17 | 1.7 | 289 | 17 | US-09-304-517A-2397  | Sequence 2397, Ap   |
| 500 | 17 | 1.7 | 258 | 37 | US-60-051-749-1399   | Sequence 1399, Ap   | 573 | 17 | 1.7 | 289 | 17 | US-09-371-167A-2397  | Sequence 2397, Ap   |
| 501 | 17 | 1.7 | 260 | 11 | US-08-740-370-890    | Sequence 890, Appl  | 574 | 17 | 1.7 | 289 | 21 | US-09-540-212A-40653 | Sequence 40653, A   |
| 502 | 17 | 1.7 | 260 | 32 | US-60-007-127-890    | Sequence 890, Appl  | 575 | 17 | 1.7 | 289 | 36 | US-60-044-082-310    | Sequence 310, Appl  |
| 503 | 17 | 1.7 | 261 | 11 | US-08-731-034-1461   | Sequence 1461, Ap   | 576 | 17 | 1.7 | 289 | 40 | US-60-085-533-782    | Sequence 782, Appl  |
| 504 | 17 | 1.7 | 261 | 21 | US-09-540-733-3422   | Sequence 3422, Ap   | 577 | 17 | 1.7 | 289 | 41 | US-60-092-036-1186   | Sequence 1186, Ap   |
| 505 | 17 | 1.7 | 261 | 32 | US-60-004-674-1461   | Sequence 1461, Ap   | 578 | 17 | 1.7 | 290 | 15 | US-09-167-461-69     | Sequence 69, Appl   |
| 506 | 17 | 1.7 | 262 | 1  | PCT-US01-00663-18726 | Sequence 18726, A   | 579 | 17 | 1.7 | 290 | 21 | US-09-340-766-72119  | Sequence 72119, A   |
| 507 | 17 | 1.7 | 262 | 17 | US-09-304-517A-34575 | Sequence 34575, A   | 580 | 17 | 1.7 | 290 | 52 | US-60-207-458-8822   | Sequence 8822, Ap   |
| 508 | 17 | 1.7 | 262 | 17 | US-09-371-146A-34575 | Sequence 34575, A   | 581 | 17 | 1.7 | 292 | 21 | US-09-540-128-183485 | Sequence 183485, A  |
| 509 | 17 | 1.7 | 263 | 21 | US-09-540-766-70834  | Sequence 70834, A   | 582 | 17 | 1.7 | 293 | 14 | US-09-075-126-1345   | Sequence 1345, Ap   |
| 510 | 17 | 1.7 | 263 | 43 | US-60-111-749-1395   | Sequence 1395, Ap   | 583 | 17 | 1.7 | 293 | 21 | US-09-540-208-49558  | Sequence 49558, A   |
| 511 | 17 | 1.7 | 264 | 5  | US-08-104-507C-6744  | Sequence 6744, Ap   | 584 | 17 | 1.7 | 293 | 36 | US-60-048-726-1345   | Sequence 1345, Ap   |
| 512 | 17 | 1.7 | 264 | 5  | US-08-847-659-1569   | Sequence 6744, Ap   | 585 | 17 | 1.7 | 296 | 14 | US-09-065-511-2345   | Sequence 2345, Ap   |
| 513 | 17 | 1.7 | 264 | 12 | US-08-858-221-2      | Sequence 2, Appl    | 586 | 17 | 1.7 | 296 | 20 | US-09-540-229-186413 | Sequence 186413, A  |
| 514 | 17 | 1.7 | 264 | 14 | US-09-032-271-266    | Sequence 266, Appl  | 587 | 17 | 1.7 | 296 | 31 | US-09-770-175-1043   | Sequence 1043, Ap   |
| 515 | 17 | 1.7 | 264 | 21 | US-09-540-229-74017  | Sequence 74017, A   | 588 | 17 | 1.7 | 298 | 15 | US-09-128-841-1141   | Sequence 1141, Ap   |
| 516 | 17 | 1.7 | 264 | 35 | US-60-038-585-266    | Sequence 266, Appl  | 589 | 17 | 1.7 | 298 | 21 | US-09-540-229-169206 | Sequence 169206, A  |
| 517 | 17 | 1.7 | 267 | 21 | US-09-540-212A-39486 | Sequence 39486, A   | 590 | 17 | 1.7 | 299 | 14 | US-08-083-894-2130   | Sequence 2130, Ap   |
| 518 | 17 | 1.7 | 267 | 50 | US-60-184-777-1059   | Sequence 1059, Ap   | 591 | 17 | 1.7 | 300 | 11 | US-08-731-034-1375   | Sequence 1375, Ap   |
| 519 | 17 | 1.7 | 267 | 50 | US-09-565-309A-2455  | Sequence 2455, Ap   | 592 | 17 | 1.7 | 300 | 14 | US-09-036-591-1707   | Sequence 1707, Ap   |
| 520 | 17 | 1.7 | 272 | 14 | US-09-066-970-532    | Sequence 532, Appl  | 593 | 17 | 1.7 | 300 | 19 | US-09-500-782-921    | Sequence 921, Appl  |
| 521 | 17 | 1.7 | 272 | 36 | US-60-044-798-532    | Sequence 532, Appl  | 594 | 17 | 1.7 | 300 | 21 | US-09-540-723-4263   | Sequence 4263, Ap   |
| 522 | 17 | 1.7 | 273 | 11 | US-08-790-776-3757   | Sequence 3757, Ap   | 595 | 17 | 1.7 | 300 | 32 | US-60-004-674-1375   | Sequence 1375, Ap   |
| 523 | 17 | 1.7 | 273 | 11 | US-08-790-776-3757   | Sequence 3757, Ap   | 596 | 17 | 1.7 | 300 | 32 | US-60-036-549-1707   | Sequence 1707, Appl |
| 524 | 17 | 1.7 | 273 | 17 | US-09-304-517A-38768 | Sequence 38768, A   | 597 | 17 | 1.7 | 300 | 43 | US-60-119-705-971    | Sequence 971, Appl  |
| 525 | 17 | 1.7 | 273 | 17 | US-09-371-146A-38768 | Sequence 38768, A   | 598 | 17 | 1.7 | 301 | 14 | US-09-040-266-1869   | Sequence 1869, Ap   |
| 526 | 17 | 1.7 | 273 | 33 | US-60-010-803-3757   | Sequence 3757, Ap   | 599 | 17 | 1.7 | 301 | 13 | US-08-936-927-1473   | Sequence 1473, Ap   |
| 527 | 17 | 1.7 | 273 | 33 | US-60-033-755-3757   | Sequence 755, Appl  | 600 | 17 | 1.7 | 302 | 15 | US-09-107-909-1196   | Sequence 1196, Ap   |
| 528 | 17 | 1.7 | 273 | 33 | US-60-033-755-3757   | Sequence 755, Appl  | 601 | 17 | 1.7 | 302 | 21 | US-09-540-212A-5492  | Sequence 5492, Ap   |
| 529 | 17 | 1.7 | 275 | 11 | US-08-731-034-1257   | Sequence 1257, Ap   | 602 | 17 | 1.7 | 302 | 32 | US-60-008-131-1473   | Sequence 1473, Ap   |
| 530 | 17 | 1.7 | 275 | 13 | US-08-922-315-1164   | Sequence 1164, Ap   | 603 | 17 | 1.7 | 302 | 32 | US-09-070-694-151    | Sequence 151, Appl  |
| 531 | 17 | 1.7 | 275 | 15 | US-09-167-860-1192   | Sequence 1192, Ap   | 604 | 17 | 1.7 | 303 | 36 | US-60-044-030-151    | Sequence 151, Appl  |
| 532 | 17 | 1.7 | 275 | 21 | US-09-540-733-720    | Sequence 720, Appl  | 605 | 17 | 1.7 | 303 | 14 | US-09-516-278-449    | Sequence 278, Appl  |
| 533 | 17 | 1.7 | 275 | 32 | US-09-004-674-1257   | Sequence 1257, Ap   | 606 | 17 | 1.7 | 307 | 19 | US-09-736-119-880    | Sequence 880, Appl  |
| 534 | 17 | 1.7 | 276 | 15 | US-09-129-789-1389   | Sequence 1389, Ap   | 607 | 17 | 1.7 | 307 | 29 | US-09-042-629-317    | Sequence 317, Appl  |
| 535 | 17 | 1.7 | 276 | 21 | US-09-540-229-167205 | Sequence 167205, A  | 608 | 17 | 1.7 | 309 | 14 | US-09-539-806-10103  | Sequence 10103, A   |
| 536 | 17 | 1.7 | 276 | 21 | US-09-540-766-77676  | Sequence 77676, A   | 609 | 17 | 1.7 | 309 | 20 | US-08-808-443A-2815  | Sequence 2815, Ap   |
| 537 | 17 | 1.7 | 276 | 40 | US-60-085-533-784    | Sequence 784, Appl  | 610 | 17 | 1.7 | 310 | 12 | US-08-880-314-1239   | Sequence 1239, Ap   |
| 538 | 17 | 1.7 | 276 | 41 | US-60-092-036-1115   | Sequence 1115, Ap   | 611 | 17 | 1.7 | 310 | 21 | US-09-540-208-25550  | Sequence 25550, A   |
| 539 | 17 | 1.7 | 276 | 66 | US-60-141-230-731    | Sequence 731, Appl  | 612 | 17 | 1.7 | 310 | 12 | US-60-012-232-2815   | Sequence 2815, Ap   |
| 540 | 17 | 1.7 | 277 | 20 | US-09-539-806-14607  | Sequence 14607, A   | 613 | 17 | 1.7 | 310 | 33 | US-09-325-239-2015   | Sequence 2015, Ap   |
| 541 | 17 | 1.7 | 277 | 21 | US-09-540-766-59323  | Sequence 59323, A   | 614 | 17 | 1.7 | 317 | 17 | US-09-088-762-2015   | Sequence 2015, Ap   |
| 542 | 17 | 1.7 | 278 | 15 | US-09-167-461-124    | Sequence 124, Appl  | 615 | 17 | 1.7 | 317 | 40 | US-09-521-640-9397   | Sequence 9397, A    |
| 543 | 17 | 1.7 | 278 | 21 | US-09-540-766-67184  | Sequence 67184, A   | 616 | 17 | 1.7 | 319 | 19 | US-08-839-968-1234   | Sequence 1234, Ap   |
| 544 | 17 | 1.7 | 280 | 11 | US-08-731-034-1435   | Sequence 1435, Ap   | 617 | 17 | 1.7 | 322 | 16 | US-09-951-198-1234   | Sequence 1234, Ap   |
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| 546 | 17 | 1.7 | 280 | 32 | US-60-004-674-1435   | Sequence 1435, Ap   | 619 | 17 | 1.7 | 322 | 16 | US-09-266-640B-3604  | Sequence 3604, Ap   |
| 547 | 17 | 1.7 | 280 | 49 | US-60-171-431-1826   | Sequence 1826, Ap   | 620 | 17 | 1.7 | 322 | 20 | US-09-539-806-8047   | Sequence 8047, Ap   |
| 548 | 17 | 1.7 | 281 | 12 | US-08-823-505-339    | Sequence 339, Appl  | 621 | 17 | 1.7 | 323 | 24 | US-09-637-086A-10436 | Sequence 10436, A   |
| 549 | 17 | 1.7 | 281 | 16 | US-09-036-310-6450   | Sequence 6450, Appl | 622 | 17 | 1.7 | 326 | 17 | US-09-321-214-6536   | Sequence 6536, Ap   |
| 550 | 17 | 1.7 | 281 | 21 | US-09-294-086A-944   | Sequence 944, Appl  | 623 | 17 | 1.7 | 326 | 17 | US-09-359-067-5584   | Sequence 5584, Ap   |
| 551 | 17 | 1.7 | 281 | 21 | US-09-540-229-19904  | Sequence 19904, A   | 624 | 17 | 1.7 | 326 | 19 | US-09-516-335-4636   | Sequence 4636, Ap   |
| 552 | 17 | 1.7 | 281 | 21 | US-09-540-229-26772  | Sequence 26772, A   | 625 | 17 | 1.7 | 326 | 29 | US-09-733-811-4636   | Sequence 4636, Ap   |
| 553 | 17 | 1.7 | 281 | 40 | US-60-084-492-783    | Sequence 783, Appl  | 626 | 17 | 1.7 | 327 | 53 | US-60-211-750-30344  | Sequence 30344, A   |
| 554 | 17 | 1.7 | 282 | 27 | US-09-654-617-358073 | Sequence 358073, A  | 627 | 17 | 1.7 | 333 | 53 | US-60-217-080-27830  | Sequence 27830, A   |
| 555 | 17 | 1.7 | 282 | 27 | US-09-684-016-358073 | Sequence 358073, A  | 628 | 17 | 1.7 |     |    |                      |                     |
| 556 | 17 | 1.7 | 284 | 11 | US-08-779-625-56     | Sequence 56, Appl   | 629 | 17 | 1.7 |     |    |                      |                     |
| 557 | 17 | 1.7 | 284 | 17 | US-09-325-237-111    | Sequence 111, Appl  | 630 | 17 | 1.7 |     |    |                      |                     |

|       |    |     |     |    |                        |                    |       |    |     |     |    |                        |                    |
|-------|----|-----|-----|----|------------------------|--------------------|-------|----|-----|-----|----|------------------------|--------------------|
| 631   | 17 | 1.7 | 336 | 16 | US-09-271-490-3557     | Sequence 3557, Ap  | C 704 | 17 | 1.7 | 424 | 14 | US-09-076-897C-5766    | Sequence 5766, Ap  |
| C 632 | 17 | 1.7 | 337 | 23 | US-09-606-755-8251     | Sequence 8251, Ap  | C 705 | 17 | 1.7 | 424 | 52 | US-09-208-063-10717    | Sequence 10717, A  |
| C 633 | 17 | 1.7 | 338 | 23 | US-09-606-755-8226     | Sequence 8226, Ap  | C 706 | 17 | 1.7 | 425 | 19 | US-09-528-409-10716    | Sequence 10716, A  |
| C 634 | 17 | 1.7 | 343 | 23 | US-09-605-702-22471    | Sequence 22471, A  | C 707 | 17 | 1.7 | 425 | 25 | US-09-652-911-2079     | Sequence 2079, Ap  |
| C 635 | 17 | 1.7 | 344 | 50 | US-09-605-702-22471    | Sequence 898, App  | C 708 | 17 | 1.7 | 425 | 25 | US-09-654-617-269791   | Sequence 269791, A |
| C 636 | 17 | 1.7 | 348 | 23 | US-09-605-701-11521    | Sequence 11521, A  | C 709 | 17 | 1.7 | 425 | 27 | US-09-684-016-269791   | Sequence 269791, A |
| C 637 | 17 | 1.7 | 362 | 16 | US-09-235-076-37610    | Sequence 37610, A  | C 710 | 17 | 1.7 | 426 | 22 | US-09-572-409-30257    | Sequence 30257, A  |
| C 638 | 17 | 1.7 | 362 | 16 | US-09-277-227-16452    | Sequence 16452, A  | C 711 | 17 | 1.7 | 426 | 50 | US-09-189-657-8116     | Sequence 8116, A   |
| C 639 | 17 | 1.7 | 362 | 17 | US-09-332-782-37610    | Sequence 37610, A  | C 712 | 17 | 1.7 | 427 | 48 | US-09-162-747-1030     | Sequence 1030, Ap  |
| C 640 | 17 | 1.7 | 362 | 29 | US-09-737-223-37610    | Sequence 37610, A  | C 713 | 17 | 1.7 | 429 | 49 | US-09-172-362-136      | Sequence 136, App  |
| C 641 | 17 | 1.7 | 362 | 53 | US-09-431-517-21753    | Sequence 470, App  | C 714 | 17 | 1.7 | 430 | 16 | US-09-234-611-4385     | Sequence 4385, A   |
| C 642 | 17 | 1.7 | 365 | 18 | US-09-431-517-21753    | Sequence 21753, A  | C 715 | 17 | 1.7 | 430 | 16 | US-09-248-799-43363    | Sequence 43363, A  |
| C 643 | 17 | 1.7 | 366 | 18 | US-09-411-999-30766    | Sequence 30766, A  | C 716 | 17 | 1.7 | 430 | 17 | US-09-394-745-52273    | Sequence 52273, A  |
| C 644 | 17 | 1.7 | 368 | 19 | US-09-521-640-94962    | Sequence 94962, A  | C 717 | 17 | 1.7 | 430 | 22 | US-09-565-306-77347    | Sequence 77347, A  |
| C 645 | 17 | 1.7 | 368 | 26 | US-09-666-355A-9679    | Sequence 9679, A   | C 718 | 17 | 1.7 | 432 | 22 | US-09-565-306-83030    | Sequence 83030, A  |
| C 646 | 17 | 1.7 | 372 | 23 | US-09-605-701-4023     | Sequence 4023, Ap  | C 719 | 17 | 1.7 | 435 | 18 | US-09-411-999-28798    | Sequence 28798, A  |
| C 647 | 17 | 1.7 | 373 | 18 | US-09-489-036-31683    | Sequence 31683, A  | C 720 | 17 | 1.7 | 437 | 23 | US-09-606-755-7578     | Sequence 7578, Ap  |
| C 648 | 17 | 1.7 | 377 | 25 | US-09-654-617-161520   | Sequence 161520, A | C 721 | 17 | 1.7 | 441 | 52 | US-09-208-063-2384     | Sequence 2384, Ap  |
| C 649 | 17 | 1.7 | 377 | 27 | US-09-684-016-161520   | Sequence 161520, A | C 722 | 17 | 1.7 | 441 | 18 | US-09-465-877-7634     | Sequence 7634, Ap  |
| C 650 | 17 | 1.7 | 378 | 24 | US-09-637-086A-39732   | Sequence 39732, A  | C 723 | 17 | 1.7 | 444 | 50 | US-09-189-657-13169    | Sequence 13169, A  |
| C 651 | 17 | 1.7 | 379 | 23 | US-09-606-755-7956     | Sequence 7956, Ap  | C 724 | 17 | 1.7 | 445 | 19 | US-09-515-128-21541    | Sequence 21541, A  |
| C 652 | 17 | 1.7 | 380 | 22 | US-09-652-240-49961    | Sequence 49961, A  | C 725 | 17 | 1.7 | 447 | 22 | US-09-572-409-66461    | Sequence 66461, A  |
| C 653 | 17 | 1.7 | 380 | 25 | US-09-652-914-3671     | Sequence 3671, Ap  | C 726 | 17 | 1.7 | 449 | 18 | US-09-411-999-28997    | Sequence 28997, A  |
| C 654 | 17 | 1.7 | 380 | 53 | US-09-217-080-441      | Sequence 441, App  | C 727 | 17 | 1.7 | 450 | 17 | US-09-371-805-5152     | Sequence 5152, Ap  |
| C 655 | 17 | 1.7 | 383 | 17 | US-09-371-805-4794     | Sequence 4794, App | C 728 | 17 | 1.7 | 450 | 17 | US-09-371-805-5152     | Sequence 5152, Ap  |
| C 656 | 17 | 1.7 | 383 | 17 | US-09-371-805-4794     | Sequence 4794, Ap  | C 729 | 17 | 1.7 | 450 | 32 | US-09-207-458-93904    | Sequence 93904, A  |
| C 657 | 17 | 1.7 | 385 | 18 | US-09-431-517-21491    | Sequence 21491, A  | C 730 | 17 | 1.7 | 451 | 19 | US-09-528-409-10717    | Sequence 10717, A  |
| C 658 | 17 | 1.7 | 385 | 51 | US-09-192-739-1665     | Sequence 1665, Ap  | C 731 | 17 | 1.7 | 452 | 22 | US-09-572-409-74513    | Sequence 74513, A  |
| C 659 | 17 | 1.7 | 385 | 51 | US-09-194-243-1220     | Sequence 1220, Ap  | C 732 | 17 | 1.7 | 456 | 25 | US-09-654-617-161371   | Sequence 161371, A |
| C 660 | 17 | 1.7 | 385 | 53 | US-09-217-080-634      | Sequence 634, App  | C 733 | 17 | 1.7 | 456 | 27 | US-09-684-016-161371   | Sequence 161371, A |
| C 661 | 17 | 1.7 | 386 | 17 | US-09-362-510A-14653   | Sequence 14653, A  | C 734 | 17 | 1.7 | 457 | 19 | US-09-528-409-49982    | Sequence 49982, A  |
| C 662 | 17 | 1.7 | 386 | 17 | US-09-362-510A-14653   | Sequence 14653, A  | C 735 | 17 | 1.7 | 457 | 19 | US-09-658-824-1775     | Sequence 1775, A   |
| C 663 | 17 | 1.7 | 391 | 31 | US-09-872-850-160      | Sequence 160, App  | C 736 | 17 | 1.7 | 458 | 26 | US-09-671-302-1775     | Sequence 1775, Ap  |
| C 664 | 17 | 1.7 | 392 | 17 | US-09-359-067-33582    | Sequence 33582, A  | C 737 | 17 | 1.7 | 458 | 28 | US-09-702-709-1775     | Sequence 1775, A   |
| C 665 | 17 | 1.7 | 392 | 17 | US-09-362-510A-59818   | Sequence 59818, A  | C 738 | 17 | 1.7 | 467 | 17 | US-09-736-457-1775     | Sequence 1775, A   |
| C 666 | 17 | 1.7 | 392 | 17 | US-09-362-510A-59818   | Sequence 59818, A  | C 739 | 17 | 1.7 | 468 | 29 | US-09-736-457-1775     | Sequence 1775, A   |
| C 667 | 17 | 1.7 | 393 | 24 | US-09-620-392-1212     | Sequence 1212, Ap  | C 740 | 17 | 1.7 | 466 | 53 | US-09-60-189-657-13068 | Sequence 13068, A  |
| C 668 | 17 | 1.7 | 394 | 51 | US-09-197-872-44698    | Sequence 44698, A  | C 741 | 17 | 1.7 | 467 | 16 | US-09-235-076-23358    | Sequence 23358, A  |
| C 669 | 17 | 1.7 | 395 | 17 | US-09-306-609-2129     | Sequence 2129, Ap  | C 742 | 17 | 1.7 | 467 | 16 | US-09-289-768-31425    | Sequence 31425, A  |
| C 670 | 17 | 1.7 | 395 | 19 | US-09-522-251-2729     | Sequence 2729, Ap  | C 743 | 17 | 1.7 | 467 | 17 | US-09-332-782-26358    | Sequence 26358, A  |
| C 671 | 17 | 1.7 | 397 | 16 | US-09-270-849B-170029  | Sequence 170029, A | C 744 | 17 | 1.7 | 467 | 21 | US-09-540-229-129339   | Sequence 129339, A |
| C 672 | 17 | 1.7 | 398 | 50 | US-09-189-657-15584    | Sequence 15584, A  | C 745 | 17 | 1.7 | 467 | 29 | US-09-737-222-26358    | Sequence 26358, A  |
| C 673 | 17 | 1.7 | 400 | 17 | US-09-321-214-13011    | Sequence 13011, A  | C 746 | 17 | 1.7 | 472 | 1  | PCR-US01-00665-5529    | Sequence 5529, Ap  |
| C 674 | 17 | 1.7 | 400 | 19 | US-09-516-335-13011    | Sequence 13011, A  | C 747 | 17 | 1.7 | 474 | 17 | US-09-306-609-9398     | Sequence 9398, Ap  |
| C 675 | 17 | 1.7 | 400 | 29 | US-09-733-811A-13011   | Sequence 13011, A  | C 748 | 17 | 1.7 | 474 | 18 | US-09-471-277-2507     | Sequence 2507, Ap  |
| C 676 | 17 | 1.7 | 400 | 29 | US-09-733-811A-13011   | Sequence 13011, A  | C 749 | 17 | 1.7 | 474 | 19 | US-09-522-251-9398     | Sequence 9398, Ap  |
| C 677 | 17 | 1.7 | 402 | 16 | US-09-248-797-15681    | Sequence 15681, A  | C 750 | 17 | 1.7 | 493 | 16 | US-09-654-617-198292   | Sequence 198292, A |
| C 678 | 17 | 1.7 | 402 | 17 | US-09-346-956-4316     | Sequence 4316, Ap  | C 751 | 17 | 1.7 | 480 | 23 | US-09-605-669-11378    | Sequence 11378, A  |
| C 679 | 17 | 1.7 | 402 | 18 | US-09-411-999-31282    | Sequence 31282, A  | C 752 | 17 | 1.7 | 480 | 52 | US-09-208-063-4320     | Sequence 4320, Ap  |
| C 680 | 17 | 1.7 | 406 | 22 | US-09-565-309A-2458    | Sequence 2458, Ap  | C 753 | 17 | 1.7 | 487 | 30 | US-09-770-175-4202     | Sequence 4202, Ap  |
| C 681 | 17 | 1.7 | 406 | 23 | US-09-605-701-22331    | Sequence 22331, A  | C 754 | 17 | 1.7 | 490 | 30 | US-09-354-899-7927     | Sequence 7927, Ap  |
| C 682 | 17 | 1.7 | 407 | 18 | US-09-411-999-28380    | Sequence 28380, A  | C 755 | 17 | 1.7 | 493 | 27 | US-09-654-617-198292   | Sequence 198292, A |
| C 683 | 17 | 1.7 | 407 | 45 | US-09-60-133-692-8679  | Sequence 8679, Ap  | C 756 | 17 | 1.7 | 493 | 25 | US-09-684-016-198292   | Sequence 198292, A |
| C 684 | 17 | 1.7 | 410 | 18 | US-09-411-999-28431    | Sequence 28431, A  | C 757 | 17 | 1.7 | 494 | 52 | US-09-60-207-458-91596 | Sequence 91596, A  |
| C 685 | 17 | 1.7 | 411 | 23 | US-09-619-643-8852     | Sequence 8852, Ap  | C 758 | 17 | 1.7 | 496 | 25 | US-09-644-871-485      | Sequence 485, App  |
| C 686 | 17 | 1.7 | 411 | 46 | US-09-145-485-1939     | Sequence 1939, Ap  | C 759 | 17 | 1.7 | 496 | 25 | US-09-644-871-6097     | Sequence 6097, App |
| C 687 | 17 | 1.7 | 412 | 17 | US-09-362-510A-59867   | Sequence 59867, A  | C 760 | 17 | 1.7 | 498 | 17 | US-09-399-932-737      | Sequence 737, App  |
| C 688 | 17 | 1.7 | 412 | 17 | US-09-362-510A-59867   | Sequence 59867, A  | C 761 | 17 | 1.7 | 500 | 25 | US-09-654-617-457215   | Sequence 457215, A |
| C 689 | 17 | 1.7 | 413 | 53 | US-09-217-080-381      | Sequence 381, App  | C 762 | 17 | 1.7 | 500 | 27 | US-09-684-016-457215   | Sequence 457215, A |
| C 690 | 17 | 1.7 | 414 | 14 | US-09-076-617-2752     | Sequence 2752, Ap  | C 763 | 17 | 1.7 | 500 | 52 | US-09-202-213-15267    | Sequence 15267, A  |
| C 691 | 17 | 1.7 | 414 | 17 | US-09-359-067-11090    | Sequence 11090, A  | C 764 | 17 | 1.7 | 501 | 51 | US-09-197-877-4311     | Sequence 4311, Ap  |
| C 692 | 17 | 1.7 | 415 | 16 | US-09-277-227-4209     | Sequence 4209, Ap  | C 765 | 17 | 1.7 | 501 | 25 | US-09-644-871-3216     | Sequence 3216, Ap  |
| C 693 | 17 | 1.7 | 416 | 27 | US-09-698-012-5122     | Sequence 5122, Ap  | C 766 | 17 | 1.7 | 505 | 5  | US-08-196-362A-5377    | Sequence 5377, Ap  |
| C 694 | 17 | 1.7 | 417 | 29 | US-09-726-175-1039     | Sequence 1039, Ap  | C 767 | 17 | 1.7 | 505 | 5  | US-08-196-362A-5377    | Sequence 5377, Ap  |
| C 695 | 17 | 1.7 | 418 | 21 | US-09-540-235-3086     | Sequence 3086, Ap  | C 768 | 17 | 1.7 | 505 | 5  | US-08-196-362A-5377    | Sequence 5377, Ap  |
| C 696 | 17 | 1.7 | 418 | 44 | US-09-60-128-439-4700  | Sequence 4700, Ap  | C 769 | 17 | 1.7 | 505 | 5  | US-08-196-362A-5377    | Sequence 5377, Ap  |
| C 697 | 17 | 1.7 | 418 | 52 | US-09-60-207-458-12481 | Sequence 12481, A  | C 770 | 17 | 1.7 | 505 | 5  | US-08-196-362A-5377    | Sequence 5377, Ap  |
| C 698 | 17 | 1.7 | 419 | 48 | US-09-162-747-6251     | Sequence 6251, Ap  | C 771 | 17 | 1.7 | 506 | 53 | US-09-211-750-8320     | Sequence 8320, Ap  |
| C 699 | 17 | 1.7 | 421 | 19 | US-09-528-409-50541    | Sequence 50541, A  | C 772 | 17 | 1.7 | 513 | 23 | US-09-605-699-16043    | Sequence 16043, A  |
| C 700 | 17 | 1.7 | 423 | 53 | US-09-211-750-81842    | Sequence 81842, A  | C 773 | 17 | 1.7 | 517 | 50 | US-09-182-316-9583     | Sequence 9583, Ap  |
| C 701 | 17 | 1.7 | 424 | 14 | US-09-076-897-5766     | Sequence 5766, Ap  | C 774 | 17 | 1.7 | 521 | 21 | US-09-540-229-117126   | Sequence 117126, A |
| C 702 | 17 | 1.7 | 424 | 14 | US-09-076-897A-5766    | Sequence 5766, Ap  | C 775 | 17 | 1.7 | 522 | 25 | US-09-652-911-8081     | Sequence 8081, Ap  |
| C 703 | 17 | 1.7 | 424 | 14 | US-09-076-897B-5766    | Sequence 5766, Ap  | C 776 | 17 | 1.7 | 522 | 25 | US-09-652-915-3112     | Sequence 3112, Ap  |



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|-------|----|-----|-----|----|----------------------|--------------------|-------|----|-----|------|----|-----------------------|-------------------|
| 777   | 17 | 1.7 | 527 | 22 | US-09-565-309A-6558  | Sequence 6558, Ap  | c 850 | 17 | 1.7 | 681  | 53 | US-60-211-750-89622   | Sequence 89622, A |
| 778   | 17 | 1.7 | 527 | 48 | US-60-169-401-328    | Sequence 328, App  | 851   | 17 | 1.7 | 688  | 51 | US-60-196-718-2863    | Sequence 2863, Ap |
| 779   | 17 | 1.7 | 530 | 17 | US-09-371-805-4613   | Sequence 4613, Ap  | 852   | 17 | 1.7 | 685  | 18 | US-09-496-914A-6289   | Sequence 6289, Ap |
| 780   | 17 | 1.7 | 530 | 17 | US-09-371-805-4613   | Sequence 4613, Ap  | 853   | 17 | 1.7 | 688  | 22 | US-09-560-875A-6289   | Sequence 6289, Ap |
| 781   | 17 | 1.7 | 530 | 25 | US-09-654-617-268058 | Sequence 268058,   | 854   | 17 | 1.7 | 690  | 52 | US-60-208-063-18846   | Sequence 18846, A |
| 782   | 17 | 1.7 | 530 | 27 | US-09-684-016-268058 | Sequence 268058,   | c 855 | 17 | 1.7 | 691  | 28 | US-09-702-134-2532    | Sequence 2532, Ap |
| 783   | 17 | 1.7 | 532 | 17 | US-09-399-932-3851   | Sequence 3851, Ap  | 856   | 17 | 1.7 | 706  | 47 | US-09-699-998-4636    | Sequence 4636, Ap |
| 784   | 17 | 1.7 | 535 | 27 | US-09-698-913-503    | Sequence 503, App  | c 857 | 17 | 1.7 | 724  | 29 | US-60-172-362-3158    | Sequence 3158, Ap |
| 785   | 17 | 1.7 | 536 | 19 | US-09-306-609-9785   | Sequence 9785, Ap  | 858   | 17 | 1.7 | 731  | 1  | PCT-US01-10485A-72    | Sequence 72, Appl |
| 786   | 17 | 1.7 | 536 | 19 | US-09-522-251-9785   | Sequence 9785, Ap  | 859   | 17 | 1.7 | 765  | 22 | US-09-565-309A-53882  | Sequence 53882, A |
| c 787 | 17 | 1.7 | 537 | 23 | US-09-605-701-3566   | Sequence 3566, Ap  | 860   | 17 | 1.7 | 765  | 22 | US-09-565-309A-59495  | Sequence 59495, A |
| c 788 | 17 | 1.7 | 545 | 27 | US-60-136-245-2428   | Sequence 2428, Ap  | 861   | 17 | 1.7 | 778  | 16 | US-09-270-849B-89505  | Sequence 89505, A |
| c 789 | 17 | 1.7 | 549 | 25 | US-09-699-997-6689   | Sequence 6689, Ap  | 862   | 17 | 1.7 | 784  | 16 | US-09-270-849B-160732 | Sequence 160732,  |
| c 790 | 17 | 1.7 | 552 | 1  | PCT-US00-08981-29    | Sequence 29, Appl  | c 863 | 17 | 1.7 | 786  | 18 | US-09-489-039A-1447   | Sequence 1447, Ap |
| 791   | 17 | 1.7 | 554 | 46 | US-60-147-499-1260   | Sequence 1260, Ap  | 864   | 17 | 1.7 | 791  | 16 | US-09-270-849B-115904 | Sequence 115904,  |
| 792   | 17 | 1.7 | 557 | 52 | US-60-209-830-44765  | Sequence 44765, A  | c 865 | 17 | 1.7 | 800  | 1  | PCT-US01-12788-32     | Sequence 32, Appl |
| c 793 | 17 | 1.7 | 560 | 17 | US-09-396-970-2582   | Sequence 2582, Ap  | 866   | 17 | 1.7 | 814  | 25 | US-09-654-617-259009  | Sequence 259009,  |
| 794   | 17 | 1.7 | 560 | 22 | US-09-565-309A-50095 | Sequence 50095, A  | 867   | 17 | 1.7 | 814  | 27 | US-09-684-016-259009  | Sequence 259009,  |
| 795   | 17 | 1.7 | 560 | 52 | US-60-207-458-107719 | Sequence 107719,   | c 868 | 17 | 1.7 | 840  | 1  | PCT-US00-35017A-564   | Sequence 564, App |
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| c 797 | 17 | 1.7 | 562 | 52 | US-60-209-830-44842  | Sequence 44842, A  | 870   | 17 | 1.7 | 876  | 30 | US-09-770-175-3164    | Sequence 3164, Ap |
| 798   | 17 | 1.7 | 567 | 17 | US-09-371-435-110    | Sequence 110, App  | 871   | 17 | 1.7 | 906  | 30 | US-09-770-175-8627    | Sequence 8627, Ap |
| 799   | 17 | 1.7 | 567 | 17 | US-09-371-435-110    | Sequence 110, App  | c 872 | 17 | 1.7 | 957  | 17 | US-09-371-168-7394    | Sequence 7394, Ap |
| 800   | 17 | 1.7 | 567 | 30 | US-09-783-062-110    | Sequence 110, App  | c 873 | 17 | 1.7 | 957  | 25 | US-09-644-870-9050    | Sequence 9050, Ap |
| 801   | 17 | 1.7 | 570 | 50 | US-60-180-489-899    | Sequence 899, App  | c 874 | 17 | 1.7 | 957  | 25 | US-09-644-873-9481    | Sequence 9481, Ap |
| 802   | 17 | 1.7 | 572 | 25 | US-09-654-617-129789 | Sequence 129789,   | c 875 | 17 | 1.7 | 957  | 31 | US-09-801-833-7394    | Sequence 7394, Ap |
| 803   | 17 | 1.7 | 572 | 27 | US-09-684-016-129789 | Sequence 129789,   | 876   | 17 | 1.7 | 997  | 16 | US-09-270-849B-101870 | Sequence 101870,  |
| c 804 | 17 | 1.7 | 572 | 52 | US-60-207-458-129329 | Sequence 129329,   | 877   | 17 | 1.7 | 1015 | 50 | US-60-182-316-483     | Sequence 483, App |
| c 805 | 17 | 1.7 | 573 | 25 | US-09-644-870-6611   | Sequence 6611, Ap  | c 878 | 17 | 1.7 | 1050 | 18 | US-09-417-507-3751    | Sequence 3751, Ap |
| 806   | 17 | 1.7 | 574 | 25 | US-09-649-164-4158   | Sequence 4158, Ap  | c 879 | 17 | 1.7 | 1152 | 16 | US-09-252-991A-13050  | Sequence 13050, A |
| 807   | 17 | 1.7 | 576 | 52 | US-60-209-830-53417  | Sequence 53417, A  | c 880 | 17 | 1.7 | 1170 | 16 | US-09-252-991-3174    | Sequence 3174, Ap |
| 808   | 17 | 1.7 | 579 | 22 | US-09-565-309A-6559  | Sequence 6559, Ap  | c 881 | 17 | 1.7 | 1170 | 16 | US-09-252-691C-3174   | Sequence 3174, Ap |
| c 809 | 17 | 1.7 | 586 | 49 | US-60-171-481-669    | Sequence 669, App  | c 882 | 17 | 1.7 | 1208 | 16 | US-09-270-849B-91034  | Sequence 91034, A |
| 810   | 17 | 1.7 | 588 | 16 | US-09-252-991A-5208  | Sequence 5208, Ap  | 883   | 17 | 1.7 | 1224 | 48 | US-60-164-285-6287    | Sequence 6287, Ap |
| 811   | 17 | 1.7 | 590 | 1  | PCT-US01-01354-391   | Sequence 391, App  | 884   | 17 | 1.7 | 1233 | 16 | US-09-252-991A-13225  | Sequence 13225, A |
| c 812 | 17 | 1.7 | 590 | 49 | US-60-173-469-854    | Sequence 854, App  | 885   | 17 | 1.7 | 1272 | 16 | US-09-565-309A-57226  | Sequence 57226, A |
| c 813 | 17 | 1.7 | 591 | 52 | US-60-207-458-107633 | Sequence 107633,   | 886   | 17 | 1.7 | 1308 | 1  | PCT-US99-03268-158    | Sequence 153, App |
| c 814 | 17 | 1.7 | 592 | 17 | US-09-396-970-1795   | Sequence 1795, Ap  | c 887 | 17 | 1.7 | 1338 | 1  | PCT-US99-03268-158    | Sequence 158, App |
| c 815 | 17 | 1.7 | 594 | 18 | US-09-421-106-25862  | Sequence 25862, A  | c 888 | 17 | 1.7 | 1338 | 13 | US-08-942-341-153     | Sequence 153, App |
| c 816 | 17 | 1.7 | 594 | 19 | US-09-521-640-294493 | Sequence 294493,   | c 889 | 17 | 1.7 | 1338 | 13 | US-08-942-341-153     | Sequence 153, App |
| 817   | 17 | 1.7 | 606 | 49 | US-60-173-462-33     | Sequence 33, Appl  | c 890 | 17 | 1.7 | 1338 | 14 | US-08-942-578-158     | Sequence 158, App |
| 818   | 17 | 1.7 | 606 | 49 | US-60-173-467-104    | Sequence 104, Appl | c 891 | 17 | 1.7 | 1338 | 14 | US-09-024-753-153     | Sequence 153, App |
| 819   | 17 | 1.7 | 606 | 49 | US-60-173-468-574    | Sequence 574, App  | c 892 | 17 | 1.7 | 1338 | 14 | US-09-025-197-158     | Sequence 158, App |
| 820   | 17 | 1.7 | 618 | 22 | US-09-565-309A-2456  | Sequence 2456, Ap  | c 893 | 17 | 1.7 | 1338 | 14 | US-09-056-556-158     | Sequence 158, App |
| 821   | 17 | 1.7 | 618 | 22 | US-09-565-309A-2459  | Sequence 2459, Ap  | c 894 | 17 | 1.7 | 1338 | 14 | US-09-072-596-153     | Sequence 153, App |
| c 822 | 17 | 1.7 | 626 | 25 | US-09-652-911-9642   | Sequence 9642, Ap  | c 895 | 17 | 1.7 | 1338 | 14 | US-09-072-967-158     | Sequence 158, App |
| c 823 | 17 | 1.7 | 628 | 52 | US-60-207-458-112200 | Sequence 112200,   | 896   | 17 | 1.7 | 1363 | 16 | US-09-205-070-14442   | Sequence 14442, A |
| c 824 | 17 | 1.7 | 633 | 16 | US-09-252-691-738    | Sequence 738, App  | 897   | 17 | 1.7 | 1363 | 17 | US-09-340-623-14442   | Sequence 14442, A |
| c 825 | 17 | 1.7 | 633 | 16 | US-09-252-691C-738   | Sequence 738, App  | 898   | 17 | 1.7 | 1368 | 28 | US-09-703-708-9484    | Sequence 9484, A  |
| 826   | 17 | 1.7 | 633 | 25 | US-09-652-814-5442   | Sequence 5442, Ap  | 899   | 17 | 1.7 | 1388 | 48 | US-60-164-320-9484    | Sequence 9484, Ap |
| 827   | 17 | 1.7 | 634 | 48 | US-60-160-189-3870   | Sequence 3870, Ap  | 900   | 17 | 1.7 | 1388 | 50 | US-60-183-791-9484    | Sequence 9484, Ap |
| 828   | 17 | 1.7 | 635 | 25 | US-09-652-915-8555   | Sequence 8555, Ap  | 901   | 17 | 1.7 | 1394 | 25 | US-09-644-869-7333    | Sequence 7333, Ap |
| 829   | 17 | 1.7 | 635 | 52 | US-60-209-830-56824  | Sequence 56824, A  | 902   | 17 | 1.7 | 1394 | 25 | US-09-652-128-7422    | Sequence 7422, Ap |
| 830   | 17 | 1.7 | 636 | 52 | US-60-209-830-50367  | Sequence 50367, A  | 903   | 17 | 1.7 | 1409 | 26 | US-09-668-688-9423    | Sequence 9423, Ap |
| 831   | 17 | 1.7 | 639 | 52 | US-60-209-830-15261  | Sequence 15261, A  | c 904 | 17 | 1.7 | 1461 | 27 | US-09-654-617-267272  | Sequence 267272,  |
| 832   | 17 | 1.7 | 640 | 17 | US-09-399-932-5599   | Sequence 5599, Ap  | c 905 | 17 | 1.7 | 1461 | 27 | US-09-684-016-267272  | Sequence 267272,  |
| 833   | 17 | 1.7 | 648 | 25 | US-09-649-164-8334   | Sequence 8334, Ap  | c 906 | 17 | 1.7 | 1463 | 49 | US-60-172-373-20594   | Sequence 20594, A |
| c 834 | 17 | 1.7 | 655 | 52 | US-60-209-830-47468  | Sequence 47468, A  | 907   | 17 | 1.7 | 1470 | 1  | PCT-US00-03882-429    | Sequence 429, App |
| 841   | 17 | 1.7 | 658 | 17 | US-09-371-752-913    | Sequence 913, App  | 908   | 17 | 1.7 | 1474 | 14 | US-09-001-403-115     | Sequence 115, App |
| 842   | 17 | 1.7 | 673 | 1  | PCT-US99-13151A-4    | Sequence 4, Appl   | 909   | 17 | 1.7 | 1501 | 48 | US-60-164-285-7371    | Sequence 7371, Ap |
| 843   | 17 | 1.7 | 673 | 15 | US-09-185-158-4      | Sequence 4, Appl   | 910   | 17 | 1.7 | 1501 | 48 | US-09-359-922-3391    | Sequence 3391, Ap |
| 844   | 17 | 1.7 | 673 | 18 | US-09-487-441-4      | Sequence 4, Appl   | 917   | 17 | 1.7 | 1563 | 16 | US-09-252-991A-12900  | Sequence 12900, A |
| 845   | 17 | 1.7 | 673 | 26 | US-09-662-270-4      | Sequence 4, Appl   | 918   | 17 | 1.7 | 1647 | 28 | US-09-703-708-2691    | Sequence 2691, Ap |
| c 846 | 17 | 1.7 | 673 | 51 | US-60-196-718-2896   | Sequence 2896, Ap  | 919   | 17 | 1.7 | 1647 | 48 | US-60-164-320-2691    | Sequence 2691, Ap |
| 847   | 17 | 1.7 | 677 | 30 | US-09-770-175-7134   | Sequence 7134, Ap  | 920   | 17 | 1.7 | 1647 | 50 | US-60-183-791-2691    | Sequence 2691, Ap |
| 848   | 17 | 1.7 | 679 | 25 | US-09-654-617-267094 | Sequence 267094,   | 921   | 17 | 1.7 | 1720 | 25 | US-09-644-871-9050    | Sequence 9050, Ap |
| 849   | 17 | 1.7 | 679 | 27 | US-09-684-016-267094 | Sequence 267094,   | c 922 | 17 | 1.7 | 1742 | 27 | US-09-637-886-9347    | Sequence 9347, Ap |



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RESULT 2  
US-09-138-736-1

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: Sequence 1, Application US/09138736
: GENERAL INFORMATION:
: APPLICANT: PARANHOS-BACALA, Glaucia
: APPLICANT: LESENECHAL, Mylene
: APPLICANT: JOLIVET, Michel
: TITLE OF INVENTION: NEW TRYPAOSOMA CRUZI ANTIGEN, AND GENE
: TITLE OF INVENTION: ENCODING THE LATTER: THEIR APPLICATION TO THE DETECTION OF
: TITLE OF INVENTION: CHAGAS DISEASE
: NUMBER OF SEQUENCES: 13
: CORRESPONDENCE ADDRESS:
: ADDRESS: 700 South Washington Street, Suite 300
: CITY: Alexandria
: STATE: Virginia
: COUNTRY: U.S.A.
: ZIP: 22314

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: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/138,736
: FILING DATE:
: CLASSIFICATION:
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: US 08/480,917
: FILING DATE: 07-JUN-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Berridge, William P.
: REGISTRATION NUMBER: 30,024
: REFERENCE/DOCKET NUMBER: WPB 36400
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703-836-6400
: TELEFAX: 703-836-2787
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3402 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: US-09-138-736-1

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Query Match: 100.0%; Score 976; DB 15; Length 3402;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 976; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2132 CTGTCTCTCTCTCGGATTCCTCTCTCGACATCATCGAAGGCGGTGAAGCGTGTGTG 2191
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RESULT 3
US-08-988-242-5
; Sequence 5, Application US/08988242
; GENERAL INFORMATION:
; APPLICANT: PARANHOS-BACCALA, GLAUCIA
; APPLICANT: LESENECHAL, MYLENE
; APPLICANT: JOLIVET, MICHEL
; APPLICANT: MANDRAND, BERNARD
; TITLE OF INVENTION: NEW TRYPANOSOMA CRUZI ANTIGEN, GENE
; TITLE OF INVENTION: ENCODING THEREFOR, AND METHODS OF DETECTING AND TREATING
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OLIVE & BERRIDGE, PLC
; STREET: P.O. BOX 19928
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/988,242
; FILING DATE: 10-DEC-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 36400A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6400
; TELEFAX: 703-836-2787
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-988-242-5
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Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
US-09-138-736-9
; Sequence 9, Application US/09138736
; GENERAL INFORMATION:
; APPLICANT: PARANHOS-BACCALA, GLAUCIA
; APPLICANT: LESENECHAL, MYLENE
; APPLICANT: JOLIVET, MICHEL
; TITLE OF INVENTION: NEW TRYPANOSOMA CRUZI ANTIGEN, AND GENE
; TITLE OF INVENTION: ENCODING THE LATTER, THEIR APPLICATION TO THE DETECTION OF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Olive & Berridge
; STREET: 700 South Washington Street, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/138,736
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,917
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 36400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6400
; TELEFAX: 703-836-2787
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-138-736-9

Query Match 2.3%; Score 22; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 cagcgacggtagctgcgtctc 56
      |||
Db 1 CAGCGACGGTAGCTGCGTCT 22

RESULT 5
US-09-606-977-3519/c
; Sequence 3519, Application US/09606977
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated W
```

```
FILE REFERENCE: 38-21(15877)B
CURRENT APPLICATION NUMBER: US/09/606,977
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 82359
SEQ ID NO 3519
LENGTH: 366
TYPE: DNA
ORGANISM: Zea mays
OTHER INFORMATION: unsure at all n locations
US-09-606-977-3519

Query Match
Best Local Similarity 100.0%; Score 22; DB 23; Length 366;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 810 gatgacagagctgcagcagacg 831
|||||
Db 269 gatgacagagctgcagcagacg 248

RESULT 6
US-08-988-242-6/c
Sequence 6, Application US/08988242
GENERAL INFORMATION:
APPLICANT: PARANHOS-BACCALA, GLAUCIA
APPLICANT: LESENECHAL, MYLENE
APPLICANT: JOLIVET, MICHEL
APPLICANT: MANDRAND, BERNARD
TITLE OF INVENTION: NEW TRYPANOSOMA CRUZI ANTIGEN, GENE
TITLE OF INVENTION: ENCODING THEREFOR, AND METHODS OF DETECTING AND TREATING
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. BOX 19928
CITY: Alexandria
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,242
FILING DATE: 10-DEC-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 36400A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
TELEFAX: 703-836-2787
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-988-242-6

Query Match
Best Local Similarity 100.0%; Score 21; DB 13; Length 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 956 gtgtgacagagcattatgt 976
|||||
Db 21 gtgtgacagagcattatgt 1
```

```
RESULT 7
US-08-988-242-7
Sequence 7, Application US/08988242
GENERAL INFORMATION:
APPLICANT: PARANHOS-BACCALA, GLAUCIA
APPLICANT: LESENECHAL, MYLENE
APPLICANT: JOLIVET, MICHEL
APPLICANT: MANDRAND, BERNARD
TITLE OF INVENTION: NEW TRYPANOSOMA CRUZI ANTIGEN, GENE
TITLE OF INVENTION: ENCODING THEREFOR, AND METHODS OF DETECTING AND TREATING
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. BOX 19928
CITY: Alexandria
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,242
FILING DATE: 10-DEC-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 36400A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
TELEFAX: 703-836-2787
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-988-242-7

Query Match
Best Local Similarity 100.0%; Score 21; DB 13; Length 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 766 cgaagagaccatgaacaactt 786
|||||
Db 1 cgaagagaccatgaacaactt 21

RESULT 8
US-09-138-736-10/c
Sequence 10, Application US/09138736
GENERAL INFORMATION:
APPLICANT: PARANHOS-BACCALA, GLAUCIA
APPLICANT: LESENECHAL, MYLENE
APPLICANT: JOLIVET, MICHEL
APPLICANT: MANDRAND, BERNARD
TITLE OF INVENTION: NEW TRYPANOSOMA CRUZI ANTIGEN, AND GENE
TITLE OF INVENTION: ENCODING THE LATTER, THEIR APPLICATION TO THE DETECTION OF
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oliff & Berridge
STREET: 700 South Washington Street, Suite 300
CITY: Alexandria
STATE: Virginia
COUNTRY: U.S.A.
```

```

; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/138,736
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,917
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: MPB 36400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6400
; TELEFAX: 703-836-2787
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-138-736-10

Query Match      2.2%; Score 21; DB 15; Length 21;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 956 gtgtgaacgagaccattgt 976
    |||||||||||||||||||
DB 21 ctctgaacgagccattatct 1

RESULT 9
; US-09-138-736-12
; Sequence 12, Application US/09138736
; GENERAL INFORMATION:
; APPLICANT: PARANHOS-BACCALA, Glaucia
; APPLICANT: LESENECHAL, Mylene
; APPLICANT: JOLIVET, Michel
; TITLE OF INVENTION: NEW TRYPAOSOMA CRUZI ANTIGEN, AND GENE
; TITLE OF INVENTION: ENCODING THE LATTER; THEIR APPLICATION TO THE DETECTION OF
; TITLE OF INVENTION: CHAGAS DISEASE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oliff & Berridge
; STREET: 700 South Washington Street, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/138,736
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,917
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: MPB 36400
```

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6400
; TELEFAX: 703-836-2787
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-138-736-12

Query Match      2.2%; Score 21; DB 15; Length 21;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 766 cgaagagaccatgaacactt 786
    |||||||||||||||||||
DB 1 CGAAGAGACCATGACCACTT 21

RESULT 10
; US-09-332-782-18690
; Sequence 18690, Application US/09332782
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-754CON1
; CURRENT APPLICATION NUMBER: US/09/332,782
; CURRENT FILING DATE: 1999-06-14
; EARLIER APPLICATION NUMBER: US 09/181,430
; EARLIER FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 21027
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18690
; LENGTH: 391
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-332-782-18690

Query Match      2.0%; Score 20; DB 17; Length 391;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 740 ttctgaagtgcctcccgac 759
    |||||||||||||||||||
DB 353 ttctgaagtgcctcccgac 372

RESULT 11
; US-09-515-694-18690
; Sequence 18690, Application US/09515694
; GENERAL INFORMATION:
; APPLICANT: Arterburn, Matthew
; APPLICANT: Asghari, Vida
; APPLICANT: Blum, Linda
; APPLICANT: Cheung, Patrick
; APPLICANT: Damavandi, Simin
; APPLICANT: Drake, Jim
; APPLICANT: Engleman, Carrie
; APPLICANT: Eymann, Radoje
; APPLICANT: Faulkner, Brandy
; APPLICANT: Fox, Melvin
; APPLICANT: Garcia, Veronica
; APPLICANT: Giedt, Gretchen
; APPLICANT: Jomek, Leni
; APPLICANT: Jones, Lee
; APPLICANT: Kita, David
; APPLICANT: Kotler, Janette
```

APPLICANT: Labat, Ivan  
APPLICANT: Lee, Mon-Jae  
APPLICANT: Lomelli, Michelle  
APPLICANT: Nguyen, Hong  
APPLICANT: Nguyen, Linh  
APPLICANT: Nguyen, Lynne  
APPLICANT: Nguyen, Phuong  
APPLICANT: Nogra, Margie  
APPLICANT: Ojeda, Jesse  
APPLICANT: Palencia, Servando  
APPLICANT: Raisi, Fariba  
APPLICANT: Randhwa, Gurpreet  
APPLICANT: Sahourieh, Hannah  
APPLICANT: Sidhu, Navjwan  
APPLICANT: Smythe, Ashleigh  
APPLICANT: Tkach, Joe  
APPLICANT: Tulpule, Mukul  
APPLICANT: Verna, Ron  
APPLICANT: Wachter, Adam  
APPLICANT: Wu, James  
APPLICANT: Yim, Kenneth  
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
FILE REFERENCE: 754CIP  
CURRENT APPLICATION NUMBER: US/09/515,694  
EARLIER APPLICATION NUMBER: 09/332,782  
EARLIER FILING DATE: 1999-06-14  
EARLIER APPLICATION NUMBER: 09/181,430  
EARLIER FILING DATE: 1998-10-28  
NUMBER OF SEQ ID NOS: 21027  
SOFTWARE: PastSeq for Windows Version 3.0  
SEQ ID NO 18690  
LENGTH: 391  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-515-694-18690

Query Match 2.0%; Score 20; DB 19; Length 391;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 740 ttctgaagtgtctccctgac 759  
|||||  
DB 353 ttctgaagtgtctccctgac 372  
RESULT 12  
US-09-332-782-12269  
Sequence 12269, Application US/09332782  
GENERAL INFORMATION:  
APPLICANT: Hyseq, Inc.  
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
FILE REFERENCE: 20411-754CON1  
CURRENT APPLICATION NUMBER: US/09/332,782  
CURRENT FILING DATE: 1999-06-14  
EARLIER APPLICATION NUMBER: US 09/181,430  
EARLIER FILING DATE: 1998-10-28  
NUMBER OF SEQ ID NOS: 21027  
SOFTWARE: PastSeq for Windows Version 3.0  
SEQ ID NO 12269  
LENGTH: 403  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-332-782-12269

Query Match 2.0%; Score 20; DB 17; Length 403;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 740 ttctgaagtgtctccctgac 759  
|||||  
DB 354 ttctgaagtgtctccctgac 373

RESULT 13  
US-09-515-694-12269  
Sequence 12269, Application US/09515694  
GENERAL INFORMATION:  
APPLICANT: Arterburn, Matthew  
APPLICANT: Asghari, Vida  
APPLICANT: Blum, Linda  
APPLICANT: Cheung, Patrick  
APPLICANT: Damavandi, Simin  
APPLICANT: Dickson, Mark  
APPLICANT: Drake, Jim  
APPLICANT: Drmanac, Radoje  
APPLICANT: Engleman, Carrie  
APPLICANT: Faulkner, Brandy  
APPLICANT: Fox, Melvin  
APPLICANT: Garcia, Veronica  
APPLICANT: Giedl, Gretchen  
APPLICANT: Jomek, Leni  
APPLICANT: Jones, Lee  
APPLICANT: Kita, David  
APPLICANT: Kofler, Janette  
APPLICANT: Labat, Ivan  
APPLICANT: Lee, Mon-Jae  
APPLICANT: Lomelli, Michelle  
APPLICANT: Nguyen, Hong  
APPLICANT: Nguyen, Linh  
APPLICANT: Nguyen, Lynne  
APPLICANT: Nguyen, Phuong  
APPLICANT: Nogra, Margie  
APPLICANT: Ojeda, Jesse  
APPLICANT: Palencia, Servando  
APPLICANT: Raisi, Fariba  
APPLICANT: Randhwa, Gurpreet  
APPLICANT: Sahourieh, Hannah  
APPLICANT: Sidhu, Navjwan  
APPLICANT: Smith, Benjamin  
APPLICANT: Smythe, Ashleigh  
APPLICANT: Tkach, Joe  
APPLICANT: Tulpule, Mukul  
APPLICANT: Verna, Ron  
APPLICANT: Wachter, Adam  
APPLICANT: Wu, James  
APPLICANT: Yim, Kenneth  
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
FILE REFERENCE: 754CIP  
CURRENT APPLICATION NUMBER: US/09/515,694  
CURRENT FILING DATE: 2000-02-29  
EARLIER APPLICATION NUMBER: 09/332,782  
EARLIER FILING DATE: 1999-06-14  
EARLIER APPLICATION NUMBER: 09/181,430  
EARLIER FILING DATE: 1998-10-28  
NUMBER OF SEQ ID NOS: 21027  
SOFTWARE: PastSeq for Windows Version 3.0  
SEQ ID NO 12269  
LENGTH: 403  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-515-694-12269

Query Match 2.0%; Score 20; DB 19; Length 403;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 740 ttctgaagtgtctccctgac 759  
|||||

Db 354 ttctgaagttgctccctgac 373

## RESULT 14

US-09-332-782-12260  
; Sequence 12260, Application US/09332782  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; FILE REFERENCE: 20411-754CON1  
; CURRENT APPLICATION NUMBER: US/09/332,782  
; CURRENT FILING DATE: 1999-06-14  
; EARLIER APPLICATION NUMBER: US 09/181,430  
; EARLIER FILING DATE: 1998-10-28  
; NUMBER OF SEQ ID NOS: 21027  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 12260  
; LENGTH: 408  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(408)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-332-782-12260

Query Match 2.0%; Score 20; DB 17; Length 408;  
Best Local Similarity 100.0%; Pred. No. 15;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 740 ttctgaagttgctccctgac 759  
|||||

Db 354 ttctgaagttgctccctgac 373

## RESULT 15

US-09-515-694-12260  
; Sequence 12260, Application US/09515694  
; GENERAL INFORMATION:  
; APPLICANT: Arterburn, Matthew  
; APPLICANT: Asghari, Vida  
; APPLICANT: Blum, Linda  
; APPLICANT: Cheung, Patrick  
; APPLICANT: Damavandi, Samin  
; APPLICANT: Dickson, Mark  
; APPLICANT: Drake, Jim  
; APPLICANT: Drmanac, Radoje  
; APPLICANT: Engleman, Carlie  
; APPLICANT: Faulkner, Brandy  
; APPLICANT: Fox, Melvin  
; APPLICANT: Garcia, Veronica  
; APPLICANT: Giedt, Gretchen  
; APPLICANT: Jomek, Leol  
; APPLICANT: Jones, Lee  
; APPLICANT: Kita, David  
; APPLICANT: Kofler, Janette  
; APPLICANT: Labat, Ivan  
; APPLICANT: Lee, Won-Jae  
; APPLICANT: Lomelli, Michelle  
; APPLICANT: Nguyen, Hong  
; APPLICANT: Nguyen, Linh  
; APPLICANT: Nguyen, Lynne  
; APPLICANT: Nguyen, Phuong  
; APPLICANT: Nogra, Margie  
; APPLICANT: Ojeda, Jesse  
; APPLICANT: Palencia, Servando  
; APPLICANT: Ralski, Farida  
; APPLICANT: Randhwa, Gurpreet  
; APPLICANT: Sabourieh, Hannah  
; APPLICANT: Sidhu, Navjivan  
; APPLICANT: Smith, Benjamin

; APPLICANT: Smythe, Ashleigh

; APPLICANT: Tkach, Joe

; APPLICANT: Tulpule, Mukul

; APPLICANT: Verna, Ron

; APPLICANT: Wachter, Adam

; APPLICANT: Wu, James

; APPLICANT: Yim, Kenneth

; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; FILE REFERENCE: 754CIP

; CURRENT APPLICATION NUMBER: US/09/515,694

; CURRENT FILING DATE: 2000-02-29

; EARLIER APPLICATION NUMBER: 09/332,782

; EARLIER FILING DATE: 1999-06-14

; EARLIER APPLICATION NUMBER: 09/181,430

; EARLIER FILING DATE: 1998-10-28

; NUMBER OF SEQ ID NOS: 21027

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 12260

; LENGTH: 408

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: (1)...(408)

; OTHER INFORMATION: n = A,T,C or G  
US-09-515-694-12260

Query Match 2.0%; Score 20; DB 19; Length 408;  
Best Local Similarity 100.0%; Pred. No. 15;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 740 ttctgaagttgctccctgac 759  
|||||

Db 354 ttctgaagttgctccctgac 373

## RESULT 16

US-09-654-617-126156  
; Sequence 126156, Application US/09654617  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Liu, Jingdong  
; TITLE OF INVENTION: Annotated Plant Genes  
; FILE REFERENCE: 38-21(15097)D  
; CURRENT APPLICATION NUMBER: US/09/654,617  
; CURRENT FILING DATE: 2000-09-05  
; NUMBER OF SEQ ID NOS: 463173  
; SEQ ID NO 126156  
; LENGTH: 718  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-654-617-126156

Query Match 2.0%; Score 20; DB 25; Length 718;  
Best Local Similarity 100.0%; Pred. No. 15;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 212 ctctgcgcgtgctgac 231  
|||||

Db 586 ctctgcgcgtgctgac 605

## RESULT 17

US-09-684-016-126156  
; Sequence 126156, Application US/09684016  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Liu, Jingdong  
; TITLE OF INVENTION: Annotated Plant Genes  
; FILE REFERENCE: 38-21(15097)D



CURRENT APPLICATION NUMBER: US/09/684,016  
CURRENT FILING DATE: 2000-10-10 US 09/654,617  
PRIOR APPLICATION NUMBER:  
PRIOR FILING DATE: 2000-09-05  
NUMBER OF SEQ ID NOS: 463173  
SEQ ID NO 126156  
LENGTH: 718  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
US-09-684-016-126156

Query Match 2.0%; Score 20; DB 27; Length 718;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 212 ctctgcgcgtcgtcgtcgc 231  
|||||  
Db 586 ctctgcgcgtcgtcgtcgc 605

RESULT 18  
US-09-620-392-64793/c  
Sequence 64793, Application US/09620392  
GENERAL INFORMATION:  
APPLICANT: Boukharov, Andrey A.  
APPLICANT: Kovalic, David K.  
APPLICANT: Liu, Jindong  
TITLE OF INVENTION: Plant Genome Sequence And Uses Thereof  
FILE REFERENCE: 38-21(51237)E  
CURRENT APPLICATION NUMBER: US/09/620,392  
CURRENT FILING DATE: 2000-07-19  
NUMBER OF SEQ ID NOS: 69652  
SEQ ID NO 64793  
LENGTH: 5679  
TYPE: DNA  
ORGANISM: Oryza sativa  
US-09-620-392-64793

Query Match 2.0%; Score 20; DB 24; Length 5679;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 215 ctgcgcgtcgtcgtcgcct 234  
|||||  
Db 3043 CTGCCGCTGTCGATCCCT 3024

RESULT 19  
US-09-702-134-21010/c  
Sequence 21010, Application US/09702134  
GENERAL INFORMATION:  
APPLICANT: Boukharov, Andrey A.  
APPLICANT: Cao, Yongwei  
APPLICANT: Kovalic, David K.  
APPLICANT: Liu, Jindong  
APPLICANT: McIninch, James  
TITLE OF INVENTION: Plant Genome Sequence and Uses Thereof  
FILE REFERENCE: 38-21(51237)F  
CURRENT APPLICATION NUMBER: US/09/702,134  
CURRENT FILING DATE: 2000-10-31  
NUMBER OF SEQ ID NOS: 52202  
SEQ ID NO 21010  
LENGTH: 5679  
TYPE: DNA  
ORGANISM: Oryza sativa  
US-09-702-134-21010

Query Match 2.0%; Score 20; DB 28; Length 5679;

Best Local Similarity 100.0%; Pred. No. 16;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 215 ctgcgcgtcgtcgtcgcct 234  
|||||  
Db 3043 CTGCCGCTGTCGATCCCT 3024

RESULT 20  
US-60-173-464-11355  
Sequence 11355, Application US/60173464  
GENERAL INFORMATION:  
APPLICANT: Li, Peter W.D.  
TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS AND USES  
TITLE OF INVENTION: THEREOF  
FILE REFERENCE: CLO00173  
CURRENT APPLICATION NUMBER: US/60/173,464  
CURRENT FILING DATE: 1999-12-29  
NUMBER OF SEQ ID NOS: 30269  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 11355  
LENGTH: 11355  
TYPE: DNA  
ORGANISM: Drosophila  
US-60-173-464-11355

Query Match 2.0%; Score 20; DB 49; Length 11335;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 50 ggcctcgtcgtcgtcgtcgtc 69  
|||||  
Db 6835 ggcctcgtcgtcgtcgtcgtc 6854

RESULT 21  
US-60-191-637-13953/c  
Sequence 13953, Application US/60191637  
GENERAL INFORMATION:  
APPLICANT: Venter, J. Craig  
TITLE OF INVENTION: NUCLEIC ACID DETECTION KITS COMPRISING  
TITLE OF INVENTION: GENE SEQUENCES EXPRESSED FROM THE DROSOPHILA GENOME, AND  
TITLE OF INVENTION: USES THEREOF  
FILE REFERENCE: CLO00392  
CURRENT APPLICATION NUMBER: US/60/191,637  
CURRENT FILING DATE: 2000-03-23  
NUMBER OF SEQ ID NOS: 42660  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 13953  
LENGTH: 11335  
TYPE: DNA  
ORGANISM: DROSOPHILA  
US-60-191-637-13953

Query Match 2.0%; Score 20; DB 51; Length 11335;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 50 ggcctcgtcgtcgtcgtcgtc 69  
|||||  
Db 4501 GGCCTCTGCTGATGTCG 4482

RESULT 22  
US-60-191-681-10986/c  
Sequence 10986, Application US/60191681  
GENERAL INFORMATION:  
APPLICANT: Li, Peter, W.D.  
TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC  
TITLE OF INVENTION: ACID MOLECULES ENCODING ISOLATED DROSOPHILA PROTEINS AND



```
US-09-620-392-32691
; Sequence 32691, Application US/09620392
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: McIninch, James
; TITLE OF INVENTION: Plant Genome Sequence And Uses Thereof
; FILE REFERENCE: 38-21(51237)E
; CURRENT APPLICATION NUMBER: US/09/620,392
; CURRENT FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 69652
; SEQ ID NO 32691
; LENGTH: 9855
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-620-392-32691

Query Match
Best Local Similarity 1.9%; Score 19; DB 24; Length 9855;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 387 gccggccacgacgaggtct 405
    |||
Db 259 gccggccacgacgaggtct 277

RESULT 28
US-09-620-392-67713
; Sequence 67713, Application US/09620392
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: McIninch, James
; TITLE OF INVENTION: Plant Genome Sequence And Uses Thereof
; FILE REFERENCE: 38-21(51237)E
; CURRENT APPLICATION NUMBER: US/09/620,392
; CURRENT FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 69652
; SEQ ID NO 67713
; LENGTH: 9895
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-620-392-67713

Query Match
Best Local Similarity 1.9%; Score 19; DB 24; Length 9895;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 387 gccggccacgacgaggtct 405
    |||
Db 8100 gccggccacgacgaggtct 8118

RESULT 29
US-09-407-562-32/C
; Sequence 32, Application US/09407562
; GENERAL INFORMATION:
; APPLICANT: Katheryn Meek
; TITLE OF INVENTION: Genetic Test For Equine Severe
; TITLE OF INVENTION: Combined Immunodeficiency Disease
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dr. Benjamin A. Adler
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77071
; COMPUTER READABLE FORM:
```

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/407,562
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/970,269
; FILING DATE: November 14, 1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler Ph.D., Benjamin A.
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D5860
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-777-2321
; TELEFAX: 713-777-6908
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11873 bp
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: other nucleic acid
; HYPOTHETICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; FEATURE:
US-09-407-562-32
```

```
Query Match
Best Local Similarity 1.9%; Score 19; DB 18; Length 11873;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 211 actctgcgctgtctgcat 229
    |||
Db 6446 actctgcgctgtctgcat 6428

RESULT 30
US-09-407-562-31/C
; Sequence 31, Application US/09407562
; GENERAL INFORMATION:
; APPLICANT: Katheryn Meek
; TITLE OF INVENTION: Genetic Test For Equine Severe
; TITLE OF INVENTION: Combined Immunodeficiency Disease
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dr. Benjamin A. Adler
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/407,562
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/970,269
; FILING DATE: November 14, 1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler Ph.D., Benjamin A.
```

```

:
:   REGISTRATION NUMBER: 35,423
:   REFERENCE/DOCKET NUMBER: D5860
:   TELECOMMUNICATION INFORMATION:
:   TELEPHONE: 713-777-2321
:   TELEFAX: 713-777-6908
:   INFORMATION FOR SEQ ID NO: 31:
:   SEQUENCE CHARACTERISTICS:
:   LENGTH: 11878 bp
:   TYPE: nucleic acid
:   STRANDEDNESS: double stranded
:   TOPOLOGY: linear
:   MOLECULE TYPE:
:   DESCRIPTION: other nucleic acid
:   HYPOTHETICAL: no
:   ANTI-SENSE: no
:   ORIGINAL SOURCE:
:   FEATURE:
:
: US-09-407-562-31

```

```

Query Match      1.9%; Score 19; DB 18; Length 11878;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 211 actctgcgcgtcgtcat 229
|||||
DB 6446 ACTCTGCCGCTGCTGCAT 6428

```

```

RESULT 31
US-09-407-562-28/C
: Sequence 28, Application US/09407562
:
:   GENERAL INFORMATION:
:   APPLICANT: Kathryn Meek
:   TITLE OF INVENTION: Genetic Test For Equine Severe
:   TITLE OF INVENTION: Combined Immunodeficiency Disease
:   NUMBER OF SEQUENCES: 32
:   CORRESPONDENCE ADDRESS:
:   ADDRESSEE: Dr. Benjamin A. Adler
:   STREET: 8011 Candle Lane
:   CITY: Houston
:   STATE: Texas
:   COUNTRY: USA
:   ZIP: 77071
:
:   COMPUTER READABLE FORM:
:   MEDIUM TYPE: Floppy disk
:   COMPUTER: Apple
:   OPERATING SYSTEM: Macintosh
:   SOFTWARE: Microsoft Word for Macintosh
:   CURRENT APPLICATION DATA:
:   APPLICATION NUMBER: US/09/407,562
:   FILING DATE:
:   CLASSIFICATION:
:   PRIOR APPLICATION DATA:
:   APPLICATION NUMBER: 08/970,269
:   FILING DATE: November 14, 1997
:   CLASSIFICATION:
:   ATTORNEY/AGENT INFORMATION:
:   NAME: Adler Ph.D., Benjamin A.
:   REGISTRATION NUMBER: 35,423
:   REFERENCE/DOCKET NUMBER: D5860
:   TELECOMMUNICATION INFORMATION:
:   TELEPHONE: 713-777-2321
:   TELEFAX: 713-777-6908
:   INFORMATION FOR SEQ ID NO: 28:
:   SEQUENCE CHARACTERISTICS:
:   LENGTH: 11883 bp
:   TYPE: nucleic acid
:   STRANDEDNESS: double stranded
:   TOPOLOGY: linear
:   MOLECULE TYPE:
:   DESCRIPTION: other nucleic acid
:   HYPOTHETICAL: no

```

```

:   ANTI-SENSE: no
:   ORIGINAL SOURCE:
:
: US-09-407-562-28

```

```

Query Match      1.9%; Score 19; DB 18; Length 11883;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 211 actctgcgcgtcgtcat 229
|||||
DB 6449 ACTTGTGCCGCTGCTGCAT 6431

```

```

RESULT 32
US-09-620-392-10632/C
: Sequence 10632, Application US/09620392
:
:   GENERAL INFORMATION:
:   APPLICANT: Boukharov, Andrey A.
:   APPLICANT: Kovalic, David K.
:   APPLICANT: Liu, Jingdong
:   APPLICANT: McIninch, James
:   TITLE OF INVENTION: Plant Genome Sequence And Uses Thereof
:   FILE REFERENCE: 38-21(51237)E
:   CURRENT APPLICATION NUMBER: US/09/620,392
:   CURRENT FILING DATE: 2000-07-19
:   NUMBER OF SEQ ID NOS: 69652
:   SEQ ID NO 10632
:   LENGTH: 19505
:   TYPE: DNA
:   ORGANISM: Oryza sativa
:
: US-09-620-392-10632

```

```

Query Match      1.9%; Score 19; DB 24; Length 19505;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 387 gccgcgcacgacgagctc 405
|||||
DB 19008 GCCGCCACGACGAGCTCT 18990

```

```

RESULT 33
US-09-620-392-4251/C
: Sequence 4251, Application US/09620392
:
:   GENERAL INFORMATION:
:   APPLICANT: Boukharov, Andrey A.
:   APPLICANT: Kovalic, David K.
:   APPLICANT: Liu, Jingdong
:   APPLICANT: McIninch, James
:   TITLE OF INVENTION: Plant Genome Sequence And Uses Thereof
:   FILE REFERENCE: 38-21(51237)E
:   CURRENT APPLICATION NUMBER: US/09/620,392
:   CURRENT FILING DATE: 2000-07-19
:   NUMBER OF SEQ ID NOS: 69652
:   SEQ ID NO 4251
:   LENGTH: 25670
:   TYPE: DNA
:   ORGANISM: Oryza sativa
:   OTHER INFORMATION: unsure at all n locations
:
: US-09-620-392-4251

```

```

Query Match      1.9%; Score 19; DB 24; Length 25670;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 387 gccgcgcacgacgagctc 405
|||||
DB 3582 GCCGCCACGACGAGCTCT 3564

```

```
RESULT 34
US-09-702-134-5295/c
: Sequence 5295, Application US/09702134
: GENERAL INFORMATION:
: APPLICANT: Boukharov, Andrey A.
: APPLICANT: Cao, Yongwei
: APPLICANT: Kovalic, David K.
: APPLICANT: Liu, Jindong
: APPLICANT: McIninch, James
: APPLICANT: Wu, Mei
: TITLE OF INVENTION: Plant Genome Sequence and Uses Thereof
: FILE REFERENCE: 38-21(51237)F
: CURRENT APPLICATION NUMBER: US/09/702.134
: CURRENT FILING DATE: 2000-10-31
: NUMBER OF SEQ ID NOS: 52202
: SEQ ID NO 5295
: LENGTH: 31556
: TYPE: DNA
: ORGANISM: Oryza sativa
: FEATURE:
: NAME/KEY: unsure
: LOCATION: (1)..(31556)
: OTHER INFORMATION: unsure at all n locations
US-09-702-134-5295

Query Match 1.9%; Score 19; DB 28; Length 31556;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 387 gccggccacgacgaggtct 405
|||||
DB 9468 GCCGCCACGACGAGGTCT 9450

RESULT 35
US-09-702-134-5301
: Sequence 5301, Application US/09702134
: GENERAL INFORMATION:
: APPLICANT: Boukharov, Andrey A.
: APPLICANT: Cao, Yongwei
: APPLICANT: Kovalic, David K.
: APPLICANT: Liu, Jindong
: APPLICANT: McIninch, James
: APPLICANT: Wu, Mei
: TITLE OF INVENTION: Plant Genome Sequence and Uses Thereof
: FILE REFERENCE: 38-21(51237)F
: CURRENT APPLICATION NUMBER: US/09/702.134
: CURRENT FILING DATE: 2000-10-31
: NUMBER OF SEQ ID NOS: 52202
: SEQ ID NO 5301
: LENGTH: 159989
: TYPE: DNA
: ORGANISM: Oryza sativa
US-09-702-134-5301

Query Match 1.9%; Score 19; DB 28; Length 159989;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 387 gccggccacgacgaggtct 405
|||||
DB 32451 gccggccacgacgaggtct 32469

RESULT 36
US-08-988-242-4/c
: Sequence 4, Application US/08988242
: GENERAL INFORMATION:
: APPLICANT: PARANHOS-BACCALA, GLAUCIA
: APPLICANT: LESENECHAL, MYLENE
: APPLICANT: JOLIVET, MICHEL
```

```
APPLICANT: MANDRAND, BERNARD
: TITLE OF INVENTION: NEW TRYPAPOSOMA CRUZI ANTIGEN, GENE
: TITLE OF INVENTION: ENCODING THEREFOR, AND METHODS OF DETECTING AND TREATING
: TITLE OF INVENTION: CHAGAS DISEASE
: NUMBER OF SEQUENCES: 19
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: OLIFF & BERRIDGE, PLC
: STREET: P.O. BOX 19928
: CITY: Alexandria
: STATE: Virginia
: COUNTRY: U.S.A.
: ZIP: 22314
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/988.242
: FILING DATE: 10-DEC-1997
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Berridge, William P.
: REGISTRATION NUMBER: 30,024
: REFERENCE/DOCKET NUMBER: MPB 36400A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703-836-6400
: TELEFAX: 703-836-2787
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 18 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
US-08-988-242-4

Query Match 1.8%; Score 18; DB 13; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 211 actctgcgcgcctcgtca 228
|||||
DB 18 ACTTCTGCCGCTGCTGCA 1

RESULT 37
US-09-138-736-5
: Sequence 5, Application US/09138736
: GENERAL INFORMATION:
: APPLICANT: PARANHOS-BACCALA, GLAUCIA
: APPLICANT: LESENECHAL, MYLENE
: APPLICANT: JOLIVET, MICHEL
: TITLE OF INVENTION: NEW TRYPAPOSOMA CRUZI ANTIGEN, AND GENE
: TITLE OF INVENTION: ENCODING THE LATTER; THEIR APPLICATION TO THE DETECTION OF
: TITLE OF INVENTION: CHAGAS DISEASE
: NUMBER OF SEQUENCES: 13
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Oliff & Berridge
: STREET: 700 South Washington Street, Suite 300
: CITY: Alexandria
: STATE: Virginia
: COUNTRY: U.S.A.
: ZIP: 22314
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/138.736
: FILING DATE:
```

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/480,917  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Berridge, William P.  
REGISTRATION NUMBER: 30,024  
REFERENCE/DOCKET NUMBER: WPB 36400  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6400  
TELEFAX: 703-836-2787  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-138-736-5

Query Match 1.8%; Score 18; DB 15; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 tcggcgactgagcgagcg 189  
|||||  
DB 1 TCGGCGACTGATCGCGCG 18

RESULT 38  
US-09-138-736-8/c  
Sequence 8, Application US/09138736  
GENERAL INFORMATION:  
APPLICANT: PARANHOS-BACCALA, Glaucia  
APPLICANT: LESENECHAL, Mylene  
APPLICANT: JOLIVET, Michel  
TITLE OF INVENTION: NEW TRYPAOSOMA CRUZI ANTIGEN, AND GENE  
TITLE OF INVENTION: ENCODING THE LATTER; THEIR APPLICATION TO THE DETECTION OF  
TITLE OF INVENTION: CHAGAS DISEASE  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Oliff & Berridge  
STREET: 700 South Washington Street, Suite 300  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22314  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/138,736  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/480,917  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Berridge, William P.  
REGISTRATION NUMBER: 30,024  
REFERENCE/DOCKET NUMBER: WPB 36400  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6400  
TELEFAX: 703-836-2787  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)  
US-09-138-736-8

Query Match 1.8%; Score 18; DB 15; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 211 actctgcgcgtgcatgcc 228  
|||||  
DB 18 ACTCTGCGCGCTGCTGCA 1

RESULT 39  
US-09-366-691A-1504/c  
Sequence 1504, Application US/09366691A  
GENERAL INFORMATION:  
APPLICANT: Rosen, Craig A., et al.  
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products. 38  
FILE REFERENCE: PO-38  
CURRENT APPLICATION NUMBER: US/09/366,691A  
CURRENT FILING DATE: 1999-08-04  
PRIOR APPLICATION NUMBER: 60/095,485  
PRIOR FILING DATE: 1998-08-05  
NUMBER OF SEQ ID NOS: 8319  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1504  
LENGTH: 70  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (10)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (60)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (65)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (70)  
OTHER INFORMATION: n equals a,t,g, or c  
US-09-366-691A-1504

Query Match 1.8%; Score 18; DB 17; Length 70;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 216 tcgcgctgtcatccccc 233  
|||||  
DB 31 TCGCGCTGCTGATCCGCC 14

RESULT 40  
US-09-076-667-928/c  
Sequence 928, Application US/09076667  
GENERAL INFORMATION:  
APPLICANT: Gooding, Douglas H.  
APPLICANT: Stuve, Laura L.  
APPLICANT: Stuart, Susan G.  
APPLICANT: Ito, Laura Y.  
APPLICANT: Akerblom, Ingrid E.  
APPLICANT: Deleageane, Angelo M.  
APPLICANT: Naughton, Rebecca E.  
APPLICANT: Klingler, Tod M.  
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM  
TITLE OF INVENTION: HUMAN BRAIN  
NUMBER OF SEQUENCES: 4483  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE

CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/076,667  
FILING DATE:  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: CERRONE, MICHAEL C.  
REGISTRATION NUMBER: 39,132  
REFERENCE/DOCKET NUMBER: PD-0370P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 855-0555  
TELEFAX: (415) 845-4166  
INFORMATION FOR SEQ ID NO: 928:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 85 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
IMMEDIATE SOURCE:  
CLONE: 3244053H1  
US-09-076-667-928

Query Match 1.8%; Score 18; DB 14; Length 85;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 111 agaacagcagccagcca 128  
|||||  
DB 29 AGAACAGCAGCCAGGCCA 12

RESULT 41  
US-09-540-229-15688/C  
Sequence 15688, Application US/09540229  
GENERAL INFORMATION:  
APPLICANT: Seilhamer, Jeffrey J.  
APPLICANT: Delegeane, Angelo M.  
APPLICANT: Stuart, Susan G.  
APPLICANT: Stuve, Laura L.  
APPLICANT: Mullaby, Sara J.  
APPLICANT: Naughton, Rebecca E.  
TITLE OF INVENTION: POLYNUCLEOTIDES OF NERVOUS SYSTEM AND SENSORY ORGANS  
FILE REFERENCE: PD-1033 CIP  
CURRENT APPLICATION NUMBER: US/09/540,229  
CURRENT FILING DATE: 2000-03-31  
Prior application data removed - refer to PALM or file wrapper  
NUMBER OF SEQ ID NOS: 193582  
SOFTWARE: PERL Program  
SEQ ID NO 15688  
LENGTH: 85  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc-feature  
OTHER INFORMATION: Incyte ID NO: hu00290743  
NAME/KEY: unsure  
LOCATION: 3, 81  
OTHER INFORMATION: a, t, c, g, or other  
US-09-540-229-15688

Query Match 1.8%; Score 18; DB 21; Length 85;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 111 agaacagcagccagcca 128  
|||||  
DB 29 AGAACAGCAGCCAGGCCA 12

RESULT 42  
US-60-048-002-928/C  
Sequence 928, Application US/60048002  
GENERAL INFORMATION:  
APPLICANT: Gooding, Douglas H.  
APPLICANT: Stuve, Laura L.  
APPLICANT: Stuart, Susan G.  
APPLICANT: Ito, Laura Y.  
APPLICANT: Akerblom, Ingrid E.  
APPLICANT: Delegeane, Angelo M.  
APPLICANT: Naughton, Rebecca E.  
APPLICANT: Klingler, Tod M.  
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM  
TITLE OF INVENTION: HUMAN BRAIN  
NUMBER OF SEQUENCES: 483  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/60/048,002  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: CERRONE, MICHAEL C.  
REGISTRATION NUMBER: 39,132  
REFERENCE/DOCKET NUMBER: PD-0370P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 855-0555  
TELEFAX: (415) 845-4166  
INFORMATION FOR SEQ ID NO: 928:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 85 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
IMMEDIATE SOURCE:  
CLONE: 3244053H1  
US-60-048-002-928

Query Match 1.8%; Score 18; DB 36; Length 85;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 agaacagcagccagcca 128  
|||||  
DB 29 AGAACAGCAGCCAGGCCA 12

RESULT 43  
US-09-513-991-2039  
Sequence 2039, Application US/09513991  
GENERAL INFORMATION:  
APPLICANT: Gearing, David P.  
APPLICANT: Fraser, Christopher C.  
APPLICANT: Holtzman, Douglas A.

```

; APPLICANT: Jakubowski, Joseph A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM
; FILE REFERENCE: 1600.1083-001
; CURRENT APPLICATION NUMBER: US/09/513,991
; EARLIER FILING DATE: 2000-03-08
; EARLIER APPLICATION NUMBER: 60/123,397
; NUMBER OF SEQ ID NOS: 3378
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2039
; LENGTH: 180
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(180)
; OTHER INFORMATION: n - A,T,C or G
US-09-513-991-2039

```

```

Query Match
Best Local Similarity 1.8%; Score 18; DB 19; Length 180;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 92 tcgcgtctccgcgcagg 109
|||||
DB 1 tcgcgtctccgcgcagg 18

```

```

RESULT 44
US-09-654-617-141143/c
; Sequence 141143, Application US/09654617
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)D
; CURRENT APPLICATION NUMBER: US/09/654,617
; CURRENT FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 463173
; SEQ ID NO 141143
; LENGTH: 194
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-654-617-141143

```

```

Query Match
Best Local Similarity 1.8%; Score 18; DB 25; Length 194;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 930 caacatcacgaaggggt 947
|||||
DB 178 CAACATCAGCAGAGGGGT 161

```

```

RESULT 45
US-09-684-016-141143/c
; Sequence 141143, Application US/09684016
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)D
; CURRENT APPLICATION NUMBER: US/09/684,016
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/654,617
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 463173
; SEQ ID NO 141143
; LENGTH: 194
; TYPE: DNA

```

```

; ORGANISM: Arabidopsis thaliana
US-09-684-016-141143

```

```

Query Match
Best Local Similarity 1.8%; Score 18; DB 27; Length 194;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 930 caacatcacgaaggggt 947
|||||
DB 178 CAACATCAGCAGAGGGGT 161

```

```

RESULT 46
US-09-654-617-162528/c
; Sequence 162528, Application US/09654617
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)D
; CURRENT APPLICATION NUMBER: US/09/654,617
; CURRENT FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 463173
; SEQ ID NO 162528
; LENGTH: 196
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana columbia
US-09-654-617-162528

```

```

Query Match
Best Local Similarity 1.8%; Score 18; DB 25; Length 196;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 930 caacatcacgaaggggt 947
|||||
DB 153 CAACATCAGCAGAGGGGT 136

```

```

RESULT 47
US-09-684-016-162528/c
; Sequence 162528, Application US/09684016
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)D
; CURRENT APPLICATION NUMBER: US/09/684,016
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/654,617
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 463173
; SEQ ID NO 162528
; LENGTH: 196
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana columbia
US-09-684-016-162528

```

```

Query Match
Best Local Similarity 1.8%; Score 18; DB 27; Length 196;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 930 caacatcacgaaggggt 947
|||||
DB 153 CAACATCAGCAGAGGGGT 136

```

```

RESULT 48
US-09-654-617-141154/c
; Sequence 141154, Application US/09654617
; GENERAL INFORMATION:

```



APPLICANT: Kovalic, David K.  
APPLICANT: Liu, Jindong  
TITLE OF INVENTION: Annotated Plant Genes  
FILE REFERENCE: 38-21(15097)D  
CURRENT APPLICATION NUMBER: US/09/654,617  
CURRENT FILING DATE: 2000-09-05  
NUMBER OF SEQ ID NOS: 463173  
SEQ ID NO 141154  
LENGTH: 217  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
US-09-654-617-141154

Query Match 1.8%: Score 18; DB 25; Length 217;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 930 caacatcacgaaggggt 947  
|||||  
DB 168 CAACATCAGGAAGGGGT 151

RESULT 49  
US-09-684-016-141154/C  
Sequence 141154, Application US/09684016  
GENERAL INFORMATION:  
APPLICANT: Kovalic, David K.  
APPLICANT: Liu, Jindong  
TITLE OF INVENTION: Annotated Plant Genes  
FILE REFERENCE: 38-21(15097)D  
CURRENT APPLICATION NUMBER: US/09/684,016  
CURRENT FILING DATE: 2000-10-10  
PRIOR APPLICATION NUMBER: US 09/654,617  
PRIOR FILING DATE: 2000-09-05  
NUMBER OF SEQ ID NOS: 463173  
SEQ ID NO 141154  
LENGTH: 217  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
US-09-684-016-141154

Query Match 1.8%: Score 18; DB 27; Length 217;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 930 caacatcacgaaggggt 947  
|||||  
DB 168 CAACATCAGGAAGGGGT 151

RESULT 50  
US-08-810-326-2151/C  
Sequence 2151, Application US/08810326  
GENERAL INFORMATION:  
APPLICANT: Gooding, Douglas H.  
APPLICANT: Stuve, Laura L.  
APPLICANT: Stuart, Susan G.  
APPLICANT: Ito, Laura Y.  
APPLICANT: Akerblom, Ingrid E.  
APPLICANT: Delegeane, Angelo M.  
APPLICANT: Naughton, Rebecca E.  
APPLICANT: Kingler, Tod M.  
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM  
TITLE OF INVENTION: HUMAN LUNG  
NUMBER OF SEQUENCES: 3314  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA

ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/810,326  
FILING DATE: HERWITH  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/012,699  
FILING DATE: FEBRUARY 29, 1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/015,173  
FILING DATE: APRIL 10, 1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: CERRONE, MICHAEL C.  
REGISTRATION NUMBER: 39,132  
REFERENCE/DOCKET NUMBER: PD-0121 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 855-0555  
TELEFAX: (415) 845-4166  
INFORMATION FOR SEQ ID NO: 2151:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 234 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: 765907  
US-08-810-326-2151

Query Match 1.8%: Score 18; DB 12; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 gtagctgcgtcctgctg 61  
|||||  
DB 136 GTAGCTGCGTCTGCTG 119

Search completed: September 21, 2001, 16:22:20  
Job time: 9685 sec

---

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 21, 2001, 13:33:10 : Search time 393.89 Seconds  
(without alignments)  
4951.220 Million cell updates/sec

Title: US-09-138-735-1\_COPY\_1232\_2207

Perfect score: 976

Sequence: 1 caggtacacgcgtacgcgtt.....ttgtgaacagcgcatatgt 976

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 1746710 seqs, 999096356 residues

Word size: 0

Total number of hits satisfying chosen parameters: 3493420

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

Pending\_Patents\_NA\_New:\*  
1: /cgnl\_7/ptodata/1/pna/PCR\_NEW\_COMB.seq:\*  
2: /cgnl\_7/ptodata/1/pna/US06\_NEW\_COMB.seq:\*  
3: /cgnl\_7/ptodata/1/pna/US07\_NEW\_COMB.seq:\*  
4: /cgnl\_7/ptodata/1/pna/US08\_NEW\_COMB.seq:\*  
5: /cgnl\_7/ptodata/1/pna/US09\_NEW\_COMB.seq:\*  
6: /cgnl\_7/ptodata/1/pna/US09\_NEW\_COMB.seq1:\*  
7: /cgnl\_7/ptodata/1/pna/US09\_NEW\_COMB.seq2:\*  
8: /cgnl\_7/ptodata/1/pna/US60\_NEW\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description         |
|------------|-------|-------------|--------|-------|---------------------|
| 1          | 976   | 100.0       | 3402   | 6     | US-09-138-735-1     |
| 2          | 22    | 2.3         | 22     | 6     | US-09-138-735-9     |
| 3          | 21    | 2.2         | 21     | 6     | US-09-138-735-10    |
| 4          | 21    | 2.2         | 21     | 6     | US-09-138-735-12    |
| 5          | 20    | 2.0         | 91470  | 6     | US-09-803-736-19    |
| 6          | 18    | 1.8         | 18     | 6     | US-09-138-735-5     |
| 7          | 18    | 1.8         | 18     | 6     | US-09-138-735-8     |
| 8          | 18    | 1.8         | 261    | 6     | US-09-866-555-4980  |
| 9          | 18    | 1.8         | 297    | 7     | US-09-863-524-3874  |
| 10         | 18    | 1.8         | 328    | 6     | US-09-764-891-1027  |
| 11         | 18    | 1.8         | 348    | 7     | US-09-540-213-5492  |
| 12         | 18    | 1.8         | 371    | 6     | US-09-667-188A-4578 |
| 13         | 18    | 1.8         | 378    | 6     | US-09-804-730-6853  |
| 14         | 18    | 1.8         | 380    | 8     | US-60-255-619-14255 |
| 15         | 18    | 1.8         | 468    | 7     | US-09-864-761-52    |
| 16         | 18    | 1.8         | 476    | 6     | US-09-904-809-19378 |
| 17         | 18    | 1.8         | 476    | 6     | US-09-909-627-11623 |
| 18         | 18    | 1.8         | 478    | 7     | US-09-864-761-16893 |
| 19         | 18    | 1.8         | 506    | 7     | US-09-840-145-13709 |
| 20         | 18    | 1.8         | 1431   | 8     | US-60-312-544-4166  |
| 21         | 18    | 1.8         | 1485   | 1     | PCR-US01-16450-789  |
| 22         | 18    | 1.8         | 1595   | 7     | US-09-867-716-17510 |
| 23         | 18    | 1.8         | 2817   | 6     | US-09-836-472-1298  |
| 24         | 18    | 1.8         | 15270  | 7     | US-09-764-905-28829 |
| 25         | 18    | 1.8         | 15270  | 7     | US-09-764-905-40566 |

|    |    |     |        |   |                     |                    |
|----|----|-----|--------|---|---------------------|--------------------|
| 26 | 18 | 1.8 | 62271  | 6 | US-09-803-736-1271  | Sequence 1271, Ap  |
| 27 | 18 | 1.8 | 78596  | 6 | US-09-803-736-896   | Sequence 896, Ap   |
| 28 | 18 | 1.8 | 87045  | 6 | US-09-803-736-1270  | Sequence 1270, Ap  |
| 29 | 18 | 1.8 | 91470  | 6 | US-09-803-736-19    | Sequence 19, Appl  |
| 30 | 18 | 1.8 | 96424  | 6 | US-09-803-736-1397  | Sequence 1397, Ap  |
| 31 | 18 | 1.8 | 110684 | 6 | US-09-803-736-1100  | Sequence 1100, Ap  |
| 32 | 17 | 1.7 | 88     | 8 | US-60-253-456-35126 | Sequence 35126, A  |
| 33 | 17 | 1.7 | 119    | 8 | US-60-253-457-47464 | Sequence 47464, A  |
| 34 | 17 | 1.7 | 216    | 7 | US-09-853-369-3951  | Sequence 3951, Ap  |
| 35 | 17 | 1.7 | 236    | 8 | US-60-253-457-6119  | Sequence 4199, Ap  |
| 36 | 17 | 1.7 | 239    | 8 | US-60-253-457-16116 | Sequence 26116, A  |
| 37 | 17 | 1.7 | 241    | 7 | US-09-724-671-17298 | Sequence 17298, A  |
| 38 | 17 | 1.7 | 241    | 7 | US-09-540-213-32685 | Sequence 52685, A  |
| 39 | 17 | 1.7 | 250    | 8 | US-60-253-457-27422 | Sequence 27422, A  |
| 40 | 17 | 1.7 | 262    | 7 | US-09-864-761-27318 | Sequence 27318, A  |
| 41 | 17 | 1.7 | 264    | 7 | US-09-540-213-44587 | Sequence 44587, A  |
| 42 | 17 | 1.7 | 268    | 8 | US-60-253-456-17545 | Sequence 17545, A  |
| 43 | 17 | 1.7 | 273    | 7 | US-09-912-292-45542 | Sequence 45542, A  |
| 44 | 17 | 1.7 | 276    | 8 | US-60-253-378-16751 | Sequence 16751, A  |
| 45 | 17 | 1.7 | 278    | 8 | US-60-253-457-27422 | Sequence 27422, A  |
| 46 | 17 | 1.7 | 279    | 8 | US-60-253-457-35043 | Sequence 35043, A  |
| 47 | 17 | 1.7 | 280    | 7 | US-09-724-750-1826  | Sequence 1826, Ap  |
| 48 | 17 | 1.7 | 289    | 7 | US-09-863-524-1238  | Sequence 1238, Ap  |
| 49 | 17 | 1.7 | 291    | 8 | US-60-253-457-35140 | Sequence 35140, A  |
| 50 | 17 | 1.7 | 300    | 7 | US-09-540-213-33702 | Sequence 33702, A  |
| 51 | 17 | 1.7 | 301    | 7 | US-09-724-671-8427  | Sequence 8427, Ap  |
| 52 | 17 | 1.7 | 303    | 7 | US-09-724-671-8448  | Sequence 8448, Ap  |
| 53 | 17 | 1.7 | 320    | 8 | US-60-253-457-46950 | Sequence 46950, A  |
| 54 | 17 | 1.7 | 321    | 8 | US-60-253-378-15959 | Sequence 15959, A  |
| 55 | 17 | 1.7 | 321    | 8 | US-60-253-457-10039 | Sequence 10039, A  |
| 56 | 17 | 1.7 | 322    | 7 | US-09-863-524-3604  | Sequence 3604, Ap  |
| 57 | 17 | 1.7 | 323    | 6 | US-09-796-692-4879  | Sequence 4879, Ap  |
| 58 | 17 | 1.7 | 331    | 8 | US-60-253-456-17152 | Sequence 17152, Ap |
| 59 | 17 | 1.7 | 335    | 8 | US-60-253-457-34545 | Sequence 34545, A  |
| 60 | 17 | 1.7 | 348    | 8 | US-60-253-378-16268 | Sequence 16268, A  |
| 61 | 17 | 1.7 | 353    | 7 | US-09-724-671-5748  | Sequence 5748, Ap  |
| 62 | 17 | 1.7 | 362    | 6 | US-09-909-627-16452 | Sequence 16452, A  |
| 63 | 17 | 1.7 | 365    | 8 | US-60-253-457-26768 | Sequence 26768, A  |
| 64 | 17 | 1.7 | 388    | 8 | US-60-253-457-43470 | Sequence 43470, A  |
| 65 | 17 | 1.7 | 396    | 7 | US-09-724-671-8945  | Sequence 4945, Ap  |
| 66 | 17 | 1.7 | 398    | 6 | US-09-804-730-15348 | Sequence 15348, A  |
| 67 | 17 | 1.7 | 399    | 6 | US-60-253-457-3369  | Sequence 3369, Ap  |
| 68 | 17 | 1.7 | 402    | 6 | US-09-904-703-4316  | Sequence 4316, Ap  |
| 69 | 17 | 1.7 | 404    | 6 | US-09-866-555-6918  | Sequence 6918, Ap  |
| 70 | 17 | 1.7 | 415    | 6 | US-09-909-627-4209  | Sequence 4209, Ap  |
| 71 | 17 | 1.7 | 419    | 7 | US-09-692-257A-6664 | Sequence 6664, Ap  |
| 72 | 17 | 1.7 | 426    | 6 | US-09-804-730-8033  | Sequence 8033, Ap  |
| 73 | 17 | 1.7 | 427    | 7 | US-09-692-257A-1034 | Sequence 1034, Ap  |
| 74 | 17 | 1.7 | 430    | 6 | US-09-904-809-4385  | Sequence 4385, Ap  |
| 75 | 17 | 1.7 | 431    | 8 | US-60-253-457-44718 | Sequence 44718, A  |
| 76 | 17 | 1.7 | 433    | 7 | US-09-861-757-3357  | Sequence 3357, Ap  |
| 77 | 17 | 1.7 | 444    | 6 | US-09-804-730-13175 | Sequence 13175, A  |
| 78 | 17 | 1.7 | 444    | 6 | US-09-906-555-7634  | Sequence 7634, Ap  |
| 79 | 17 | 1.7 | 444    | 6 | US-09-724-671-4408  | Sequence 4408, Ap  |
| 80 | 17 | 1.7 | 458    | 6 | US-09-849-626-1775  | Sequence 1775, Ap  |
| 81 | 17 | 1.7 | 458    | 7 | US-09-902-941-1755  | Sequence 1755, Ap  |
| 82 | 17 | 1.7 | 466    | 6 | US-09-804-730-13074 | Sequence 13074, A  |
| 83 | 17 | 1.7 | 468    | 6 | US-09-758-463-219   | Sequence 219, Ap   |
| 84 | 17 | 1.7 | 472    | 7 | US-09-864-761-10670 | Sequence 10670, A  |
| 85 | 17 | 1.7 | 474    | 7 | US-09-881-797-3356  | Sequence 3356, Ap  |
| 86 | 17 | 1.7 | 481    | 8 | US-60-253-652-24408 | Sequence 24408, A  |
| 87 | 17 | 1.7 | 492    | 6 | US-09-823-241-6683  | Sequence 6683, Ap  |
| 88 | 17 | 1.7 | 498    | 8 | US-60-253-457-23050 | Sequence 23050, A  |
| 89 | 17 | 1.7 | 500    | 7 | US-09-850-147-15830 | Sequence 15830, A  |
| 90 | 17 | 1.7 | 501    | 6 | US-09-83-366-4311   | Sequence 4311, Ap  |
| 91 | 17 | 1.7 | 514    | 6 | US-09-758-463-239   | Sequence 239, Ap   |
| 92 | 17 | 1.7 | 562    | 7 | US-09-821-837-41107 | Sequence 4107, Ap  |
| 93 | 17 | 1.7 | 571    | 6 | US-09-655-125A-6941 | Sequence 6941, Ap  |
| 94 | 17 | 1.7 | 575    | 7 | US-09-824-518-6780  | Sequence 6780, Ap  |
| 95 | 17 | 1.7 | 588    | 8 | US-60-253-457-22558 | Sequence 22558, A  |
| 96 | 17 | 1.7 | 590    | 7 | US-09-764-905-391   | Sequence 391, Ap   |
| 97 | 17 | 1.7 | 591    | 8 | US-60-253-457-22533 | Sequence 22533, A  |
| 98 | 17 | 1.7 | 594    | 6 | US-09-823-241-9297  | Sequence 9297, Ap  |

|       |    |     |        |   |                      |                    |       |    |     |     |   |                      |                    |
|-------|----|-----|--------|---|----------------------|--------------------|-------|----|-----|-----|---|----------------------|--------------------|
| C 99  | 17 | 1.7 | 604    | 8 | US-60-253-457-22414  | Sequence 22414, A  | C 172 | 16 | 1.6 | 236 | 7 | US-09-863-524-4502   | Sequence 4502, Ap  |
| C 100 | 17 | 1.7 | 607    | 7 | US-09-824-518-6753   | Sequence 6753, Ap  | 173   | 16 | 1.6 | 236 | 8 | US-60-253-378-35947  | Sequence 35947, A  |
| C 101 | 17 | 1.7 | 615    | 8 | US-60-279-526-973    | Sequence 973, App  | 174   | 16 | 1.6 | 239 | 8 | US-60-253-378-35896  | Sequence 35896, A  |
| C 102 | 17 | 1.7 | 643    | 7 | US-09-823-327-3506   | Sequence 3606, Ap  | 175   | 16 | 1.6 | 241 | 7 | US-09-853-369-7623   | Sequence 7623, Ap  |
| C 103 | 17 | 1.7 | 697    | 6 | US-09-623-746A-60    | Sequence 60, Appl  | 176   | 16 | 1.6 | 245 | 7 | US-09-540-213-10234  | Sequence 10234, Ap |
| C 104 | 17 | 1.7 | 721    | 1 | PCT-US01-08631-9801  | Sequence 9801, Ap  | 177   | 16 | 1.6 | 245 | 7 | US-09-877-486-3251   | Sequence 3251, Ap  |
| C 105 | 17 | 1.7 | 781    | 1 | PCT-US01-08631-9802  | Sequence 9802, Ap  | 178   | 16 | 1.6 | 255 | 8 | US-60-253-457-34193  | Sequence 34193, A  |
| C 106 | 17 | 1.7 | 790    | 6 | US-09-883-152-20     | Sequence 20, Appl  | 179   | 16 | 1.6 | 275 | 7 | US-09-912-292-52592  | Sequence 52592, A  |
| C 107 | 17 | 1.7 | 812    | 8 | US-60-278-561-2143   | Sequence 2143, Ap  | 180   | 16 | 1.6 | 279 | 7 | US-09-853-366-1403   | Sequence 1403, Ap  |
| C 108 | 17 | 1.7 | 944    | 1 | PCT-US01-08631-535   | Sequence 535, App  | 181   | 16 | 1.6 | 283 | 7 | US-09-540-213-15809  | Sequence 15809, Ap |
| C 109 | 17 | 1.7 | 954    | 1 | PCT-US01-18569-775   | Sequence 775, App  | 182   | 16 | 1.6 | 285 | 7 | US-09-859-490-835    | Sequence 835, App  |
| C 110 | 17 | 1.7 | 1269   | 1 | PCT-US01-08631-10338 | Sequence 10338, A  | 183   | 16 | 1.6 | 288 | 8 | US-60-253-457-47688  | Sequence 47688, A  |
| C 111 | 17 | 1.7 | 1342   | 8 | US-60-278-561-7253   | Sequence 7263, Ap  | 184   | 16 | 1.6 | 290 | 6 | US-09-617-681A-3535  | Sequence 3535, Ap  |
| C 112 | 17 | 1.7 | 1363   | 6 | US-09-898-888-14442  | Sequence 14442, A  | 185   | 16 | 1.6 | 293 | 8 | US-60-252-823-38373  | Sequence 38373, A  |
| C 113 | 17 | 1.7 | 1470   | 1 | PCT-US01-16450-431   | Sequence 431, App  | 186   | 16 | 1.6 | 297 | 7 | US-09-867-716-7328   | Sequence 7328, Ap  |
| C 114 | 17 | 1.7 | 1470   | 5 | US-09-925-301-429    | Sequence 429, App  | 187   | 16 | 1.6 | 302 | 6 | US-09-783-589-1286   | Sequence 1286, Ap  |
| C 115 | 17 | 1.7 | 1513   | 6 | US-09-898-888-7596   | Sequence 7596, Ap  | 188   | 16 | 1.6 | 302 | 7 | US-09-912-292-38493  | Sequence 38493, A  |
| C 116 | 17 | 1.7 | 1518   | 1 | PCT-US01-08631-745   | Sequence 745, App  | 189   | 16 | 1.6 | 306 | 7 | US-09-853-369-3588   | Sequence 3588, Ap  |
| C 117 | 17 | 1.7 | 1707   | 1 | PCT-US01-08631-28984 | Sequence 28984, A  | 190   | 16 | 1.6 | 311 | 7 | US-09-877-486-3861   | Sequence 3861, Ap  |
| C 118 | 17 | 1.7 | 1959   | 8 | US-60-278-561-12846  | Sequence 12846, A  | 191   | 16 | 1.6 | 315 | 6 | US-09-504-576A-12465 | Sequence 12465, A  |
| C 119 | 17 | 1.7 | 1970   | 1 | PCT-US01-08631-21764 | Sequence 21764, A  | 192   | 16 | 1.6 | 315 | 7 | US-09-867-716-6790   | Sequence 6790, Ap  |
| C 120 | 17 | 1.7 | 2205   | 1 | PCT-US01-08631-8851  | Sequence 8851, Ap  | 193   | 16 | 1.6 | 326 | 7 | US-09-724-671-18201  | Sequence 18201, Ap |
| C 121 | 17 | 1.7 | 2211   | 7 | US-09-764-874-12555  | Sequence 12555, A  | 194   | 16 | 1.6 | 328 | 8 | US-60-253-456-26975  | Sequence 26975, A  |
| C 122 | 17 | 1.7 | 2545   | 6 | US-09-849-626-1900   | Sequence 1900, Ap  | 195   | 16 | 1.6 | 328 | 8 | US-09-724-671-4901   | Sequence 4901, Ap  |
| C 123 | 17 | 1.7 | 2545   | 7 | US-09-902-941-1900   | Sequence 1900, Ap  | 196   | 16 | 1.6 | 335 | 7 | US-09-724-671-5022   | Sequence 5022, Ap  |
| C 124 | 17 | 1.7 | 2689   | 7 | US-09-902-540-2831   | Sequence 2831, Ap  | 197   | 16 | 1.6 | 337 | 8 | US-60-253-457-29711  | Sequence 29711, A  |
| C 125 | 17 | 1.7 | 2710   | 6 | US-09-652-125A-9381  | Sequence 9381, Ap  | 198   | 16 | 1.6 | 338 | 7 | US-09-724-671-18461  | Sequence 18461, A  |
| C 126 | 17 | 1.7 | 2914   | 8 | US-60-278-258-10032  | Sequence 10032, A  | 199   | 16 | 1.6 | 346 | 8 | US-60-253-378-39233  | Sequence 39233, Ap |
| C 127 | 17 | 1.7 | 2942   | 6 | US-09-758-440-168    | Sequence 168, App  | 200   | 16 | 1.6 | 349 | 7 | US-09-912-292-8604   | Sequence 8604, Ap  |
| C 128 | 17 | 1.7 | 2975   | 7 | US-09-838-601-3647   | Sequence 3647, Ap  | 201   | 16 | 1.6 | 362 | 7 | US-09-834-366-49569  | Sequence 49569, A  |
| C 129 | 17 | 1.7 | 3103   | 7 | US-09-808-384-986    | Sequence 986, App  | 202   | 16 | 1.6 | 363 | 7 | US-09-724-671-18790  | Sequence 18790, A  |
| C 130 | 17 | 1.7 | 3331   | 5 | US-09-617-746A-8     | Sequence 8, Appl   | 203   | 16 | 1.6 | 369 | 6 | US-09-904-871-12595  | Sequence 12595, A  |
| C 131 | 17 | 1.7 | 3465   | 8 | US-60-278-232-8890   | Sequence 8890, Ap  | 204   | 16 | 1.6 | 371 | 6 | US-09-898-888-12081  | Sequence 12081, A  |
| C 132 | 17 | 1.7 | 3617   | 7 | US-09-764-874-12556  | Sequence 12556, A  | 205   | 16 | 1.6 | 371 | 6 | US-09-866-555-19255  | Sequence 19255, A  |
| C 133 | 17 | 1.7 | 3618   | 7 | US-09-764-874-12554  | Sequence 12554, A  | 206   | 16 | 1.6 | 372 | 8 | US-60-253-378-35457  | Sequence 35457, A  |
| C 134 | 17 | 1.7 | 3690   | 6 | US-09-922-279-1518   | Sequence 1518, Ap  | 207   | 16 | 1.6 | 382 | 8 | US-60-252-833-28803  | Sequence 28803, A  |
| C 135 | 17 | 1.7 | 3764   | 6 | US-09-652-125A-9079  | Sequence 9079, Ap  | 208   | 16 | 1.6 | 383 | 8 | US-60-252-833-28803  | Sequence 28803, A  |
| C 136 | 17 | 1.7 | 3846   | 7 | US-09-902-540-2350   | Sequence 2350, Ap  | 209   | 16 | 1.6 | 387 | 7 | US-09-724-750-24153  | Sequence 24153, A  |
| C 137 | 17 | 1.7 | 4815   | 1 | PCT-US01-08631-24178 | Sequence 24178, A  | 210   | 16 | 1.6 | 396 | 1 | PCT-US01-08631-16672 | Sequence 16672, A  |
| C 138 | 17 | 1.7 | 4815   | 1 | PCT-US01-08631-26102 | Sequence 26102, A  | 211   | 16 | 1.6 | 397 | 6 | US-09-904-703-2778   | Sequence 2778, Ap  |
| C 139 | 17 | 1.7 | 4826   | 8 | US-60-260-483-126    | Sequence 126, App  | 212   | 16 | 1.6 | 400 | 6 | US-09-760-476-768    | Sequence 768, App  |
| C 140 | 17 | 1.7 | 4835   | 8 | US-60-278-258-4418   | Sequence 4418, Ap  | 213   | 16 | 1.6 | 400 | 6 | US-09-909-627-13906  | Sequence 13906, A  |
| C 141 | 17 | 1.7 | 5491   | 1 | PCT-US01-08631-21772 | Sequence 21772, A  | 214   | 16 | 1.6 | 401 | 7 | US-09-850-147-3027   | Sequence 3027, Ap  |
| C 142 | 17 | 1.7 | 6238   | 1 | PCT-US01-08656-4045  | Sequence 4045, Ap  | 215   | 16 | 1.6 | 406 | 6 | US-09-790-435-4023   | Sequence 4023, Ap  |
| C 143 | 17 | 1.7 | 6266   | 8 | US-60-278-232-9933   | Sequence 9933, Ap  | 216   | 16 | 1.6 | 409 | 8 | US-60-253-654-23916  | Sequence 23916, A  |
| C 144 | 17 | 1.7 | 7114   | 6 | US-09-760-457-463    | Sequence 463, App  | 217   | 16 | 1.6 | 410 | 8 | US-60-255-592-32916  | Sequence 32916, A  |
| C 145 | 17 | 1.7 | 7714   | 6 | US-09-760-457-463    | Sequence 463, App  | 218   | 16 | 1.6 | 411 | 8 | US-60-253-456-7084   | Sequence 7084, Ap  |
| C 146 | 17 | 1.7 | 14271  | 1 | PCT-US01-14827-6329  | Sequence 6329, Ap  | 219   | 16 | 1.6 | 411 | 7 | US-09-692-257A-11306 | Sequence 11306, A  |
| C 147 | 17 | 1.7 | 14391  | 1 | PCT-US01-14827-5802  | Sequence 5802, Ap  | 220   | 16 | 1.6 | 412 | 6 | US-09-922-279-1000   | Sequence 1000, Ap  |
| C 148 | 17 | 1.7 | 14301  | 1 | PCT-US01-08631-18513 | Sequence 18513, A  | 221   | 16 | 1.6 | 421 | 7 | US-09-692-257A-6018  | Sequence 6018, Ap  |
| C 149 | 17 | 1.7 | 14464  | 7 | US-09-902-540-1135   | Sequence 1135, Ap  | 222   | 16 | 1.6 | 422 | 7 | US-09-724-750-22736  | Sequence 22736, A  |
| C 150 | 17 | 1.7 | 17503  | 7 | US-09-902-540-1114   | Sequence 1114, Ap  | 223   | 16 | 1.6 | 425 | 7 | US-09-724-750-21484  | Sequence 21484, A  |
| C 151 | 17 | 1.7 | 22259  | 6 | US-09-764-891-7064   | Sequence 7064, Ap  | 224   | 16 | 1.6 | 427 | 6 | US-09-667-188A-1299  | Sequence 1299, Ap  |
| C 152 | 17 | 1.7 | 27804  | 7 | US-09-764-905-41288  | Sequence 41288, A  | 225   | 16 | 1.6 | 431 | 6 | US-09-909-629-35857  | Sequence 35857, A  |
| C 153 | 17 | 1.7 | 32189  | 6 | US-09-764-877-3291   | Sequence 3291, Ap  | 226   | 16 | 1.6 | 432 | 8 | US-60-253-654-6659   | Sequence 6659, Ap  |
| C 154 | 17 | 1.7 | 32189  | 7 | US-09-764-874-8672   | Sequence 8672, Ap  | 227   | 16 | 1.6 | 433 | 8 | US-60-253-592-6659   | Sequence 6659, Ap  |
| C 155 | 17 | 1.7 | 32189  | 7 | US-09-764-874-9823   | Sequence 9823, Ap  | 228   | 16 | 1.6 | 433 | 6 | US-09-909-629-31791  | Sequence 31791, A  |
| C 156 | 17 | 1.7 | 32189  | 7 | US-09-764-874-10121  | Sequence 10121, A  | 229   | 16 | 1.6 | 437 | 7 | US-09-834-366-1534   | Sequence 1534, Ap  |
| C 157 | 17 | 1.7 | 35896  | 6 | US-09-803-736-927    | Sequence 927, App  | 230   | 16 | 1.6 | 437 | 7 | US-09-834-366-32015  | Sequence 32015, A  |
| C 158 | 17 | 1.7 | 46626  | 6 | US-09-803-736-164    | Sequence 164, App  | 231   | 16 | 1.6 | 437 | 7 | US-09-773-476-127    | Sequence 127, App  |
| C 159 | 17 | 1.7 | 88009  | 6 | US-09-803-736-1287   | Sequence 1287, Ap  | 232   | 16 | 1.6 | 441 | 7 | US-09-834-366-3658   | Sequence 3658, A   |
| C 160 | 17 | 1.7 | 88401  | 6 | US-09-803-736-71     | Sequence 71, Appl  | 233   | 16 | 1.6 | 443 | 6 | US-09-909-629-37049  | Sequence 37049, A  |
| C 161 | 17 | 1.7 | 94029  | 6 | US-09-803-736-147    | Sequence 147, Appl | 234   | 16 | 1.6 | 446 | 6 | US-09-909-629-32626  | Sequence 32626, A  |
| C 162 | 17 | 1.7 | 240825 | 6 | US-09-790-289-1      | Sequence 1, Appl1  | 235   | 16 | 1.6 | 450 | 7 | US-09-902-540-2380   | Sequence 2380, Ap  |
| C 163 | 17 | 1.6 | 51     | 8 | US-60-278-232-7294   | Sequence 7294, Ap  | 236   | 16 | 1.6 | 451 | 8 | US-60-253-654-23636  | Sequence 23636, A  |
| C 164 | 16 | 1.6 | 51     | 8 | US-60-278-232-12391  | Sequence 12391, A  | 237   | 16 | 1.6 | 451 | 8 | US-60-255-529-22631  | Sequence 22631, A  |
| C 165 | 16 | 1.6 | 65     | 8 | US-09-908-975-27555  | Sequence 27555, A  | 238   | 16 | 1.6 | 453 | 6 | US-09-909-629-26031  | Sequence 26031, A  |
| C 166 | 16 | 1.6 | 65     | 8 | US-60-287-724-27555  | Sequence 27555, A  | 239   | 16 | 1.6 | 455 | 7 | US-09-843-620-863    | Sequence 863, App  |
| C 167 | 16 | 1.6 | 73     | 8 | US-60-253-457-27555  | Sequence 27555, A  | 240   | 16 | 1.6 | 461 | 7 | US-09-834-366-12022  | Sequence 12022, A  |
| C 168 | 16 | 1.6 | 139    | 7 | US-09-864-761-27193  | Sequence 27193, A  | 241   | 16 | 1.6 | 463 | 6 | US-09-667-188A-2226  | Sequence 2226, Ap  |
| C 169 | 16 | 1.6 | 197    | 6 | US-09-790-435-6810   | Sequence 6810, Ap  | 242   | 16 | 1.6 | 465 | 7 | US-09-692-257A-8032  | Sequence 8032, Ap  |
| C 170 | 16 | 1.6 | 207    | 7 | US-09-540-213-6493   | Sequence 6493, Ap  | 243   | 16 | 1.6 | 467 | 8 | US-60-255-619-6600   | Sequence 6600, Ap  |
| C 171 | 16 | 1.6 | 235    | 7 | US-09-724-671-4868   | Sequence 4868, Ap  | 244   | 16 | 1.6 | 468 | 8 | US-60-255-619-8270   | Sequence 8270, Ap  |

|       |    |     |      |   |                      |                   |       |    |     |       |   |                      |                   |
|-------|----|-----|------|---|----------------------|-------------------|-------|----|-----|-------|---|----------------------|-------------------|
| C 245 | 16 | 1.6 | 470  | 6 | US-09-804-730-22592  | Sequence 22592, A | 318   | 16 | 1.6 | 1146  | 6 | US-09-803-110-2857   | Sequence 2857, Ap |
| C 246 | 16 | 1.6 | 473  | 7 | US-09-864-761-2646   | Sequence 2646, Ap | 319   | 16 | 1.6 | 1178  | 7 | US-09-881-797-4070   | Sequence 4070, Ap |
| C 247 | 16 | 1.6 | 473  | 7 | US-09-821-837-3341   | Sequence 3341, Ap | 320   | 16 | 1.6 | 1213  | 7 | US-09-982-540-3750   | Sequence 3750, Ap |
| C 248 | 16 | 1.6 | 475  | 7 | US-09-834-366-5538   | Sequence 5538, Ap | 321   | 16 | 1.6 | 1236  | 1 | PCT-US01-16450-742   | Sequence 742, Ap  |
| C 249 | 16 | 1.6 | 475  | 8 | US-60-233-652-14468  | Sequence 14468, A | C 322 | 16 | 1.6 | 1238  | 8 | US-60-309-870-58     | Sequence 58, Ap   |
| C 250 | 16 | 1.6 | 476  | 7 | US-09-834-366-29018  | Sequence 29018, A | C 323 | 16 | 1.6 | 1266  | 8 | US-60-279-526-251    | Sequence 251, Ap  |
| C 251 | 16 | 1.6 | 476  | 8 | US-60-253-653-3489   | Sequence 3489, A  | C 324 | 16 | 1.6 | 1267  | 1 | PCT-US01-16450-1306  | Sequence 1306, Ap |
| C 252 | 16 | 1.6 | 482  | 7 | US-09-864-761-10572  | Sequence 10572, A | C 325 | 16 | 1.6 | 1294  | 6 | US-09-898-888-8734   | Sequence 8734, Ap |
| C 253 | 16 | 1.6 | 484  | 8 | US-60-255-619-8590   | Sequence 8590, Ap | C 326 | 16 | 1.6 | 1296  | 7 | US-09-902-540-6682   | Sequence 6682, Ap |
| C 254 | 16 | 1.6 | 486  | 7 | US-09-824-518-5079   | Sequence 5079, Ap | C 327 | 16 | 1.6 | 1318  | 6 | US-09-758-471-362    | Sequence 362, Ap  |
| C 255 | 16 | 1.6 | 487  | 7 | US-09-864-761-5296   | Sequence 5296, Ap | C 328 | 16 | 1.6 | 1324  | 7 | US-09-850-118-1432   | Sequence 1432, Ap |
| C 256 | 16 | 1.6 | 488  | 6 | US-09-652-125A-3022  | Sequence 3022, Ap | C 329 | 16 | 1.6 | 1341  | 6 | US-09-738-626-3482   | Sequence 3482, Ap |
| C 257 | 16 | 1.6 | 488  | 7 | US-09-912-292-43627  | Sequence 43627, A | C 330 | 16 | 1.6 | 1368  | 7 | US-09-902-540-9028   | Sequence 9028, Ap |
| C 258 | 16 | 1.6 | 489  | 7 | US-09-902-540-3851   | Sequence 3851, A  | C 331 | 16 | 1.6 | 1403  | 6 | US-09-760-466-561    | Sequence 561, Ap  |
| C 259 | 16 | 1.6 | 491  | 8 | US-60-252-833-13471  | Sequence 13471, A | C 332 | 16 | 1.6 | 1500  | 1 | PCT-US01-14827-6399  | Sequence 6399, Ap |
| C 260 | 16 | 1.6 | 497  | 6 | US-09-866-555-6172   | Sequence 6172, Ap | C 333 | 16 | 1.6 | 1502  | 7 | US-09-902-540-6160   | Sequence 6160, Ap |
| C 261 | 16 | 1.6 | 499  | 7 | US-09-840-145-4699   | Sequence 4699, Ap | C 334 | 16 | 1.6 | 1504  | 7 | US-09-902-540-301    | Sequence 301, Ap  |
| C 262 | 16 | 1.6 | 501  | 6 | US-09-796-692-4449   | Sequence 4449, Ap | C 335 | 16 | 1.6 | 1572  | 6 | US-09-760-469-116    | Sequence 116, Ap  |
| C 263 | 16 | 1.6 | 503  | 6 | US-09-796-692-5825   | Sequence 5825, Ap | C 336 | 16 | 1.6 | 1668  | 1 | PCT-US01-08631-9677  | Sequence 9677, Ap |
| C 264 | 16 | 1.6 | 507  | 7 | US-09-840-145-11795  | Sequence 11795, A | C 337 | 16 | 1.6 | 1692  | 1 | PCT-US01-08631-22519 | Sequence 22519, A |
| C 265 | 16 | 1.6 | 510  | 7 | US-09-834-366-13222  | Sequence 13222, A | C 338 | 16 | 1.6 | 1729  | 7 | US-60-278-561-7091   | Sequence 7091, Ap |
| C 266 | 16 | 1.6 | 511  | 7 | US-09-850-147-13070  | Sequence 13070, A | C 339 | 16 | 1.6 | 1770  | 7 | US-09-902-540-4547   | Sequence 4547, Ap |
| C 267 | 16 | 1.6 | 517  | 8 | US-60-255-619-14863  | Sequence 14863, A | C 340 | 16 | 1.6 | 1806  | 1 | PCT-US01-08631-27810 | Sequence 27810, A |
| C 268 | 16 | 1.6 | 523  | 8 | US-60-255-619-8610   | Sequence 8610, Ap | C 341 | 16 | 1.6 | 1877  | 8 | US-60-278-232-863    | Sequence 863, Ap  |
| C 269 | 16 | 1.6 | 525  | 7 | US-09-902-540-9559   | Sequence 9559, Ap | C 342 | 16 | 1.6 | 1975  | 6 | US-09-760-466-472    | Sequence 472, Ap  |
| C 270 | 16 | 1.6 | 534  | 6 | US-09-898-888-3145   | Sequence 3145, Ap | C 343 | 16 | 1.6 | 1992  | 1 | PCT-US01-08631-26331 | Sequence 26331, A |
| C 271 | 16 | 1.6 | 542  | 6 | US-60-255-619-10472  | Sequence 10472, A | C 344 | 16 | 1.6 | 2058  | 7 | US-09-758-469-179    | Sequence 179, Ap  |
| C 272 | 16 | 1.6 | 549  | 6 | US-09-504-576A-11777 | Sequence 11777, A | C 345 | 16 | 1.6 | 2066  | 7 | US-09-902-540-357    | Sequence 357, Ap  |
| C 273 | 16 | 1.6 | 553  | 8 | US-60-255-619-5452   | Sequence 5452, Ap | C 346 | 16 | 1.6 | 2140  | 8 | US-60-278-258-11997  | Sequence 11997, A |
| C 275 | 16 | 1.6 | 556  | 6 | US-09-758-471-2563   | Sequence 2563, Ap | C 347 | 16 | 1.6 | 2188  | 6 | US-09-620-3128-409   | Sequence 409, Ap  |
| C 276 | 16 | 1.6 | 560  | 6 | US-09-845-674-428    | Sequence 428, Ap  | C 348 | 16 | 1.6 | 2268  | 1 | PCT-US01-08631-19259 | Sequence 19259, A |
| C 277 | 16 | 1.6 | 563  | 6 | US-09-804-730-6011   | Sequence 6011, Ap | C 349 | 16 | 1.6 | 2275  | 6 | US-09-620-3128-410   | Sequence 410, Ap  |
| C 278 | 16 | 1.6 | 567  | 6 | US-09-758-472-2247   | Sequence 2247, Ap | C 350 | 16 | 1.6 | 2310  | 6 | US-09-603-207-257    | Sequence 25, Ap   |
| C 279 | 16 | 1.6 | 570  | 7 | US-09-861-478-1889   | Sequence 1889, Ap | C 351 | 16 | 1.6 | 2332  | 8 | US-60-278-561-12029  | Sequence 12029, A |
| C 280 | 16 | 1.6 | 585  | 7 | US-09-902-540-5518   | Sequence 5518, Ap | C 352 | 16 | 1.6 | 2332  | 1 | PCT-US01-08631-22380 | Sequence 22380, A |
| C 281 | 16 | 1.6 | 594  | 8 | US-60-255-619-9706   | Sequence 9706, Ap | C 353 | 16 | 1.6 | 2345  | 8 | US-60-278-258-998    | Sequence 4998, Ap |
| C 282 | 16 | 1.6 | 596  | 7 | US-09-861-478-273    | Sequence 273, Ap  | C 354 | 16 | 1.6 | 2424  | 7 | US-09-902-540-4231   | Sequence 4231, Ap |
| C 283 | 16 | 1.6 | 596  | 8 | US-60-253-457-42814  | Sequence 42814, A | C 355 | 16 | 1.6 | 2460  | 1 | PCT-US01-08631-20712 | Sequence 20712, A |
| C 284 | 16 | 1.6 | 598  | 7 | US-09-898-888-1049   | Sequence 1049, Ap | C 356 | 16 | 1.6 | 2550  | 7 | US-09-902-540-8526   | Sequence 8526, Ap |
| C 285 | 16 | 1.6 | 601  | 6 | US-09-861-478-29     | Sequence 29, Ap   | C 357 | 16 | 1.6 | 2688  | 6 | US-09-598-075-154    | Sequence 154, Ap  |
| C 286 | 16 | 1.6 | 601  | 6 | US-09-758-450-458    | Sequence 458, Ap  | C 358 | 16 | 1.6 | 2688  | 6 | US-09-598-075A-154   | Sequence 154, Ap  |
| C 287 | 16 | 1.6 | 614  | 1 | PCT-US01-08656-3926  | Sequence 3926, Ap | C 359 | 16 | 1.6 | 2880  | 8 | US-60-278-232-858    | Sequence 858, Ap  |
| C 288 | 16 | 1.6 | 624  | 8 | US-60-253-378-36331  | Sequence 36331, A | C 360 | 16 | 1.6 | 2891  | 6 | US-60-278-232-858    | Sequence 858, Ap  |
| C 289 | 16 | 1.6 | 624  | 8 | US-60-253-652-11254  | Sequence 11254, A | C 361 | 16 | 1.6 | 2891  | 6 | US-09-602-740-561    | Sequence 561, Ap  |
| C 290 | 16 | 1.6 | 636  | 7 | US-09-834-366-48902  | Sequence 48902, A | C 362 | 16 | 1.6 | 3167  | 1 | PCT-US01-16450-776   | Sequence 776, Ap  |
| C 291 | 16 | 1.6 | 645  | 6 | US-09-834-366-10416  | Sequence 10416, A | C 363 | 16 | 1.6 | 3331  | 6 | US-09-235-810-31     | Sequence 31, Ap   |
| C 292 | 16 | 1.6 | 651  | 6 | US-09-803-110-8094   | Sequence 8094, A  | C 364 | 16 | 1.6 | 3331  | 6 | US-09-373-658-31     | Sequence 31, Ap   |
| C 293 | 16 | 1.6 | 651  | 6 | US-09-738-626-982    | Sequence 982, Ap  | C 365 | 16 | 1.6 | 3342  | 8 | US-60-171-503-31     | Sequence 31, Ap   |
| C 294 | 16 | 1.6 | 660  | 8 | US-60-252-833-27834  | Sequence 27834, A | C 366 | 16 | 1.6 | 3429  | 1 | PCT-US01-08631-29177 | Sequence 29177, A |
| C 295 | 16 | 1.6 | 667  | 7 | US-09-902-540-4299   | Sequence 4299, Ap | C 367 | 16 | 1.6 | 3659  | 6 | US-09-764-864-1568   | Sequence 1568, Ap |
| C 296 | 16 | 1.6 | 703  | 6 | US-09-898-888-1682   | Sequence 1682, Ap | C 368 | 16 | 1.6 | 3659  | 6 | US-09-764-891-7820   | Sequence 7820, Ap |
| C 297 | 16 | 1.6 | 713  | 7 | US-09-861-478-316    | Sequence 316, Ap  | C 369 | 16 | 1.6 | 3684  | 8 | US-60-278-258-6146   | Sequence 6146, Ap |
| C 298 | 16 | 1.6 | 733  | 6 | US-09-845-674-452    | Sequence 452, Ap  | C 370 | 16 | 1.6 | 3718  | 6 | US-09-620-3128-74    | Sequence 74, Ap   |
| C 299 | 16 | 1.6 | 756  | 7 | US-09-902-540-5475   | Sequence 5475, Ap | C 371 | 16 | 1.6 | 3731  | 6 | PCT-US01-14827-6410  | Sequence 6410, Ap |
| C 300 | 16 | 1.6 | 813  | 1 | PCT-US01-08631-17135 | Sequence 17135, A | C 372 | 16 | 1.6 | 3771  | 6 | US-09-738-626-1250   | Sequence 1250, Ap |
| C 301 | 16 | 1.6 | 813  | 1 | PCT-US01-08631-18137 | Sequence 18137, A | C 373 | 16 | 1.6 | 4369  | 6 | US-09-764-891-8870   | Sequence 8870, Ap |
| C 302 | 16 | 1.6 | 852  | 6 | US-09-764-864-285    | Sequence 285, Ap  | C 374 | 16 | 1.6 | 4641  | 1 | PCT-US01-08631-25987 | Sequence 25987, A |
| C 303 | 16 | 1.6 | 852  | 6 | US-09-764-891-1407   | Sequence 1407, Ap | C 375 | 16 | 1.6 | 5228  | 7 | US-09-902-540-789    | Sequence 789, Ap  |
| C 304 | 16 | 1.6 | 876  | 6 | US-09-760-451-93     | Sequence 93, Ap   | C 376 | 16 | 1.6 | 7213  | 7 | US-09-764-905-9933   | Sequence 9933, A  |
| C 305 | 16 | 1.6 | 876  | 6 | US-09-758-471-2206   | Sequence 2206, Ap | C 377 | 16 | 1.6 | 7671  | 8 | US-60-278-232-8827   | Sequence 8827, Ap |
| C 306 | 16 | 1.6 | 909  | 6 | US-09-758-474-223    | Sequence 223, Ap  | C 378 | 16 | 1.6 | 8046  | 1 | PCT-US01-08631-29175 | Sequence 29175, A |
| C 307 | 16 | 1.6 | 919  | 6 | US-09-760-451-45     | Sequence 45, Ap   | C 379 | 16 | 1.6 | 8773  | 7 | US-09-902-540-965    | Sequence 965, Ap  |
| C 308 | 16 | 1.6 | 930  | 7 | US-09-902-540-5570   | Sequence 5570, Ap | C 380 | 16 | 1.6 | 9321  | 7 | US-09-902-540-998    | Sequence 998, Ap  |
| C 309 | 16 | 1.6 | 945  | 7 | US-09-902-540-5859   | Sequence 5859, Ap | C 381 | 16 | 1.6 | 10276 | 7 | US-09-902-540-975    | Sequence 975, Ap  |
| C 310 | 16 | 1.6 | 956  | 6 | US-09-760-466-85     | Sequence 85, Ap   | C 382 | 16 | 1.6 | 10644 | 7 | US-09-902-540-1028   | Sequence 1028, Ap |
| C 311 | 16 | 1.6 | 1017 | 1 | PCT-US01-08656-3925  | Sequence 3925, Ap | C 383 | 16 | 1.6 | 13874 | 6 | US-09-803-376-722    | Sequence 722, Ap  |
| C 312 | 16 | 1.6 | 1020 | 7 | US-09-902-540-3902   | Sequence 3902, Ap | C 384 | 16 | 1.6 | 14898 | 6 | US-09-898-888-8846   | Sequence 8846, Ap |
| C 313 | 16 | 1.6 | 1038 | 6 | US-09-803-110-6914   | Sequence 6914, Ap | C 385 | 16 | 1.6 | 15172 | 7 | US-09-902-540-1086   | Sequence 1086, Ap |
| C 314 | 16 | 1.6 | 1063 | 6 | US-09-898-888-217    | Sequence 217, Ap  | C 386 | 16 | 1.6 | 15651 | 7 | US-09-764-905-56332  | Sequence 56332, A |
| C 315 | 16 | 1.6 | 1070 | 7 | US-09-867-716-17316  | Sequence 17316, A | C 387 | 16 | 1.6 | 16584 | 7 | US-09-902-540-1119   | Sequence 1119, Ap |
| C 316 | 16 | 1.6 | 1089 | 6 | US-09-738-626-1956   | Sequence 1956, Ap | C 388 | 16 | 1.6 | 16924 | 7 | US-09-902-540-1178   | Sequence 1178, Ap |
| C 317 | 16 | 1.6 | 1107 | 8 | US-60-309-870-59     | Sequence 59, Ap   | C 389 | 16 | 1.6 | 17315 | 7 | US-09-902-540-1103   | Sequence 1103, Ap |
|       |    |     |      |   |                      |                   | C 390 | 16 | 1.6 | 17897 | 7 | US-09-902-540-1182   | Sequence 1182, Ap |

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| C 391 | 16 | 1.6 | 18339   | 7 | US-09-881-797-808   | Sequence 808, App  | 464   | 15 | 1.5 | 256 | 7 | US-09-773-476-37    | Sequence 37, Appl  |
| C 392 | 16 | 1.6 | 19222   | 7 | US-09-902-540-1192  | Sequence 1192, Ap  | C 465 | 15 | 1.5 | 256 | 7 | US-09-864-761-18722 | Sequence 18722, A  |
| C 393 | 16 | 1.6 | 20303   | 7 | US-09-902-540-1183  | Sequence 1183, Ap  | C 466 | 15 | 1.5 | 256 | 7 | US-09-540-213-46447 | Sequence 46447, A  |
| C 394 | 16 | 1.6 | 21964   | 7 | US-09-902-540-1190  | Sequence 1190, Ap  | C 467 | 15 | 1.5 | 259 | 7 | US-09-692-254-7708  | Sequence 7708, Ap  |
| C 395 | 16 | 1.6 | 21988   | 6 | US-09-803-736-147   | Sequence 347, App  | C 468 | 15 | 1.5 | 259 | 7 | US-09-540-213-4719  | Sequence 4719, Ap  |
| C 396 | 16 | 1.6 | 22807   | 7 | US-09-902-540-1214  | Sequence 1214, Ap  | C 469 | 15 | 1.5 | 259 | 7 | US-09-540-213-12022 | Sequence 12022, A  |
| C 397 | 16 | 1.6 | 24757   | 6 | US-09-764-868-1347  | Sequence 1347, Ap  | C 470 | 15 | 1.5 | 263 | 7 | US-09-859-490-10688 | Sequence 10688, A  |
| C 398 | 16 | 1.6 | 25497   | 7 | US-09-902-540-1284  | Sequence 1284, Ap  | C 471 | 15 | 1.5 | 264 | 7 | US-09-724-671-10646 | Sequence 10646, A  |
| C 399 | 16 | 1.6 | 29899   | 7 | US-09-902-540-1265  | Sequence 1265, Ap  | C 472 | 15 | 1.5 | 266 | 7 | US-09-855-807-2007  | Sequence 2007, Ap  |
| C 400 | 16 | 1.6 | 39678   | 7 | US-09-764-905-39808 | Sequence 39808, A  | C 473 | 15 | 1.5 | 268 | 7 | US-09-855-807-3146  | Sequence 3146, Ap  |
| C 401 | 16 | 1.6 | 41768   | 7 | US-09-902-540-1286  | Sequence 1286, Ap  | C 474 | 15 | 1.5 | 269 | 7 | US-09-540-213-53081 | Sequence 53081, A  |
| C 402 | 16 | 1.6 | 41927   | 7 | US-09-902-540-1288  | Sequence 1288, Ap  | C 475 | 15 | 1.5 | 269 | 7 | US-09-540-213-53081 | Sequence 53081, A  |
| C 403 | 16 | 1.6 | 76304   | 8 | US-60-299-426-1     | Sequence 1, Appl1  | C 476 | 15 | 1.5 | 269 | 8 | US-60-253-654-7719  | Sequence 7719, Ap  |
| C 404 | 16 | 1.6 | 81662   | 6 | US-09-803-736-951   | Sequence 951, App  | C 477 | 15 | 1.5 | 269 | 8 | US-60-253-654-7719  | Sequence 7719, Ap  |
| C 405 | 16 | 1.6 | 84702   | 6 | US-09-803-736-474   | Sequence 474, App  | C 478 | 15 | 1.5 | 271 | 8 | US-60-253-457-47280 | Sequence 47280, A  |
| C 406 | 16 | 1.6 | 87210   | 6 | US-09-803-736-767   | Sequence 767, App  | C 479 | 15 | 1.5 | 273 | 8 | US-60-252-833-17089 | Sequence 17089, A  |
| C 407 | 16 | 1.6 | 99547   | 6 | US-09-803-736-1121  | Sequence 1121, Ap  | C 480 | 15 | 1.5 | 273 | 8 | US-60-253-653-27807 | Sequence 27807, A  |
| C 408 | 16 | 1.6 | 100887  | 6 | US-09-803-736-1289  | Sequence 1289, Ap  | C 481 | 15 | 1.5 | 274 | 8 | US-60-252-833-35665 | Sequence 35665, A  |
| C 409 | 16 | 1.6 | 101647  | 6 | US-09-803-736-380   | Sequence 380, App  | C 482 | 15 | 1.5 | 276 | 7 | US-09-692-257A-1149 | Sequence 1149, Ap  |
| C 410 | 16 | 1.6 | 101647  | 6 | US-09-803-736-1173  | Sequence 1173, Ap  | C 483 | 15 | 1.5 | 277 | 7 | US-09-850-147-6691  | Sequence 6691, Ap  |
| C 411 | 16 | 1.6 | 112862  | 6 | US-09-803-736-1173  | Sequence 1173, Ap  | C 484 | 15 | 1.5 | 277 | 7 | US-09-850-147-6691  | Sequence 6691, Ap  |
| C 412 | 16 | 1.6 | 114418  | 6 | US-09-803-736-129   | Sequence 129, App  | C 485 | 15 | 1.5 | 277 | 7 | US-09-894-949-6094  | Sequence 6094, Ap  |
| C 413 | 16 | 1.6 | 114505  | 6 | US-09-803-736-100   | Sequence 100, App  | C 486 | 15 | 1.5 | 279 | 8 | US-60-253-653-17410 | Sequence 17410, A  |
| C 414 | 16 | 1.6 | 145744  | 6 | US-09-803-736-1465  | Sequence 1465, Ap  | C 487 | 15 | 1.5 | 281 | 7 | US-09-540-213-19496 | Sequence 19496, A  |
| C 415 | 16 | 1.6 | 165200  | 6 | US-09-803-110-205   | Sequence 205, App  | C 488 | 15 | 1.5 | 282 | 7 | US-09-724-671-14888 | Sequence 14888, A  |
| C 416 | 16 | 1.6 | 186449  | 7 | US-09-881-797-715   | Sequence 715, App  | C 489 | 15 | 1.5 | 282 | 7 | US-09-783-590-7613  | Sequence 7613, Ap  |
| C 417 | 16 | 1.6 | 189268  | 7 | US-09-881-797-715   | Sequence 697, App  | C 490 | 15 | 1.5 | 282 | 7 | US-09-839-976-288   | Sequence 288, App  |
| C 418 | 16 | 1.6 | 206606  | 6 | US-09-803-736-581   | Sequence 581, App  | C 491 | 15 | 1.5 | 282 | 7 | US-09-853-369-6301  | Sequence 6301, Ap  |
| C 419 | 16 | 1.6 | 542340  | 6 | US-09-803-110-219   | Sequence 219, App  | C 492 | 15 | 1.5 | 282 | 8 | US-60-253-456-17347 | Sequence 17347, A  |
| C 420 | 16 | 1.6 | 3309400 | 6 | US-09-738-626-1     | Sequence 1, Appl1  | C 493 | 15 | 1.5 | 284 | 7 | US-09-764-874-9875  | Sequence 9875, Ap  |
| C 421 | 15 | 1.5 | 51      | 8 | US-60-278-258-2188  | Sequence 2188, Ap  | C 494 | 15 | 1.5 | 284 | 8 | US-60-253-653-6571  | Sequence 6571, Ap  |
| C 422 | 15 | 1.5 | 51      | 8 | US-60-278-232-1843  | Sequence 1843, Ap  | C 495 | 15 | 1.5 | 285 | 7 | US-09-855-807-3263  | Sequence 3263, Ap  |
| C 423 | 15 | 1.5 | 51      | 8 | US-60-278-232-3958  | Sequence 3958, Ap  | C 496 | 15 | 1.5 | 287 | 6 | US-09-790-435-2160  | Sequence 2160, Ap  |
| C 424 | 15 | 1.5 | 57      | 5 | US-09-752-514-4     | Sequence 4, Appl1  | C 497 | 15 | 1.5 | 287 | 6 | US-60-253-652-24155 | Sequence 24155, A  |
| C 425 | 15 | 1.5 | 65      | 8 | US-09-908-975-28318 | Sequence 28318, A  | C 498 | 15 | 1.5 | 289 | 7 | US-09-888-347-2939  | Sequence 2939, Ap  |
| C 426 | 15 | 1.5 | 65      | 8 | US-60-287-724-28318 | Sequence 28318, A  | C 499 | 15 | 1.5 | 289 | 8 | US-60-253-378-36075 | Sequence 36075, A  |
| C 427 | 15 | 1.5 | 106     | 7 | US-09-834-366-33225 | Sequence 33225, A  | C 500 | 15 | 1.5 | 290 | 7 | US-09-867-716-2318  | Sequence 2318, Ap  |
| C 428 | 15 | 1.5 | 118     | 7 | US-09-692-257A-2050 | Sequence 2050, Ap  | C 501 | 15 | 1.5 | 291 | 7 | US-09-859-490-4217  | Sequence 4217, Ap  |
| C 429 | 15 | 1.5 | 155     | 8 | US-60-253-457-40041 | Sequence 40041, A  | C 502 | 15 | 1.5 | 291 | 7 | US-09-853-369-2731  | Sequence 2731, Ap  |
| C 430 | 15 | 1.5 | 157     | 8 | US-60-253-378-40066 | Sequence 40066, A  | C 503 | 15 | 1.5 | 292 | 7 | US-09-880-107-1581  | Sequence 1581, Ap  |
| C 431 | 15 | 1.5 | 163     | 7 | US-09-667-716-1690  | Sequence 1690, Ap  | C 504 | 15 | 1.5 | 292 | 7 | US-09-823-327-5930  | Sequence 5930, Ap  |
| C 432 | 15 | 1.5 | 167     | 6 | US-09-804-730-21002 | Sequence 21002, A  | C 505 | 15 | 1.5 | 292 | 7 | US-09-540-213-38802 | Sequence 38802, A  |
| C 433 | 15 | 1.5 | 171     | 7 | US-09-724-671-14218 | Sequence 14218, A  | C 506 | 15 | 1.5 | 293 | 7 | US-09-840-145-5109  | Sequence 5109, Ap  |
| C 434 | 15 | 1.5 | 181     | 7 | US-09-834-366-28038 | Sequence 28038, A  | C 507 | 15 | 1.5 | 293 | 7 | US-09-894-949-5365  | Sequence 5365, Ap  |
| C 435 | 15 | 1.5 | 188     | 6 | US-09-803-110-2777  | Sequence 2777, Ap  | C 508 | 15 | 1.5 | 293 | 8 | US-60-253-653-283   | Sequence 283, App  |
| C 436 | 15 | 1.5 | 188     | 6 | US-60-253-378-40212 | Sequence 40212, A  | C 509 | 15 | 1.5 | 294 | 6 | US-09-803-110-7207  | Sequence 7207, Ap  |
| C 437 | 15 | 1.5 | 209     | 7 | US-09-440-305A-72   | Sequence 72, Appl1 | C 510 | 15 | 1.5 | 294 | 8 | US-09-863-524-3586  | Sequence 3586, Ap  |
| C 438 | 15 | 1.5 | 213     | 4 | US-08-798-074B-605  | Sequence 605, App  | C 511 | 15 | 1.5 | 294 | 8 | US-60-253-457-48133 | Sequence 48133, A  |
| C 439 | 15 | 1.5 | 213     | 4 | US-08-798-074B-605  | Sequence 605, App  | C 512 | 15 | 1.5 | 296 | 7 | US-09-912-292-53521 | Sequence 53521, A  |
| C 440 | 15 | 1.5 | 213     | 4 | US-08-798-074C-605  | Sequence 605, App  | C 513 | 15 | 1.5 | 296 | 7 | US-09-540-213-47732 | Sequence 47732, A  |
| C 441 | 15 | 1.5 | 213     | 4 | US-08-798-074C-605  | Sequence 605, App  | C 514 | 15 | 1.5 | 297 | 7 | US-09-839-976-1736  | Sequence 1736, Ap  |
| C 442 | 15 | 1.5 | 218     | 7 | US-09-724-671-17170 | Sequence 17170, A  | C 515 | 15 | 1.5 | 297 | 8 | US-09-922-217-31    | Sequence 31, Appl1 |
| C 443 | 15 | 1.5 | 219     | 8 | US-60-253-652-18012 | Sequence 18012, A  | C 516 | 15 | 1.5 | 297 | 8 | US-60-253-652-19466 | Sequence 19466, A  |
| C 444 | 15 | 1.5 | 219     | 8 | US-09-877-486-4991  | Sequence 4991, Ap  | C 517 | 15 | 1.5 | 298 | 5 | US-09-824-559-3170  | Sequence 3170, Ap  |
| C 445 | 15 | 1.5 | 222     | 7 | US-09-804-730-17124 | Sequence 17124, A  | C 518 | 15 | 1.5 | 299 | 7 | US-09-783-590-3890  | Sequence 3890, Ap  |
| C 446 | 15 | 1.5 | 224     | 7 | US-09-877-486-2809  | Sequence 2809, Ap  | C 519 | 15 | 1.5 | 299 | 8 | US-60-253-457-4190  | Sequence 4190, Ap  |
| C 447 | 15 | 1.5 | 224     | 7 | US-09-877-486-7079  | Sequence 7079, Ap  | C 520 | 15 | 1.5 | 300 | 7 | US-09-894-949-52547 | Sequence 52547, Ap |
| C 448 | 15 | 1.5 | 225     | 5 | US-09-824-559-3218  | Sequence 3218, Ap  | C 521 | 15 | 1.5 | 301 | 1 | PCR-US01-08656-4893 | Sequence 4893, Ap  |
| C 449 | 15 | 1.5 | 228     | 7 | US-09-540-213-7393  | Sequence 7393, Ap  | C 522 | 15 | 1.5 | 301 | 7 | US-09-877-486-3646  | Sequence 3646, Ap  |
| C 450 | 15 | 1.5 | 229     | 7 | US-09-853-369-5293  | Sequence 5293, Ap  | C 523 | 15 | 1.5 | 301 | 8 | US-60-253-653-3462  | Sequence 3462, App |
| C 451 | 15 | 1.5 | 232     | 6 | US-09-796-692-4188  | Sequence 4188, Ap  | C 524 | 15 | 1.5 | 302 | 8 | US-60-253-378-22144 | Sequence 22144, A  |
| C 452 | 15 | 1.5 | 236     | 7 | US-09-877-486-588   | Sequence 588, App  | C 525 | 15 | 1.5 | 303 | 6 | US-09-804-730-20147 | Sequence 20147, A  |
| C 453 | 15 | 1.5 | 236     | 7 | US-09-877-486-588   | Sequence 588, App  | C 526 | 15 | 1.5 | 304 | 8 | US-60-252-833-12574 | Sequence 12574, A  |
| C 454 | 15 | 1.5 | 238     | 8 | US-60-253-378-36184 | Sequence 36184, A  | C 527 | 15 | 1.5 | 307 | 8 | US-09-724-671-8599  | Sequence 8599, Ap  |
| C 455 | 15 | 1.5 | 238     | 8 | US-60-252-833-35084 | Sequence 35084, A  | C 528 | 15 | 1.5 | 307 | 8 | US-60-253-378-36054 | Sequence 36054, A  |
| C 456 | 15 | 1.5 | 243     | 7 | US-60-253-457-48223 | Sequence 48223, A  | C 529 | 15 | 1.5 | 311 | 8 | US-60-253-378-40145 | Sequence 40145, A  |
| C 457 | 15 | 1.5 | 243     | 7 | US-09-540-213-9093  | Sequence 9093, Ap  | C 530 | 15 | 1.5 | 312 | 8 | US-60-253-378-6598  | Sequence 6598, Ap  |
| C 458 | 15 | 1.5 | 244     | 7 | US-09-853-369-5124  | Sequence 5124, Ap  | C 531 | 15 | 1.5 | 313 | 7 | US-09-724-671-626   | Sequence 626, App  |
| C 459 | 15 | 1.5 | 245     | 7 | US-09-864-761-22230 | Sequence 22230, A  | C 532 | 15 | 1.5 | 313 | 7 | US-09-724-671-13915 | Sequence 13915, A  |
| C 460 | 15 | 1.5 | 246     | 7 | US-09-724-671-20713 | Sequence 20713, A  | C 533 | 15 | 1.5 | 313 | 7 | US-09-850-147-16619 | Sequence 16619, A  |
| C 461 | 15 | 1.5 | 249     | 6 | US-09-758-470-98    | Sequence 98, Appl1 | C 534 | 15 | 1.5 | 313 | 8 | US-60-253-653-11686 | Sequence 11686, A  |
| C 462 | 15 | 1.5 | 250     | 6 | US-60-253-378-40213 | Sequence 40213, A  | C 535 | 15 | 1.5 | 314 | 6 | US-09-866-555-13756 | Sequence 13756, A  |
| C 463 | 15 | 1.5 | 256     | 6 | US-09-804-730-9797  | Sequence 9797, Ap  | C 536 | 15 | 1.5 | 314 | 7 | US-09-764-905-25631 | Sequence 25631, A  |

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| C 537 | 15 | 1.5 | 314 | 8 | US-60-253-456-4867  | Sequence 4867, Ap   | 610 | 15 | 1.5 | 354 | 7 | US-09-904-456-138   | Sequence 138, App  |
| C 538 | 15 | 1.5 | 315 | 8 | US-60-253-378-44506 | Sequence 34506, A   | 611 | 15 | 1.5 | 354 | 8 | US-60-253-456-14698 | Sequence 14698, A  |
| C 539 | 15 | 1.5 | 316 | 8 | US-60-253-378-40070 | Sequence 40070, A   | 612 | 15 | 1.5 | 354 | 7 | US-09-859-490-12486 | Sequence 12486, A  |
| C 540 | 15 | 1.5 | 317 | 7 | US-09-912-292-46375 | Sequence 46375, A   | 613 | 15 | 1.5 | 356 | 8 | US-60-252-833-35845 | Sequence 35845, A  |
| C 541 | 15 | 1.5 | 317 | 8 | US-60-253-456-6964  | Sequence 6964, Ap   | 614 | 15 | 1.5 | 357 | 6 | US-09-688-848-3358  | Sequence 2358, Ap  |
| C 542 | 15 | 1.5 | 318 | 7 | US-60-253-456-83323 | Sequence 8323, Ap   | 615 | 15 | 1.5 | 359 | 6 | US-09-878-178-2119  | Sequence 2119, Ap  |
| C 543 | 15 | 1.5 | 319 | 8 | US-60-253-456-23377 | Sequence 23377, A   | 616 | 15 | 1.5 | 359 | 8 | US-60-253-457-13176 | Sequence 11776, A  |
| C 544 | 15 | 1.5 | 321 | 7 | US-09-724-671-3935  | Sequence 3935, Ap   | 617 | 15 | 1.5 | 360 | 6 | US-09-846-041-1057  | Sequence 1057, Ap  |
| C 545 | 15 | 1.5 | 321 | 7 | US-09-912-292-28740 | Sequence 28740, A   | 618 | 15 | 1.5 | 360 | 8 | US-60-252-833-27830 | Sequence 37830, A  |
| C 546 | 15 | 1.5 | 321 | 7 | US-09-853-369-726   | Sequence 726, App   | 619 | 15 | 1.5 | 360 | 8 | US-60-252-833-42501 | Sequence 42501, A  |
| C 547 | 15 | 1.5 | 322 | 8 | US-60-252-833-35763 | Sequence 35763, App | 620 | 15 | 1.5 | 360 | 8 | US-60-253-378-40178 | Sequence 40178, A  |
| C 548 | 15 | 1.5 | 322 | 8 | US-60-253-653-22384 | Sequence 22384, A   | 621 | 15 | 1.5 | 361 | 6 | US-09-804-730-18458 | Sequence 18458, A  |
| C 549 | 15 | 1.5 | 323 | 6 | US-09-922-279-286   | Sequence 286, App   | 622 | 15 | 1.5 | 361 | 8 | US-60-252-833-29974 | Sequence 29974, A  |
| C 550 | 15 | 1.5 | 325 | 6 | US-60-253-653-23219 | Sequence 23219, A   | 623 | 15 | 1.5 | 361 | 8 | US-60-256-867-1490  | Sequence 1490, Ap  |
| C 551 | 15 | 1.5 | 328 | 6 | US-09-804-730-18928 | Sequence 18928, A   | 624 | 15 | 1.5 | 362 | 7 | US-09-912-292-32540 | Sequence 32540, A  |
| C 552 | 15 | 1.5 | 328 | 8 | US-60-252-833-23255 | Sequence 23255, A   | 625 | 15 | 1.5 | 364 | 7 | US-09-912-292-32540 | Sequence 32540, A  |
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| C 554 | 15 | 1.5 | 329 | 7 | US-09-877-486-6154  | Sequence 6154, Ap   | 627 | 15 | 1.5 | 365 | 6 | US-09-504-576A-2428 | Sequence 2428, Ap  |
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| C 557 | 15 | 1.5 | 329 | 8 | US-60-255-592-24353 | Sequence 24353, A   | 630 | 15 | 1.5 | 366 | 8 | US-60-252-833-27326 | Sequence 27326, A  |
| C 558 | 15 | 1.5 | 330 | 8 | US-60-253-378-40197 | Sequence 40197, A   | 631 | 15 | 1.5 | 367 | 6 | US-09-804-730-2639  | Sequence 2639, Ap  |
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| C 560 | 15 | 1.5 | 331 | 8 | US-60-253-456-34134 | Sequence 34134, A   | 633 | 15 | 1.5 | 367 | 6 | US-09-688-848-2356  | Sequence 2356, Ap  |
| C 561 | 15 | 1.5 | 332 | 6 | US-09-898-888-42956 | Sequence 42956, A   | 634 | 15 | 1.5 | 367 | 7 | US-09-724-671-7727  | Sequence 7727, Ap  |
| C 562 | 15 | 1.5 | 334 | 7 | US-09-724-671-10249 | Sequence 10249, A   | 635 | 15 | 1.5 | 367 | 7 | US-09-840-145-1533  | Sequence 1533, Ap  |
| C 563 | 15 | 1.5 | 334 | 7 | US-09-912-292-17876 | Sequence 17876, A   | 636 | 15 | 1.5 | 369 | 8 | US-60-253-378-16816 | Sequence 16816, A  |
| C 564 | 15 | 1.5 | 334 | 7 | US-09-859-490-10762 | Sequence 10762, A   | 637 | 15 | 1.5 | 370 | 6 | US-09-758-472-140   | Sequence 740, App  |
| C 565 | 15 | 1.5 | 334 | 8 | US-60-253-456-33763 | Sequence 23763, A   | 638 | 15 | 1.5 | 370 | 6 | US-09-667-188A-6735 | Sequence 6735, Ap  |
| C 566 | 15 | 1.5 | 334 | 8 | US-60-253-651-22124 | Sequence 22124, A   | 639 | 15 | 1.5 | 370 | 7 | US-09-724-671-18825 | Sequence 18825, A  |
| C 567 | 15 | 1.5 | 335 | 6 | US-09-823-241-7965  | Sequence 7965, Ap   | 640 | 15 | 1.5 | 371 | 7 | US-09-724-671-7274  | Sequence 7274, App |
| C 568 | 15 | 1.5 | 335 | 7 | US-09-724-671-12312 | Sequence 12312, A   | 641 | 15 | 1.5 | 371 | 8 | US-60-253-652-20359 | Sequence 20359, A  |
| C 569 | 15 | 1.5 | 336 | 7 | US-09-888-347-3619  | Sequence 3619, Ap   | 642 | 15 | 1.5 | 373 | 6 | US-09-898-888-3587  | Sequence 3587, Ap  |
| C 570 | 15 | 1.5 | 336 | 8 | US-60-253-457-47692 | Sequence 47692, A   | 643 | 15 | 1.5 | 373 | 6 | US-09-804-730-13731 | Sequence 13731, A  |
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| C 572 | 15 | 1.5 | 339 | 7 | US-09-724-671-16425 | Sequence 16425, A   | 645 | 15 | 1.5 | 374 | 6 | US-09-757-034-693   | Sequence 693, App  |
| C 573 | 15 | 1.5 | 339 | 7 | US-09-718-455-505   | Sequence 505, App   | 646 | 15 | 1.5 | 374 | 6 | US-60-253-378-40062 | Sequence 40062, A  |
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| C 575 | 15 | 1.5 | 339 | 8 | US-60-253-378-2631  | Sequence 2631, Ap   | 648 | 15 | 1.5 | 375 | 7 | US-09-724-671-12222 | Sequence 12222, A  |
| C 576 | 15 | 1.5 | 339 | 8 | US-60-253-378-40201 | Sequence 40201, Ap  | 649 | 15 | 1.5 | 376 | 7 | US-09-881-797-2177  | Sequence 2177, Ap  |
| C 577 | 15 | 1.5 | 339 | 8 | US-60-253-653-21923 | Sequence 21923, A   | 650 | 15 | 1.5 | 377 | 7 | US-09-783-590-10476 | Sequence 10476, A  |
| C 578 | 15 | 1.5 | 340 | 1 | PCT-US01-14827-5278 | Sequence 5278, Ap   | 651 | 15 | 1.5 | 377 | 8 | US-60-253-457-26048 | Sequence 26048, A  |
| C 579 | 15 | 1.5 | 340 | 6 | US-09-804-730-16368 | Sequence 16368, A   | 652 | 15 | 1.5 | 378 | 8 | US-60-253-378-6338  | Sequence 6338, Ap  |
| C 580 | 15 | 1.5 | 341 | 4 | US-08-798-074B-8882 | Sequence 8882, Ap   | 653 | 15 | 1.5 | 381 | 7 | US-09-692-257A-7435 | Sequence 7435, Ap  |
| C 581 | 15 | 1.5 | 341 | 4 | US-08-798-074B-8882 | Sequence 8882, Ap   | 654 | 15 | 1.5 | 381 | 8 | US-60-253-378-1838  | Sequence 1838, Ap  |
| C 582 | 15 | 1.5 | 341 | 4 | US-08-798-074B-8882 | Sequence 8882, Ap   | 655 | 15 | 1.5 | 381 | 8 | US-60-253-456-5468  | Sequence 5468, Ap  |
| C 583 | 15 | 1.5 | 341 | 6 | US-09-718-454-130   | Sequence 130, App   | 656 | 15 | 1.5 | 382 | 7 | US-09-850-147-5245  | Sequence 5245, Ap  |
| C 584 | 15 | 1.5 | 341 | 6 | US-60-253-457-16677 | Sequence 16677, A   | 657 | 15 | 1.5 | 384 | 6 | US-09-611-527A-896  | Sequence 896, App  |
| C 585 | 15 | 1.5 | 342 | 4 | US-08-798-074B-5584 | Sequence 5584, Ap   | 658 | 15 | 1.5 | 384 | 7 | US-09-764-874-1413  | Sequence 1413, Ap  |
| C 586 | 15 | 1.5 | 342 | 4 | US-08-798-074B-5584 | Sequence 5584, Ap   | 659 | 15 | 1.5 | 388 | 7 | US-09-912-292-14559 | Sequence 4559, A   |
| C 587 | 15 | 1.5 | 342 | 4 | US-08-798-074C-5584 | Sequence 5584, Ap   | 660 | 15 | 1.5 | 390 | 7 | US-09-834-366-47236 | Sequence 47236, A  |
| C 588 | 15 | 1.5 | 342 | 6 | US-09-866-555-13048 | Sequence 13048, A   | 661 | 15 | 1.5 | 390 | 7 | US-09-724-671-69    | Sequence 69, App1  |
| C 589 | 15 | 1.5 | 342 | 6 | US-09-667-188A-234  | Sequence 234, App   | 662 | 15 | 1.5 | 390 | 7 | US-09-864-761-1279  | Sequence 4279, App |
| C 590 | 15 | 1.5 | 343 | 7 | US-09-724-671-5341  | Sequence 5341, Ap   | 663 | 15 | 1.5 | 390 | 7 | US-09-864-761-21032 | Sequence 21032, A  |
| C 591 | 15 | 1.5 | 344 | 7 | US-09-850-147-15518 | Sequence 15518, A   | 664 | 15 | 1.5 | 391 | 7 | US-09-864-761-3379  | Sequence 3379, Ap  |
| C 592 | 15 | 1.5 | 345 | 7 | US-09-834-366-7468  | Sequence 7468, Ap   | 665 | 15 | 1.5 | 393 | 6 | US-09-909-629-16965 | Sequence 16965, A  |
| C 593 | 15 | 1.5 | 345 | 8 | US-60-253-457-27686 | Sequence 27686, A   | 666 | 15 | 1.5 | 393 | 7 | US-09-834-366-48608 | Sequence 48608, A  |
| C 594 | 15 | 1.5 | 346 | 7 | US-09-540-213-38719 | Sequence 38719, A   | 667 | 15 | 1.5 | 394 | 6 | US-09-866-535-11628 | Sequence 11628, A  |
| C 595 | 15 | 1.5 | 346 | 7 | US-09-888-347-2222  | Sequence 2222, Ap   | 668 | 15 | 1.5 | 394 | 6 | US-60-252-833-37793 | Sequence 37793, A  |
| C 596 | 15 | 1.5 | 347 | 5 | US-09-824-559-7087  | Sequence 7087, Ap   | 669 | 15 | 1.5 | 395 | 6 | US-09-611-527A-2444 | Sequence 2444, Ap  |
| C 597 | 15 | 1.5 | 348 | 7 | US-09-770-791-739   | Sequence 739, App   | 670 | 15 | 1.5 | 396 | 5 | US-09-824-559-17303 | Sequence 4703, Ap  |
| C 598 | 15 | 1.5 | 348 | 8 | US-60-253-653-21899 | Sequence 21899, A   | 671 | 15 | 1.5 | 397 | 6 | US-09-907-421-18    | Sequence 18, App1  |
| C 599 | 15 | 1.5 | 351 | 8 | US-60-253-653-24184 | Sequence 24184, A   | 672 | 15 | 1.5 | 397 | 6 | US-09-611-527A-895  | Sequence 895, App  |
| C 600 | 15 | 1.5 | 351 | 8 | US-60-253-654-2279  | Sequence 2279, App  | 673 | 15 | 1.5 | 397 | 7 | US-09-840-145-10776 | Sequence 10776, A  |
| C 601 | 15 | 1.5 | 351 | 8 | US-60-253-592-2279  | Sequence 2279, App  | 674 | 15 | 1.5 | 398 | 6 | US-09-904-703-8217  | Sequence 8217, Ap  |
| C 602 | 15 | 1.5 | 352 | 6 | US-09-728-445-108   | Sequence 108, App   | 675 | 15 | 1.5 | 399 | 1 | PCT-US01-08631-8261 | Sequence 8261, App |
| C 603 | 15 | 1.5 | 352 | 7 | US-09-764-874-7543  | Sequence 7543, App  | 676 | 15 | 1.5 | 399 | 6 | US-09-611-527A-686  | Sequence 686, App  |
| C 604 | 15 | 1.5 | 352 | 7 | US-09-859-490-10177 | Sequence 10177, A   | 677 | 15 | 1.5 | 399 | 8 | US-60-253-456-2997  | Sequence 2997, App |
| C 605 | 15 | 1.5 | 352 | 8 | US-60-252-833-3404  | Sequence 3404, Ap   | 678 | 15 | 1.5 | 400 | 6 | US-09-898-888-9289  | Sequence 9289, Ap  |
| C 606 | 15 | 1.5 | 353 | 8 | US-60-253-654-18328 | Sequence 18328, A   | 679 | 15 | 1.5 | 400 | 7 | US-09-632-257A-2826 | Sequence 2826, Ap  |
| C 607 | 15 | 1.5 | 353 | 8 | US-60-255-592-18328 | Sequence 18328, A   | 680 | 15 | 1.5 | 400 | 7 | US-09-850-147-14568 | Sequence 14568, Ap |
| C 608 | 15 | 1.5 | 354 | 6 | US-09-878-722-138   | Sequence 138, App   | 681 | 15 | 1.5 | 401 | 8 | US-60-253-457-12676 | Sequence 12676, A  |
| C 609 | 15 | 1.5 | 354 | 6 | US-09-898-888-19058 | Sequence 19058, A   | 682 | 15 | 1.5 | 401 | 7 | US-09-724-671-16990 | Sequence 16990, A  |

|       |    |     |     |   |                     |                    |       |    |     |     |   |                         |                    |
|-------|----|-----|-----|---|---------------------|--------------------|-------|----|-----|-----|---|-------------------------|--------------------|
| C 683 | 15 | 1.5 | 401 | 7 | US-09-764-905-2714  | Sequence 2714, Ap  | C 756 | 15 | 1.5 | 425 | 7 | US-09-864-761-19140     | Sequence 19140, A  |
| C 684 | 15 | 1.5 | 402 | 1 | PCT-US01-08631-9009 | Sequence 9009, Ap  | C 757 | 15 | 1.5 | 426 | 7 | US-09-838-601-1588      | Sequence 1588, Ap  |
| C 685 | 15 | 1.5 | 402 | 6 | US-09-667-188A-6861 | Sequence 6861, Ap  | C 758 | 15 | 1.5 | 427 | 8 | US-09-60-253-652-26649  | Sequence 26649, A  |
| C 686 | 15 | 1.5 | 403 | 6 | US-09-904-703-6175  | Sequence 6175, Ap  | C 759 | 15 | 1.5 | 428 | 6 | US-09-667-188A-5567     | Sequence 5567, Ap  |
| C 687 | 15 | 1.5 | 403 | 6 | US-09-611-527A-2636 | Sequence 2636, Ap  | C 760 | 15 | 1.5 | 428 | 7 | US-09-834-366-46453     | Sequence 46453, A  |
| C 688 | 15 | 1.5 | 403 | 6 | US-09-617-681A-4429 | Sequence 4429, Ap  | C 761 | 15 | 1.5 | 429 | 7 | US-09-834-366-50354     | Sequence 50354, A  |
| C 689 | 15 | 1.5 | 403 | 7 | US-09-692-257A-1123 | Sequence 1123, Ap  | C 762 | 15 | 1.5 | 429 | 7 | US-09-834-366-50354     | Sequence 50354, A  |
| C 690 | 15 | 1.5 | 403 | 7 | US-09-724-750-8032  | Sequence 8032, Ap  | C 763 | 15 | 1.5 | 430 | 6 | US-09-764-905-28958     | Sequence 28958, A  |
| C 691 | 15 | 1.5 | 405 | 7 | US-09-724-671-17006 | Sequence 17006, A  | C 764 | 15 | 1.5 | 431 | 6 | US-09-906-555-10397     | Sequence 10397, A  |
| C 692 | 15 | 1.5 | 405 | 7 | US-09-824-518-1921  | Sequence 1921, Ap  | C 765 | 15 | 1.5 | 431 | 6 | US-09-906-555-10397     | Sequence 10397, A  |
| C 693 | 15 | 1.5 | 405 | 7 | US-09-824-556-5294  | Sequence 5294, Ap  | C 766 | 15 | 1.5 | 431 | 7 | US-09-850-147-66460     | Sequence 66460, Ap |
| C 694 | 15 | 1.5 | 405 | 7 | US-09-824-628-5284  | Sequence 5284, Ap  | C 767 | 15 | 1.5 | 431 | 7 | US-09-821-710-6102      | Sequence 6102, Ap  |
| C 695 | 15 | 1.5 | 406 | 7 | US-09-834-366-39556 | Sequence 39556, A  | C 768 | 15 | 1.5 | 433 | 6 | US-09-760-493-141       | Sequence 141, App  |
| C 696 | 15 | 1.5 | 408 | 5 | US-09-824-559-7947  | Sequence 7947, Ap  | C 769 | 15 | 1.5 | 434 | 7 | US-09-747-360-891       | Sequence 891, App  |
| C 697 | 15 | 1.5 | 410 | 5 | US-09-824-559-6730  | Sequence 6730, Ap  | C 770 | 15 | 1.5 | 435 | 6 | US-09-758-466-125       | Sequence 125, App  |
| C 698 | 15 | 1.5 | 410 | 6 | US-09-898-888-37682 | Sequence 37682, A  | C 771 | 15 | 1.5 | 435 | 6 | US-09-823-241-1012      | Sequence 1012, Ap  |
| C 699 | 15 | 1.5 | 410 | 6 | US-09-804-730-3741  | Sequence 3741, Ap  | C 772 | 15 | 1.5 | 435 | 6 | US-09-823-241-1012      | Sequence 1012, Ap  |
| C 700 | 15 | 1.5 | 410 | 6 | US-09-909-629-8222  | Sequence 8222, Ap  | C 773 | 15 | 1.5 | 435 | 7 | US-09-649-866A-1128     | Sequence 1128, Ap  |
| C 701 | 15 | 1.5 | 411 | 1 | PCT-US01-04926A-431 | Sequence 431, App  | C 774 | 15 | 1.5 | 435 | 7 | US-09-692-257A-13364    | Sequence 13364, A  |
| C 702 | 15 | 1.5 | 411 | 1 | PCT-US01-04926A-432 | Sequence 432, App  | C 775 | 15 | 1.5 | 435 | 7 | US-09-902-540-6102      | Sequence 6102, Ap  |
| C 703 | 15 | 1.5 | 411 | 1 | PCT-US01-04926A-433 | Sequence 433, App  | C 776 | 15 | 1.5 | 436 | 6 | US-09-667-188A-4285     | Sequence 4285, Ap  |
| C 704 | 15 | 1.5 | 411 | 6 | US-09-804-730-19842 | Sequence 19842, A  | C 777 | 15 | 1.5 | 436 | 6 | US-09-906-555-9182      | Sequence 9182, Ap  |
| C 705 | 15 | 1.5 | 412 | 6 | US-09-909-629-22790 | Sequence 22790, A  | C 778 | 15 | 1.5 | 437 | 6 | US-09-823-241-1012      | Sequence 1012, Ap  |
| C 706 | 15 | 1.5 | 412 | 7 | US-09-813-155-10939 | Sequence 10939, A  | C 779 | 15 | 1.5 | 437 | 6 | US-09-823-241-7856      | Sequence 7856, Ap  |
| C 707 | 15 | 1.5 | 412 | 7 | US-09-923-779-23    | Sequence 23, Appl  | C 780 | 15 | 1.5 | 438 | 6 | US-09-804-730-19150     | Sequence 19150, A  |
| C 708 | 15 | 1.5 | 412 | 8 | US-60-253-654-11685 | Sequence 11685, A  | C 781 | 15 | 1.5 | 438 | 6 | US-09-688-848-84        | Sequence 84, Appl  |
| C 709 | 15 | 1.5 | 412 | 8 | US-60-255-592-11685 | Sequence 11685, A  | C 782 | 15 | 1.5 | 438 | 8 | US-09-692-257A-5521     | Sequence 5521, Ap  |
| C 710 | 15 | 1.5 | 413 | 6 | US-09-909-629-37    | Sequence 37, Appl  | C 783 | 15 | 1.5 | 438 | 8 | US-09-692-257A-2157     | Sequence 2157, Ap  |
| C 711 | 15 | 1.5 | 413 | 6 | US-09-909-629-45    | Sequence 45, Appl  | C 784 | 15 | 1.5 | 440 | 6 | US-09-909-629-22658     | Sequence 22658, A  |
| C 712 | 15 | 1.5 | 413 | 6 | US-09-909-629-32493 | Sequence 32493, A  | C 785 | 15 | 1.5 | 440 | 7 | US-09-867-701-6255      | Sequence 6255, Ap  |
| C 713 | 15 | 1.5 | 413 | 7 | US-09-692-257A-5534 | Sequence 5534, Ap  | C 786 | 15 | 1.5 | 440 | 7 | US-09-850-147-1602      | Sequence 1602, Ap  |
| C 714 | 15 | 1.5 | 413 | 7 | US-09-922-217-676   | Sequence 676, App  | C 787 | 15 | 1.5 | 441 | 4 | US-08-798-074B-5078     | Sequence 5078, Ap  |
| C 715 | 15 | 1.5 | 414 | 6 | US-09-904-703-4865  | Sequence 4865, Ap  | C 788 | 15 | 1.5 | 441 | 4 | US-08-798-074B-5078     | Sequence 5078, Ap  |
| C 716 | 15 | 1.5 | 414 | 6 | US-09-909-629-36    | Sequence 36, Appl  | C 789 | 15 | 1.5 | 441 | 8 | US-08-798-074C-5078     | Sequence 5078, Ap  |
| C 717 | 15 | 1.5 | 414 | 6 | US-09-909-629-39    | Sequence 39, Appl  | C 790 | 15 | 1.5 | 443 | 7 | US-09-724-671-3267      | Sequence 3267, Ap  |
| C 718 | 15 | 1.5 | 414 | 6 | US-09-909-629-81    | Sequence 81, Appl  | C 791 | 15 | 1.5 | 443 | 7 | US-09-764-869-443       | Sequence 443, App  |
| C 719 | 15 | 1.5 | 414 | 6 | US-09-909-629-81    | Sequence 81, Appl  | C 792 | 15 | 1.5 | 444 | 6 | US-09-764-869-2117      | Sequence 2117, Ap  |
| C 720 | 15 | 1.5 | 415 | 6 | US-09-804-730-2144  | Sequence 2144, Ap  | C 793 | 15 | 1.5 | 444 | 6 | US-09-904-703-10308     | Sequence 10308, A  |
| C 721 | 15 | 1.5 | 415 | 6 | US-09-758-463-176   | Sequence 176, App  | C 794 | 15 | 1.5 | 444 | 7 | US-09-692-257A-1029     | Sequence 1029, Ap  |
| C 722 | 15 | 1.5 | 415 | 6 | US-09-904-809-18884 | Sequence 18884, A  | C 795 | 15 | 1.5 | 445 | 8 | US-09-692-257A-6912     | Sequence 6912, Ap  |
| C 723 | 15 | 1.5 | 416 | 1 | PCT-US01-14827-7046 | Sequence 7046, Ap  | C 796 | 15 | 1.5 | 445 | 7 | US-09-692-253-378-25021 | Sequence 25021, A  |
| C 724 | 15 | 1.5 | 416 | 5 | US-09-824-559-2436  | Sequence 2436, Ap  | C 797 | 15 | 1.5 | 446 | 6 | US-09-809-629-2986      | Sequence 2986, Ap  |
| C 725 | 15 | 1.5 | 416 | 6 | US-09-909-629-4339  | Sequence 4339, Ap  | C 798 | 15 | 1.5 | 446 | 7 | US-09-850-147-4384      | Sequence 4384, Ap  |
| C 726 | 15 | 1.5 | 416 | 6 | US-09-909-629-19    | Sequence 19, Appl  | C 799 | 15 | 1.5 | 448 | 7 | US-09-692-257A-4781     | Sequence 4781, Ap  |
| C 727 | 15 | 1.5 | 416 | 6 | US-09-909-629-23    | Sequence 23, Appl  | C 800 | 15 | 1.5 | 449 | 6 | US-09-909-629-922       | Sequence 922, App  |
| C 728 | 15 | 1.5 | 417 | 6 | US-09-898-888-18442 | Sequence 18442, A  | C 801 | 15 | 1.5 | 449 | 6 | US-09-909-629-926       | Sequence 926, App  |
| C 729 | 15 | 1.5 | 417 | 6 | US-09-909-629-22    | Sequence 22, Appl  | C 802 | 15 | 1.5 | 449 | 6 | US-09-909-629-926       | Sequence 926, App  |
| C 730 | 15 | 1.5 | 417 | 7 | US-09-692-257A-5420 | Sequence 5420, Ap  | C 803 | 15 | 1.5 | 449 | 6 | US-09-909-629-926       | Sequence 926, App  |
| C 731 | 15 | 1.5 | 418 | 6 | US-09-804-703-4703  | Sequence 4703, Ap  | C 804 | 15 | 1.5 | 449 | 7 | US-09-912-292-22281     | Sequence 22281, A  |
| C 732 | 15 | 1.5 | 418 | 6 | US-09-809-629-83    | Sequence 83, Appl  | C 805 | 15 | 1.5 | 449 | 7 | US-09-912-292-22281     | Sequence 22281, A  |
| C 733 | 15 | 1.5 | 419 | 6 | US-09-909-629-17    | Sequence 17, Appl  | C 806 | 15 | 1.5 | 450 | 6 | US-09-821-710-4229      | Sequence 4229, Ap  |
| C 734 | 15 | 1.5 | 419 | 7 | US-09-540-213-20738 | Sequence 20738, A  | C 807 | 15 | 1.5 | 450 | 6 | US-09-909-629-916       | Sequence 916, App  |
| C 735 | 15 | 1.5 | 420 | 5 | US-09-824-559-8115  | Sequence 8115, Ap  | C 808 | 15 | 1.5 | 451 | 6 | US-09-764-855-76        | Sequence 76, Appl  |
| C 736 | 15 | 1.5 | 420 | 6 | US-09-760-469-357   | Sequence 357, App  | C 809 | 15 | 1.5 | 451 | 6 | US-09-764-855-76        | Sequence 76, Appl  |
| C 737 | 15 | 1.5 | 420 | 6 | US-09-904-703-5528  | Sequence 528, App  | C 810 | 15 | 1.5 | 451 | 6 | US-09-866-555-17982     | Sequence 17982, Ap |
| C 738 | 15 | 1.5 | 420 | 6 | US-09-909-627-3452  | Sequence 3452, App | C 811 | 15 | 1.5 | 451 | 6 | US-09-909-629-932       | Sequence 932, App  |
| C 739 | 15 | 1.5 | 420 | 8 | US-60-253-619-11539 | Sequence 11539, A  | C 812 | 15 | 1.5 | 451 | 7 | US-09-692-257A-6939     | Sequence 6939, Ap  |
| C 740 | 15 | 1.5 | 421 | 6 | US-09-866-555-17334 | Sequence 17334, A  | C 813 | 15 | 1.5 | 452 | 6 | US-09-909-629-19588     | Sequence 19588, A  |
| C 741 | 15 | 1.5 | 421 | 6 | US-09-906-555-12121 | Sequence 12121, Ap | C 814 | 15 | 1.5 | 452 | 6 | US-09-909-629-963       | Sequence 963, App  |
| C 742 | 15 | 1.5 | 421 | 7 | US-09-867-701-5805  | Sequence 5805, Ap  | C 815 | 15 | 1.5 | 452 | 6 | US-09-909-629-963       | Sequence 963, App  |
| C 743 | 15 | 1.5 | 421 | 7 | US-09-850-147-11141 | Sequence 11141, A  | C 816 | 15 | 1.5 | 452 | 7 | US-09-821-837-8744      | Sequence 8744, Ap  |
| C 744 | 15 | 1.5 | 421 | 7 | US-09-859-490-13288 | Sequence 13288, A  | C 817 | 15 | 1.5 | 453 | 6 | US-09-866-555-1963      | Sequence 1963, Ap  |
| C 745 | 15 | 1.5 | 421 | 7 | US-09-867-716-16011 | Sequence 16011, A  | C 818 | 15 | 1.5 | 453 | 6 | US-09-866-555-1345      | Sequence 1345, A   |
| C 746 | 15 | 1.5 | 422 | 5 | US-09-824-559-4800  | Sequence 4800, Ap  | C 819 | 15 | 1.5 | 453 | 6 | US-09-823-241-2237      | Sequence 2237, Ap  |
| C 747 | 15 | 1.5 | 422 | 6 | US-09-909-629-11410 | Sequence 11410, A  | C 820 | 15 | 1.5 | 453 | 6 | US-09-912-292-16270     | Sequence 16270, A  |
| C 748 | 15 | 1.5 | 422 | 6 | US-09-617-681A-908  | Sequence 908, App  | C 821 | 15 | 1.5 | 453 | 7 | US-09-912-292-5535      | Sequence 5535, A   |
| C 749 | 15 | 1.5 | 422 | 7 | US-09-724-671-19895 | Sequence 19895, A  | C 822 | 15 | 1.5 | 453 | 7 | US-09-460-595-32        | Sequence 32, Appl  |
| C 750 | 15 | 1.5 | 422 | 7 | US-09-912-292-40783 | Sequence 40783, A  | C 823 | 15 | 1.5 | 453 | 7 | US-09-764-905-39346     | Sequence 39346, A  |
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| C 755 | 15 | 1.5 | 425 | 6 | US-09-909-629-16210 | Sequence 16210, A  | C 828 | 15 | 1.5 | 455 | 7 | US-09-834-366-6856      | Sequence 6856, App |



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| C 834 | 15 | 1.5 | 459 | 6 | US-09-909-627-20302  | Sequence 20302, A  | C 907 | 15 | 1.5 | 504 | 4 | US-08-798-0748-11713 | Sequence 11713, A  |
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| C 840 | 15 | 1.5 | 461 | 6 | US-09-617-681A-3191  | Sequence 3191, Ap  | C 913 | 15 | 1.5 | 507 | 6 | US-09-795-300-252    | Sequence 252, App  |
| C 841 | 15 | 1.5 | 461 | 7 | US-09-846-038-652    | Sequence 652, App  | C 914 | 15 | 1.5 | 507 | 6 | US-09-866-555-3694   | Sequence 3694, App |
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| C 845 | 15 | 1.5 | 465 | 6 | US-09-904-809-9914   | Sequence 9914, Ap  | C 918 | 15 | 1.5 | 508 | 7 | US-09-838-601-1311   | Sequence 1311, Ap  |
| C 846 | 15 | 1.5 | 465 | 6 | US-09-864-761-5455   | Sequence 5455, Ap  | C 919 | 15 | 1.5 | 508 | 7 | US-09-840-145-14017  | Sequence 14017, A  |
| C 847 | 15 | 1.5 | 465 | 8 | US-60-253-456-2430   | Sequence 2430, Ap  | C 920 | 15 | 1.5 | 510 | 7 | US-09-834-366-4533   | Sequence 4533, Ap  |
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| C 851 | 15 | 1.5 | 467 | 7 | US-09-834-366-6099   | Sequence 6099, Ap  | C 924 | 15 | 1.5 | 512 | 6 | US-09-904-703-15373  | Sequence 15373, A  |
| C 852 | 15 | 1.5 | 468 | 6 | US-09-813-155-171    | Sequence 171, App  | C 925 | 15 | 1.5 | 512 | 6 | US-09-849-626-875    | Sequence 875, App  |
| C 853 | 15 | 1.5 | 469 | 6 | US-09-882-171-18     | Sequence 18, App1  | C 926 | 15 | 1.5 | 512 | 6 | US-09-909-627-10775  | Sequence 10775, A  |
| C 854 | 15 | 1.5 | 470 | 6 | US-09-904-809-16387  | Sequence 16387, A  | C 927 | 15 | 1.5 | 512 | 7 | US-09-902-941-875    | Sequence 875, App  |
| C 855 | 15 | 1.5 | 471 | 6 | US-09-866-555-17936  | Sequence 17936, A  | C 928 | 15 | 1.5 | 513 | 7 | US-09-838-601-1855   | Sequence 1855, Ap  |
| C 856 | 15 | 1.5 | 472 | 6 | US-09-898-888-199328 | Sequence 299328, A | C 929 | 15 | 1.5 | 513 | 6 | US-09-904-703-17498  | Sequence 17498, A  |
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| C 859 | 15 | 1.5 | 474 | 7 | US-09-834-366-39650  | Sequence 39650, A  | C 932 | 15 | 1.5 | 514 | 8 | US-09-724-671-21459  | Sequence 21459, A  |
| C 860 | 15 | 1.5 | 475 | 6 | US-09-898-888-31642  | Sequence 31642, A  | C 933 | 15 | 1.5 | 514 | 8 | US-60-279-536-883    | Sequence 983, App  |
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| C 862 | 15 | 1.5 | 476 | 6 | US-09-909-627-22243  | Sequence 22243, A  | C 935 | 15 | 1.5 | 519 | 6 | US-09-904-703-15738  | Sequence 15738, A  |
| C 863 | 15 | 1.5 | 476 | 7 | US-09-912-292-35058  | Sequence 35058, A  | C 936 | 15 | 1.5 | 519 | 6 | US-09-909-627-10792  | Sequence 10792, A  |
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| C 867 | 15 | 1.5 | 480 | 6 | US-09-909-629-29553  | Sequence 29553, A  | C 940 | 15 | 1.5 | 525 | 6 | US-09-652-125A-7910  | Sequence 7910, Ap  |
| C 868 | 15 | 1.5 | 482 | 7 | US-09-834-366-33347  | Sequence 33347, A  | C 941 | 15 | 1.5 | 525 | 7 | US-09-834-366-31710  | Sequence 31710, A  |
| C 869 | 15 | 1.5 | 483 | 5 | US-09-847-662-415    | Sequence 415, App  | C 942 | 15 | 1.5 | 525 | 7 | US-09-652-125A-2874  | Sequence 2874, Ap  |
| C 870 | 15 | 1.5 | 483 | 5 | US-09-834-366-7299   | Sequence 7299, Ap  | C 943 | 15 | 1.5 | 528 | 8 | US-60-253-652-13651  | Sequence 13651, A  |
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| C 873 | 15 | 1.5 | 487 | 7 | US-09-824-518-8605   | Sequence 8605, Ap  | C 946 | 15 | 1.5 | 534 | 7 | US-09-902-540-8822   | Sequence 8822, Ap  |
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| C 878 | 15 | 1.5 | 490 | 6 | US-09-904-809-16865  | Sequence 16865, A  | C 951 | 15 | 1.5 | 542 | 7 | US-09-764-905-39182  | Sequence 39182, A  |
| C 879 | 15 | 1.5 | 490 | 6 | US-09-617-681A-8456  | Sequence 8456, Ap  | C 952 | 15 | 1.5 | 543 | 6 | US-09-803-110-5861   | Sequence 5861, Ap  |
| C 880 | 15 | 1.5 | 490 | 8 | US-60-253-654-6097   | Sequence 6097, Ap  | C 953 | 15 | 1.5 | 543 | 7 | US-09-864-761-6716   | Sequence 6716, Ap  |
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| C 884 | 15 | 1.5 | 491 | 4 | US-08-798-074C-6707  | Sequence 6707, Ap  | C 957 | 15 | 1.5 | 546 | 8 | US-60-252-833-4272   | Sequence 4272, Ap  |
| C 885 | 15 | 1.5 | 492 | 5 | US-09-847-662-1626   | Sequence 1626, Ap  | C 958 | 15 | 1.5 | 549 | 6 | US-09-803-110-3234   | Sequence 3234, Ap  |
| C 886 | 15 | 1.5 | 493 | 6 | US-09-904-809-14460  | Sequence 14460, A  | C 959 | 15 | 1.5 | 549 | 6 | US-60-253-476A-10089 | Sequence 10089, A  |
| C 887 | 15 | 1.5 | 493 | 6 | US-09-834-366-890    | Sequence 890, App  | C 960 | 15 | 1.5 | 552 | 8 | US-60-253-378-26131  | Sequence 26131, A  |
| C 888 | 15 | 1.5 | 493 | 7 | US-09-834-366-31238  | Sequence 31238, A  | C 961 | 15 | 1.5 | 555 | 6 | US-09-808-383-3510   | Sequence 3510, Ap  |
| C 889 | 15 | 1.5 | 494 | 7 | US-09-838-601-1312   | Sequence 1312, Ap  | C 962 | 15 | 1.5 | 555 | 6 | US-09-796-692-8108   | Sequence 8108, Ap  |
| C 890 | 15 | 1.5 | 495 | 1 | PCT-US01-08631-23443 | Sequence 23443, A  | C 963 | 15 | 1.5 | 556 | 7 | US-09-912-292-41507  | Sequence 41507, A  |
| C 891 | 15 | 1.5 | 495 | 7 | US-09-813-155-5459   | Sequence 5459, Ap  | C 964 | 15 | 1.5 | 559 | 5 | US-09-824-559-3870   | Sequence 3870, Ap  |
| C 892 | 15 | 1.5 | 495 | 8 | US-60-253-654-17086  | Sequence 17086, Ap | C 965 | 15 | 1.5 | 560 | 7 | US-09-540-213-38806  | Sequence 38806, Ap |
| C 893 | 15 | 1.5 | 495 | 8 | US-60-253-552-17086  | Sequence 17086, Ap | C 966 | 15 | 1.5 | 563 | 8 | US-60-253-654-6932   | Sequence 6932, Ap  |
| C 894 | 15 | 1.5 | 496 | 6 | US-09-904-809-6450   | Sequence 6450, Ap  | C 967 | 15 | 1.5 | 563 | 8 | US-60-255-592-6932   | Sequence 6932, Ap  |
| C 895 | 15 | 1.5 | 496 | 7 | US-09-867-701-6032   | Sequence 4032, Ap  | C 968 | 15 | 1.5 | 565 | 8 | US-60-253-619-9535   | Sequence 8535, Ap  |
| C 896 | 15 | 1.5 | 496 | 7 | US-09-912-292-6037   | Sequence 6037, Ap  | C 969 | 15 | 1.5 | 565 | 8 | US-60-253-652-30664  | Sequence 23064, A  |
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| C 898 | 15 | 1.5 | 497 | 7 | US-09-825-774-1243   | Sequence 1243, Ap  | C 971 | 15 | 1.5 | 567 | 8 | US-60-253-652-27169  | Sequence 27169, A  |
| C 899 | 15 | 1.5 | 497 | 8 | US-60-278-238-8077   | Sequence 8077, Ap  | C 972 | 15 | 1.5 | 569 | 8 | US-09-825-422-123    | Sequence 123, App  |
| C 900 | 15 | 1.5 | 500 | 7 | US-09-813-155-5726   | Sequence 5726, Ap  | C 973 | 15 | 1.5 | 571 | 6 | US-09-898-888-13891  | Sequence 13891, A  |
| C 901 | 15 | 1.5 | 500 | 7 | US-09-846-038-735    | Sequence 735, App  | C 974 | 15 | 1.5 | 571 | 7 | US-09-838-601-3526   | Sequence 3526, Ap  |



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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: probe/primer
US-09-138-735-9
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; GENERAL INFORMATION:
; APPLICANT: PARANHOS-BACCALA, Glaucia
; APPLICANT: LESENECHAL, Mylene
; APPLICANT: JOLIVET, Michel
; TITLE OF INVENTION: TRYPANOSOMA CRUZI ANTIGEN, GENE ENCODING THEREFOR AND METHODS OF
; TITLE OF INVENTION: DETECTING AND TREATING CHAGAS DISEASE
; FILE REFERENCE: WPB 36400B
; CURRENT APPLICATION NUMBER: US/09/138,735
; CURRENT FILING DATE: 1998-08-24
; PRIOR APPLICATION NUMBER: US 08/480,917
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: FR 94/10132
; PRIOR FILING DATE: 1994-08-12
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: probe/primer
US-09-138-735-10
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; Sequence 12, Application US/09138735
; GENERAL INFORMATION:
; APPLICANT: PARANHOS-BACCALA, Glaucia
; APPLICANT: LESENECHAL, Mylene
; APPLICANT: JOLIVET, Michel
; TITLE OF INVENTION: TRYPANOSOMA CRUZI ANTIGEN, GENE ENCODING THEREFOR AND METHODS OF
; TITLE OF INVENTION: DETECTING AND TREATING CHAGAS DISEASE
; FILE REFERENCE: WPB 36400B
; CURRENT APPLICATION NUMBER: US/09/138,735
; CURRENT FILING DATE: 1998-08-24
; PRIOR APPLICATION NUMBER: US 08/480,917
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: FR 94/10132
; PRIOR FILING DATE: 1994-08-12
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
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; OTHER INFORMATION: probe/primer
US-09-138-735-12
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; Sequence 19, Application US/09803736
; GENERAL INFORMATION:
; APPLICANT: Bush, David F.
; APPLICANT: Levin, Irena M.
; APPLICANT: Norris, Susan R.
; APPLICANT: Rounsley, Steven D.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof
; FILE REFERENCE: 38-10(15493)D
; CURRENT APPLICATION NUMBER: US/09/803,736
; CURRENT FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 09/534,859
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: Identified by Attorney Docket number 04983.0206CPUS01 38
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 1582
; SEQ ID NO 19
; LENGTH: 91470
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-803-736-19
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; Sequence 5, Application US/09138735
; GENERAL INFORMATION:
; APPLICANT: PARANHOS-BACCALA, Glaucia
; APPLICANT: LESENECHAL, Mylene
; APPLICANT: JOLIVET, Michel
; TITLE OF INVENTION: TRYPANOSOMA CRUZI ANTIGEN, GENE ENCODING THEREFOR AND METHODS
; TITLE OF INVENTION: DETECTING AND TREATING CHAGAS DISEASE
; FILE REFERENCE: WPB 36400B
; CURRENT APPLICATION NUMBER: US/09/138,735
; CURRENT FILING DATE: 1998-08-24
; PRIOR APPLICATION NUMBER: US 08/480,917
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: FR 94/10132
; PRIOR FILING DATE: 1994-08-12
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
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## RESULT 11

US-09-540-213-5492  
; Sequence 5492, Application US/09540213  
; GENERAL INFORMATION:  
; APPLICANT: Seilhamer, Jeffrey J.  
; APPLICANT: Deleage, Angelo M.  
; APPLICANT: Stuart, Susan G.  
; APPLICANT: Stuve, Laura L.  
; APPLICANT: Mullaly, Sara J.  
; APPLICANT: Naughton, Rebecca E.  
; TITLE OF INVENTION: POLYNUCLEOTIDES OF LIVER AND PANCREAS  
; FILE REFERENCE: PD-1031 CIP  
; CURRENT APPLICATION NUMBER: US/09/540,213  
; CURRENT FILING DATE: 2000-03-31  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 53844  
; SEQ ID NO 5492  
; LENGTH: 348  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; OTHER INFORMATION: Incyte ID No: hu00532370  
; NAME/KEY: unsure  
; LOCATION: 4, 8, 304, 307  
; OTHER INFORMATION: a, t, c, g, or other  
US-09-540-213-5492

## Query Match

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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 230 cccctgcacccctg 247

Db 29 cccctgcacccctg 46

## RESULT 12

US-09-667-188A-4578/c  
; Sequence 4578, Application US/09667188A  
; GENERAL INFORMATION:  
; APPLICANT: Andersen, Scott E.  
; APPLICANT: Masucci, James D.  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; FILE REFERENCE: 38-21(51464)B  
; CURRENT APPLICATION NUMBER: US/09/667,188A  
; CURRENT FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/155,006  
; PRIOR FILING DATE: 1999-09-22  
; NUMBER OF SEQ ID NOS: 8135  
; SEQ ID NO 4578  
; LENGTH: 371  
; TYPE: DNA  
; ORGANISM: Triticum aestivum  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3281-014-P1-K1-E7  
US-09-667-188A-4578

## Query Match

1.8%; Score 18; DB 6; Length 371;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 274 cctctgcgcgcgcgcga 291

Db 153 cctctgcgcgcgcgcga 136

## RESULT 13

US-09-804-730-6853/c  
; Sequence 6853, Application US/09804730  
; GENERAL INFORMATION:  
; APPLICANT: Andersen, Scott E.  
; APPLICANT: Hammond-Kosack, Kim  
; APPLICANT: Masucci, James D.  
; APPLICANT: Urban, Martin  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; FILE REFERENCE: 38-21(51838)B  
; CURRENT APPLICATION NUMBER: US/09/804,730  
; CURRENT FILING DATE: 2001-03-13  
; PRIOR APPLICATION NUMBER: US 60/189,657  
; PRIOR FILING DATE: 2000-03-15  
; NUMBER OF SEQ ID NOS: 22828  
; SEQ ID NO 6853  
; LENGTH: 378  
; TYPE: DNA  
; ORGANISM: Triticum aestivum  
; OTHER INFORMATION: Clone ID: LIB3351-055-P1-K1-F5  
US-09-804-730-6853

## Query Match

1.8%; Score 18; DB 6; Length 378;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 616 cacacgcctctcccg 633

Db 173 CACACGCCTCTCCCG 156

## RESULT 14

US-60-255-619-14255/c  
; Sequence 14255, Application US/60255619  
; GENERAL INFORMATION:  
; APPLICANT: Deikman, Jill  
; APPLICANT: Feng, Paul C.C.  
; APPLICANT: Fincher, Karen L.  
; APPLICANT: Ziegler, Todd E.  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; FILE REFERENCE: 38-21(52274)A  
; CURRENT APPLICATION NUMBER: US/60/255,619  
; CURRENT FILING DATE: 2000-12-14  
; NUMBER OF SEQ ID NOS: 17880  
; SEQ ID NO 14255  
; LENGTH: 380  
; TYPE: DNA  
; ORGANISM: Gossypium hirsutum  
; OTHER INFORMATION: Clone ID: LIB3829-031-06-N6-D5  
US-60-255-619-14255

## Query Match

1.8%; Score 18; DB 8; Length 380;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 641 caacgatgcgtttg 658

Db 326 CAACGATGCGCTTTGG 309

## RESULT 15

US-09-864-761-52/c  
; Sequence 52, Application US/09864761  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO

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: GENERAL INFORMATION:
: APPLICANT: Hyseq, Inc.
: TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
: TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
: FILE REFERENCE: 20411-757
: CURRENT FILING DATE: 2001-07-12
: PRIOR APPLICATION NUMBER: 09/234,611
: PRIOR FILING DATE: 1999-01-22
: NUMBER OF SEQ ID NOS: 21025
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 19378
: LENGTH: 476
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc-feature
: LOCATION: (1)...(476)
: OTHER INFORMATION: n = A,T,C or G
US-09/904-809-19378

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RESULT# 17
US-09-909-627-11623/C
Sequence 11623, Application US/09909627
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-766
CURRENT APPLICATION NUMBER: US/09/909,627
CURRENT FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 09/2717,227
PRIOR FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 23680
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 11623
LENGTH: 476
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(476)
OTHER INFORMATION: n = A,T,C or G
US-09-909-627-11623

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RESULT 18  
US-09-864-761-16893/c  
; Sequence 16893, Application US/09864761/c  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
FILE REFERENCE: Aecm1ca-x-1  
CURRENT APPLICATION NUMBER: US/09/864,761  
PRIOR FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263,6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 16893  
LENGTH: 478  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AC005921.3  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.4  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3  
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.9  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4  
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.3  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3  
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 6.9  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2  
OTHER INFORMATION: SWISSPROT HIT: P50555, EVALUATE 5.60e-01  
OTHER INFORMATION: EST HUMAN HIT: BE741337.1, EVALUATE 0.00e+00  
OTHER INFORMATION: NT HIT: X99000.1, EVALUATE 3.00e-01  
US-09-864-761-16893

Query Match 1.8%; Score 18; DB 7; Length 478;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 230 cccctgcacaccacctg 247  
|||||  
DB 298 CCCCTGCATCACCCCTG 281

RESULT 19  
US-09-840-145-13709/c  
Sequence 13709, Application US/09840145  
GENERAL INFORMATION:  
APPLICANT: Adams, et. al.  
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products  
FILE REFERENCE: P014C1  
CURRENT APPLICATION NUMBER: US/09/840,145  
PRIOR FILING DATE: 2001-04-24  
PRIOR APPLICATION NUMBER: 08/276,163  
PRIOR FILING DATE: 1994-07-15  
NUMBER OF SEQ ID NOS: 15314  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 13709  
LENGTH: 506  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (11)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (30)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (44)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (46)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (51)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (60)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (66)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (148)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (185)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (306)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (321)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (345)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (359)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (364)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (375)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (385)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (425)  
OTHER INFORMATION: n equals a,t,g, or c

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; NAME/KEY: misc_feature
; LOCATION: (427)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
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; OTHER INFORMATION: n equals a,t,g, or c
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; LOCATION: (440)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (443)
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; LOCATION: (470)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (473)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (476)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (478)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (489)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (492)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (494)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (501)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-840-145-13709

Query Match          1.8%; Score 18; DB 7; Length 506;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 211 acctctgcccgtctgca 228
    |||||||
Db 243 ACTTCTGCCCTGCTGCA 226

RESULT 20
US-60-312-544-4166/C
; Sequence 4166, Application US/60312544
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Edgerton, Michael D
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: Stein, Joshua
; TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-10(52726)A
; CURRENT APPLICATION NUMBER: US/60/312,544
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 10730
; SEQ ID NO 4166
; LENGTH: 1431
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(778)
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; OTHER INFORMATION: Clone ID: LIB3205-113-E12.FLI
; US-60-312-544-4166

Query Match          1.8%; Score 18; DB 8; Length 1431;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 386 cgcgcgcacacagagt 403
    |||||||
Db 542 CGCGCGCCACAGAGGT 525

RESULT 21
PCT-US01-16450-789/C
; Sequence 789, Application PC/FUS0116450
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: P4131PCT
; CURRENT APPLICATION NUMBER: PCT/US01/16450
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2820
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 789
; LENGTH: 1485
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (158)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (749)
; OTHER INFORMATION: n equals a,t,g, or c
; PCT-US01-16450-789

Query Match          1.8%; Score 18; DB 1; Length 1485;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 gtacgtgcctcgtcgtc 61
    |||||||
Db 669 GTAGCTGCGTCGTGCTG 652

RESULT 22
US-09-867-716-17510
; Sequence 17510, Application US/09867716
; GENERAL INFORMATION:
; APPLICANT: Havukkala, Ilkka
; TITLE OF INVENTION: Polynucleotides, Polypeptides Expressed
; FILE REFERENCE: 11000.1009c1
; CURRENT APPLICATION NUMBER: US/09/867,716
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 09/215,179
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 19860
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17510
; LENGTH: 1595
; TYPE: DNA
; ORGANISM: Pinus radiata
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1595)
; OTHER INFORMATION: n = A,T,C or G
; US-09-867-716-17510
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Query Match 1.8%: Score 18; DB 7; Length 1595;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 814 acagagctgcagcagc 831  
|||||  
Db 1054 acagagctgcagcagc 1071

RESULT 23  
US-09-836-472-1298/C  
; Sequence 1298, Application US/09836472  
; GENERAL INFORMATION:  
; APPLICANT: Geating, David P.  
; APPLICANT: Holtzman, Douglas A.  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A  
; FILE REFERENCE: 1600.1033-002  
; CURRENT APPLICATION NUMBER: US/09/836,472  
; CURRENT FILING DATE: 2001-04-17  
; PRIOR APPLICATION NUMBER: 60/090,245  
; PRIOR FILING DATE: 1998-06-22  
; PRIOR APPLICATION NUMBER: 09/338,663  
; PRIOR FILING DATE: 1999-06-22  
; NUMBER OF SEQ ID NOS: 1364  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1298  
; LENGTH: 2817  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(2817)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-836-472-1298

Query Match 1.8%: Score 18; DB 6; Length 2817;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 44 gtacgtcgctctgctg 61  
|||||  
Db 1980 gtacgtcgctctgctg 1963

RESULT 24  
US-09-764-905-28829/C  
; Sequence 28829, Application US/09764905  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PC004  
; CURRENT APPLICATION NUMBER: US/09/764,905  
; CURRENT FILING DATE: 2001-01-17  
; PRIOR APPLICATION NUMBER: 60/179,065  
; PRIOR FILING DATE: 2000-01-31  
; PRIOR APPLICATION NUMBER: 60/180,628  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: 60/214,886  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: 60/217,487  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 60/225,758  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/220,963  
; PRIOR FILING DATE: 2000-07-26  
; PRIOR APPLICATION NUMBER: 60/217,496  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 60/225,447  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/218,290

; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: 60/225,757  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/226,868  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/216,647  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR APPLICATION NUMBER: 60/225,267  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/216,880  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR APPLICATION NUMBER: 60/225,270  
; PRIOR FILING DATE: 2000-08-14  
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; PRIOR FILING DATE: 2000-12-08  
; PRIOR APPLICATION NUMBER: 60/235,834  
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; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: 60/234,223  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: 60/228,924  
; PRIOR FILING DATE: 2000-08-30  
; PRIOR APPLICATION NUMBER: 60/224,518  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/236,369  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/224,519  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/220,964  
; PRIOR FILING DATE: 2000-07-26  
; PRIOR APPLICATION NUMBER: 60/241,809  
; PRIOR FILING DATE: 2000-10-20  
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; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/236,327  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/241,785  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/244,617  
; PRIOR FILING DATE: 2000-11-01  
; PRIOR APPLICATION NUMBER: 60/225,268  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/236,368  
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; PRIOR FILING DATE: 2000-12-08  
; PRIOR APPLICATION NUMBER: 60/251,868  
; PRIOR FILING DATE: 2000-12-08  
; PRIOR APPLICATION NUMBER: 60/229,344  
; PRIOR FILING DATE: 2000-09-01  
; PRIOR APPLICATION NUMBER: 60/234,997  
; PRIOR FILING DATE: 2000-09-25  
; PRIOR APPLICATION NUMBER: 60/229,343  
; PRIOR FILING DATE: 2000-09-01  
; PRIOR APPLICATION NUMBER: 60/229,345  
; PRIOR FILING DATE: 2000-09-01  
; PRIOR APPLICATION NUMBER: 60/229,287  
; PRIOR FILING DATE: 2000-09-01  
; PRIOR APPLICATION NUMBER: 60/229,513  
; PRIOR FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 60/231,413  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/229,509  
; PRIOR FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 60/236,367  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/237,039  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/237,038  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/236,370  
; PRIOR FILING DATE: 2000-09-29

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| 1  | PRIOR APPLICATION NUMBER: 60/236,802 |
| 2  | PRIOR FILING DATE: 2000-10-02        |
| 3  | PRIOR APPLICATION NUMBER: 60/237,037 |
| 4  | PRIOR FILING DATE: 2000-10-02        |
| 5  | PRIOR APPLICATION NUMBER: 60/237,040 |
| 6  | PRIOR FILING DATE: 2000-10-02        |
| 7  | PRIOR APPLICATION NUMBER: 60/240,960 |
| 8  | PRIOR FILING DATE: 2000-10-20        |
| 9  | PRIOR APPLICATION NUMBER: 60/239,955 |
| 10 | PRIOR FILING DATE: 2000-10-13        |
| 11 | PRIOR APPLICATION NUMBER: 60/239,937 |
| 12 | PRIOR FILING DATE: 2000-10-13        |
| 13 | PRIOR APPLICATION NUMBER: 60/241,787 |
| 14 | PRIOR FILING DATE: 2000-10-20        |
| 15 | PRIOR APPLICATION NUMBER: 60/246,474 |
| 16 | PRIOR FILING DATE: 2000-11-08        |
| 17 | PRIOR APPLICATION NUMBER: 60/246,532 |
| 18 | PRIOR FILING DATE: 2000-11-08        |
| 19 | PRIOR APPLICATION NUMBER: 60/249,216 |
| 20 | PRIOR FILING DATE: 2000-11-17        |
| 21 | PRIOR APPLICATION NUMBER: 60/249,210 |
| 22 | PRIOR FILING DATE: 2000-11-17        |
| 23 | PRIOR APPLICATION NUMBER: 60/226,661 |
| 24 | PRIOR FILING DATE: 2000-08-22        |
| 25 | PRIOR APPLICATION NUMBER: 60/225,759 |
| 26 | PRIOR FILING DATE: 2000-08-14        |
| 27 | PRIOR APPLICATION NUMBER: 60/225,213 |
| 28 | PRIOR FILING DATE: 2000-08-14        |
| 29 | PRIOR APPLICATION NUMBER: 60/227,182 |
| 30 | PRIOR FILING DATE: 2000-08-22        |
| 31 | PRIOR APPLICATION NUMBER: 60/225,214 |
| 32 | PRIOR FILING DATE: 2000-08-14        |
| 33 | PRIOR APPLICATION NUMBER: 60/233,836 |
| 34 | PRIOR FILING DATE: 2000-09-27        |
| 35 | PRIOR APPLICATION NUMBER: 60/230,438 |
| 36 | PRIOR FILING DATE: 2000-09-06        |
| 37 | PRIOR APPLICATION NUMBER: 60/215,135 |
| 38 | PRIOR FILING DATE: 2000-06-30        |
| 39 | PRIOR APPLICATION NUMBER: 60/225,266 |
| 40 | PRIOR FILING DATE: 2000-08-14        |
| 41 | PRIOR APPLICATION NUMBER: 60/249,218 |
| 42 | PRIOR FILING DATE: 2000-11-17        |
| 43 | PRIOR APPLICATION NUMBER: 60/249,208 |
| 44 | PRIOR FILING DATE: 2000-11-17        |
| 45 | PRIOR APPLICATION NUMBER: 60/249,213 |
| 46 | PRIOR FILING DATE: 2000-11-17        |
| 47 | PRIOR APPLICATION NUMBER: 60/249,212 |
| 48 | PRIOR FILING DATE: 2000-11-17        |
| 49 | PRIOR APPLICATION NUMBER: 60/249,207 |
| 50 | PRIOR FILING DATE: 2000-11-17        |
| 51 | PRIOR APPLICATION NUMBER: 60/249,245 |
| 52 | PRIOR FILING DATE: 2000-11-17        |
| 53 | PRIOR APPLICATION NUMBER: 60/249,244 |
| 54 | PRIOR FILING DATE: 2000-11-17        |
| 55 | PRIOR APPLICATION NUMBER: 60/249,217 |
| 56 | PRIOR FILING DATE: 2000-11-17        |
| 57 | PRIOR APPLICATION NUMBER: 60/249,211 |
| 58 | PRIOR FILING DATE: 2000-11-17        |
| 59 | PRIOR APPLICATION NUMBER: 60/249,215 |
| 60 | PRIOR FILING DATE: 2000-11-17        |
| 61 | PRIOR APPLICATION NUMBER: 60/249,264 |
| 62 | PRIOR FILING DATE: 2000-11-17        |
| 63 | PRIOR APPLICATION NUMBER: 60/249,214 |
| 64 | PRIOR FILING DATE: 2000-11-17        |
| 65 | PRIOR APPLICATION NUMBER: 60/249,237 |
| 66 | PRIOR FILING DATE: 2000-11-17        |
| 67 | PRIOR APPLICATION NUMBER: 60/233,400 |
| 68 | PRIOR FILING DATE: 2000-09-14        |
| 69 | PRIOR APPLICATION NUMBER: 60/231,242 |
| 70 | PRIOR FILING DATE: 2000-09-08        |
| 71 | PRIOR APPLICATION NUMBER: 60/232,081 |
| 72 | PRIOR FILING DATE: 2000-09-08        |
| 73 | PRIOR APPLICATION NUMBER: 60/233,080 |

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| 1  | PRIOR FILING DATE:        | 2000-09-08 |  |
| 2  | PRIOR APPLICATION NUMBER: | 60/231,414 |  |
| 3  | PRIOR FILING DATE:        | 2000-09-08 |  |
| 4  | PRIOR APPLICATION NUMBER: | 60/231,244 |  |
| 5  | PRIOR FILING DATE:        | 2000-09-08 |  |
| 6  | PRIOR APPLICATION NUMBER: | 60/233,064 |  |
| 7  | PRIOR FILING DATE:        | 2000-09-14 |  |
| 8  | PRIOR APPLICATION NUMBER: | 60/233,063 |  |
| 9  | PRIOR FILING DATE:        | 2000-09-14 |  |
| 10 | PRIOR APPLICATION NUMBER: | 60/233,397 |  |
| 11 | PRIOR FILING DATE:        | 2000-09-14 |  |
| 12 | PRIOR APPLICATION NUMBER: | 60/232,359 |  |
| 13 | PRIOR FILING DATE:        | 2000-09-14 |  |
| 14 | PRIOR APPLICATION NUMBER: | 60/232,401 |  |
| 15 | PRIOR FILING DATE:        | 2000-09-14 |  |
| 16 | PRIOR APPLICATION NUMBER: | 60/241,808 |  |
| 17 | PRIOR FILING DATE:        | 2000-10-20 |  |
| 18 | PRIOR APPLICATION NUMBER: | 60/241,826 |  |
| 19 | PRIOR FILING DATE:        | 2000-10-20 |  |
| 20 | PRIOR APPLICATION NUMBER: | 60/241,766 |  |
| 21 | PRIOR FILING DATE:        | 2000-10-20 |  |
| 22 | PRIOR APPLICATION NUMBER: | 60/241,221 |  |
| 23 | PRIOR FILING DATE:        | 2000-10-20 |  |
| 24 | PRIOR APPLICATION NUMBER: | 60/246,475 |  |
| 25 | PRIOR FILING DATE:        | 2000-11-08 |  |
| 26 | PRIOR APPLICATION NUMBER: | 60/231,243 |  |
| 27 | PRIOR FILING DATE:        | 2000-09-08 |  |
| 28 | PRIOR APPLICATION NUMBER: | 60/233,065 |  |
| 29 | PRIOR FILING DATE:        | 2000-09-14 |  |
| 30 | PRIOR APPLICATION NUMBER: | 60/233,398 |  |

|                       |                 |               |           |               |
|-----------------------|-----------------|---------------|-----------|---------------|
| Query Match           | 1.8%;           | Score 18;     | DB 7;     | Length 15270; |
| Best Local Similarity | 100.0%;         | Pred. No. 33; |           |               |
| Matches 18;           | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0        |

| QY | 227   | catccctgcatcacc  | 244   |
|----|-------|------------------|-------|
|    |       |                  |       |
| Db | 11976 | CATCCCTGCATCACCC | 11959 |

RESULT 25  
US-09-764-905-40566/c  
Sequence 40566, Application US/09764905  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.,  
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: PC004  
CURRENT APPLICATION NUMBER: US/09/764,905  
CURRENT FILING DATE: 2001-01-17  
PRIOR APPLICATION NUMBER: 60/179,065  
PRIOR FILING DATE: 2000-01-31  
PRIOR APPLICATION NUMBER: 60/180,628  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: 60/214,886  
PRIOR FILING DATE: 2000-06-28  
PRIOR APPLICATION NUMBER: 60/217,487  
PRIOR FILING DATE: 2000-07-11  
PRIOR APPLICATION NUMBER: 60/225,758  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/220,963  
PRIOR FILING DATE: 2000-07-26  
PRIOR APPLICATION NUMBER: 60/217,496  
PRIOR FILING DATE: 2000-07-11  
PRIOR APPLICATION NUMBER: 60/225,447  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/218,290  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: 60/225,757  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/226,868  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 60/216,647  
PRIOR FILING DATE: 2000-07-07

PRIOR APPLICATION NUMBER: 60/225,267  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/216,880  
PRIOR FILING DATE: 2000-07-07  
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PRIOR FILING DATE: 2000-12-08  
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PRIOR APPLICATION NUMBER: 60/234,223  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: 60/228,924  
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PRIOR APPLICATION NUMBER: 60/224,518  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/236,369  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/224,519  
PRIOR FILING DATE: 2000-08-14  
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PRIOR FILING DATE: 2000-07-26  
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PRIOR FILING DATE: 2000-09-29  
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PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/244,617  
PRIOR FILING DATE: 2000-11-01  
PRIOR APPLICATION NUMBER: 60/225,268  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/236,368  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/225,856  
PRIOR FILING DATE: 2000-12-08  
PRIOR APPLICATION NUMBER: 60/251,868  
PRIOR FILING DATE: 2000-12-08  
PRIOR APPLICATION NUMBER: 60/229,344  
PRIOR FILING DATE: 2000-09-01  
PRIOR APPLICATION NUMBER: 60/234,997  
PRIOR FILING DATE: 2000-09-25  
PRIOR APPLICATION NUMBER: 60/229,343  
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PRIOR APPLICATION NUMBER: 60/229,345  
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PRIOR APPLICATION NUMBER: 60/229,287  
PRIOR FILING DATE: 2000-09-01  
PRIOR APPLICATION NUMBER: 60/229,513  
PRIOR FILING DATE: 2000-09-05  
PRIOR APPLICATION NUMBER: 60/231,413  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: 60/229,509  
PRIOR FILING DATE: 2000-09-05  
PRIOR APPLICATION NUMBER: 60/236,367  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/237,039  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 60/237,038  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 60/236,370  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/236,802  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 60/237,037  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 60/237,040  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 60/240,960

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PRIOR FILING DATE: 2000-10-13  
PRIOR APPLICATION NUMBER: 60/239,937  
PRIOR FILING DATE: 2000-10-13  
PRIOR APPLICATION NUMBER: 60/241,787  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/246,474  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: 60/246,532  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: 60/249,216  
PRIOR FILING DATE: 2000-11-17  
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PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/226,681  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 60/225,759  
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PRIOR APPLICATION NUMBER: 60/225,214  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/235,836  
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PRIOR APPLICATION NUMBER: 60/230,438  
PRIOR FILING DATE: 2000-09-06  
PRIOR APPLICATION NUMBER: 60/215,135  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: 60/225,266  
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PRIOR APPLICATION NUMBER: 60/249,264  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,214  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,297  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/232,400  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: 60/231,242  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: 60/232,081  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: 60/232,080  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: 60/231,414  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: 60/231,244  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: 60/233,064  
PRIOR FILING DATE: 2000-09-14

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; PRIOR APPLICATION NUMBER: 60/233,063
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,397
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,399
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,401
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/241,808
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,826
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,786
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,221
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,475
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/231,243
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/233,065
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,398
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Query Match 1.8%; Score 18; DB 7; Length 15270;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 227 catccctcatcacc 244
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Db 11976 CATCCCTCATCACC 11959
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RESULT 26
; Sequence 1271, Application US/09803736
; GENERAL INFORMATION:
; APPLICANT: Bush, David F.
; APPLICANT: Levin, Irena M.
; APPLICANT: Norris, Susan R.
; APPLICANT: Rounsley, Steven D.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof
; FILE REFERENCE: 38-10(15493)D
; CURRENT APPLICATION NUMBER: US/09/803,736
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 09/534,859
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: Identified by Attorney Docket number 04983.0206CPUS01 38-10
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 1582
; SEQ ID NO 1271
; LENGTH: 62271
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-803-736-1271
```

```
Query Match 1.8%; Score 18; DB 6; Length 62271;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 779 aacaactctgaatcgg 796
```

```
Db 57285 aacaactctgaatcgg 57302
```

```
RESULT 27
US-09-803-736-896/c
; Sequence 896, Application US/09803736
; GENERAL INFORMATION:
; APPLICANT: Bush, David F.
; APPLICANT: Levin, Irena M.
```

```
; APPLICANT: Norris, Susan R.
; APPLICANT: Rounsley, Steven D.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof
; FILE REFERENCE: 38-10(15493)D
; CURRENT APPLICATION NUMBER: US/09/803,736
; CURRENT FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 09/534,859
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: Identified by Attorney Docket number 04983.0206CPUS01 38
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 1582
; SEQ ID NO 896
; LENGTH: 78596
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-803-736-896
```

```
Query Match 1.8%; Score 18; DB 6; Length 78596;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 930 caacatcaggaagggt 947
```

```
Db 41282 CAACATCAGGAGG 41265
```

```
RESULT 28
US-09-803-736-1270/c
; Sequence 1270, Application US/09803736
; GENERAL INFORMATION:
; APPLICANT: Bush, David F.
; APPLICANT: Levin, Irena M.
; APPLICANT: Norris, Susan R.
; APPLICANT: Rounsley, Steven D.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof
; FILE REFERENCE: 38-10(15493)D
; CURRENT APPLICATION NUMBER: US/09/803,736
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 09/534,859
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: Identified by Attorney Docket number 04983.0206CPUS01 38
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 1582
; SEQ ID NO 1270
; LENGTH: 87045
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-803-736-1270
```

```
Query Match 1.8%; Score 18; DB 6; Length 87045;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 779 aacaactctgaatcgg 796
```

```
Db 67036 AACAACCTTGATCTGG 67019
```

```
RESULT 29
US-09-803-736-19
; Sequence 19, Application US/09803736
; GENERAL INFORMATION:
; APPLICANT: Bush, David F.
; APPLICANT: Levin, Irena M.
; APPLICANT: Norris, Susan R.
; APPLICANT: Rounsley, Steven D.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof
; FILE REFERENCE: 38-10(15493)D
```

```
; CURRENT APPLICATION NUMBER: US/09/803,736
; CURRENT FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 09/534,859
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: Identified by Attorney Docket number 04983.0206CPUS01 38-10
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 1582
; SEQ ID NO 19
; LENGTH: 91470
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-803-736-19
```

```
Query Match          1.8%; Score 18; DB 6; Length 91470;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 797 gtttaggcgacagatga 814
|||||
Db 63394 gtttaggcgacagatga 63411
```

```
RESULT 30
US-09-803-736-1397/c
; Sequence 1397, Application US/09803736
; GENERAL INFORMATION:
; APPLICANT: Bush, David F.
; APPLICANT: Levin, Irena M.
; APPLICANT: Norris, Susan R.
; APPLICANT: Rounsley, Steven D.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof
; FILE REFERENCE: 38-10(15493)D
; CURRENT APPLICATION NUMBER: US/09/803,736
; CURRENT FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 09/534,859
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: Identified by Attorney Docket number 04983.0206CPUS01 38-10
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 1382
; SEQ ID NO 1397
; LENGTH: 96424
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-803-736-1397
```

```
Query Match          1.8%; Score 18; DB 6; Length 96424;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 202 accaatcgactctgcc 219
|||||
Db 81927 ACCAATCGACTCTGCC 81910
```

```
RESULT 31
US-09-803-736-1100
; Sequence 1100, Application US/09803736
; GENERAL INFORMATION:
; APPLICANT: Bush, David F.
; APPLICANT: Levin, Irena M.
; APPLICANT: Norris, Susan R.
; APPLICANT: Rounsley, Steven D.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof
; FILE REFERENCE: 38-10(15493)D
; CURRENT APPLICATION NUMBER: US/09/803,736
; CURRENT FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 09/534,859
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: Identified by Attorney Docket number 04983.0206CPUS01 38-10
```

```
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 1582
; SEQ ID NO 1100
; LENGTH: 110684
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-803-736-1100
```

```
Query Match          1.8%; Score 18; DB 6; Length 110684;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 652 gtttgcgcgcagcagta 669
|||||
Db 34775 gtttgcgcgcagcagta 34792
```

```
RESULT 32
US-60-253-456-35126/c
; Sequence 35126, Application US/60253456
; GENERAL INFORMATION:
; APPLICANT: Havukkala, Ilkka J
; TITLE OF INVENTION: Polynucleotides, isolated from
; TITLE OF INVENTION: plants, and methods for their use.
; FILE REFERENCE: 1054p1
; CURRENT APPLICATION NUMBER: US/60/253,456
; CURRENT FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 37096
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35126
; LENGTH: 88
; TYPE: DNA
; ORGANISM: Pinus radiata
US-60-253-456-35126
```

```
Query Match          1.7%; Score 17; DB 8; Length 88;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 842 cgcacaacacagccgaga 858
|||||
Db 74 CGCAACACAGCCGAGA 58
```

```
RESULT 33
US-60-253-457-47464/c
; Sequence 47464, Application US/60253457
; GENERAL INFORMATION:
; APPLICANT: Havukkala, Ilkka J
; TITLE OF INVENTION: Polynucleotides, isolated from plants
; TITLE OF INVENTION: and methods for their use.
; FILE REFERENCE: 1054p2
; CURRENT APPLICATION NUMBER: US/60/253,457
; CURRENT FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 48893
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47464
; LENGTH: 119
; TYPE: DNA
; ORGANISM: Pinus radiata
US-60-253-457-47464
```

```
Query Match          1.7%; Score 17; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 842 cgcacaacacagccgaga 858
|||||
Db 100 CGCAACACAGCCGAGA 84
```

```

RESULT 34
US-09-853-369-3951
: Sequence 3951, Application US/09853369
: GENERAL INFORMATION:
: APPLICANT: Ruan, Yijun
: APPLICANT: Ico, Laura Y.
: APPLICANT: Sherman, Bradley
: TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN ROOT
: FILE REFERENCE: PL-0005 CON
: CURRENT APPLICATION NUMBER: US/09/853,369
: CURRENT FILING DATE: 2001-05-14
: PRIOR APPLICATION NUMBER: 09/275,082
: PRIOR FILING DATE: 1999-03-23
: PRIOR APPLICATION NUMBER: 60/079,234
: PRIOR FILING DATE: 1998-03-25
: NUMBER OF SEQ ID NOS: 7696
: SOFTWARE: PERL Program
: SEQ ID NO 3951
: LENGTH: 216
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: Incyte ID No: 700150103H1
: US-09-853-369-3951

```

|         | Query Match            | Score 17; | DB 7;         | Length 216; |
|---------|------------------------|-----------|---------------|-------------|
|         | Best Local Similarity  | 100.0%;   | Pred. No. 92; |             |
| Matches | 17; Conservative       | 0;        | Mismatches    | 0; Indels   |
| Qy      | 658 cgcctggagcgcgtcgag | 714       |               |             |
| Db      | 149 cgcctggagcgcgtcgag | 165       |               |             |

```

RESULT 35
US-60-253-457-4199/C
: Sequence 4199, Application US/60253457
: GENERAL INFORMATION:
: APPLICANT: Havukkala, Ilkka J
: TITLE OF INVENTION: Polynucleotides, isolated from plants
: TITLE OF INVENTION: and methods for their use.
: FILE REFERENCE: 1054P2
: CURRENT APPLICATION NUMBER: US/60/253,457
: CURRENT FILING DATE: 2000-11-27
: NUMBER OF SEQ ID NOS: 48893
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 4199
: LENGTH: 216
: TYPE: DNA
: ORGANISM: Pinus radiata
: US-60-253-457-4199

```

|                       |                |                      |          |            |
|-----------------------|----------------|----------------------|----------|------------|
| Query Match           | 1.7%           | Score 17             | DB 8     | Length 215 |
| Best Local Similarity | 100.0%         | Pred. No. 92         |          |            |
| Matches 17            | Conservative 0 | Mismatches 0         | Indels 0 | Gaps 0     |
| Qy                    | 842            | cgcacaacacagccgcgaga | 858      |            |
|                       |                |                      |          |            |
|                       |                |                      |          |            |
|                       |                |                      |          |            |
|                       |                |                      |          |            |
| Db                    | 125            | CGCAAAACACAGCCCGAGA  | 109      |            |

```

: RESULT 36
: US-60-253-457-26116/C
: Sequence 26116, Application US/60253457
: GENERAL INFORMATION:
: APPLICANT: Havukkala, Ilkka J
: TITLE OF INVENTION: Polynucleotides, isolated from plants
: TITLE OF INVENTION: and methods for their use.
: FILE REFERENCE: 105442

```

```

? CURRENT APPLICATION NUMBER: US/60/253,457
? CURRENT FILING DATE: 2000-11-17
? NUMBER OF SEQ ID NOS: 48893
? SOFTWARE: FASTSQ for Windows Version 4.0.0
? SEQ ID NO: 26116
? LENGTH: 2319
? TYPE: DNA
? ORGANISM: Pinus radiata
US-60-253-457 -26116
```

|                       |                |                   |          |            |
|-----------------------|----------------|-------------------|----------|------------|
| Query Match           | 1.7%           | Score 17          | DB 8     | Length 239 |
| Best Local Similarity | 100.0%         | Pred. No. 93      |          |            |
| Matches 17            | Conservative 0 | Mismatches 0      | Indels 0 | Gaps 0     |
| Qy                    | 842            | CGCAACACAGCGCGAGA | 858      |            |
|                       |                |                   |          |            |
| Db                    | 33             | CGCAACACAGCGCGAGA | 17       |            |

```

RESULT 37
US-09-724-671-17298
: Sequence 17298, Application US/09724671
: GENERAL INFORMATION:
: APPLICANT: Watson, James D
: APPLICANT: Morrison, James G
: TITLE OF INVENTION: Polynucleotides, polypeptides expressed
: TITLE OF INVENTION: by the polynucleotides and methods for their use
: FILE REFERENCE: 105002
: CURRENT APPLICATION NUMBER: US/09/724,671
: CURRENT FILING DATE: 2000-11-28
: PRIOR APPLICATION NUMBER: U.S. No. 60/171,678
: PRIOR FILING DATE: 1999-12-23
: NUMBER OF SEQ. ID NOS: 21907
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ. ID NO 17298
: LENGTH: 241
: TYPE: DNA
: ORGANISM: Mouse
: US-09-724-671-17298

```

|    | Query Match           | 1.7%           | Score 17     | DB 7     | Length 241 |
|----|-----------------------|----------------|--------------|----------|------------|
|    | Best Local Similarity | 100.0%         | Pred. No. 93 |          |            |
|    | Matches 17            | Conservative 0 | Mismatches 0 | Indels 0 | Gaps 0     |
| Qy | 113 aacagcagccagccca  | 129            |              |          |            |
|    |                       |                |              |          |            |
| Db | 98 aacagcagccagccca   | 114            |              |          |            |

```

RESULT 38
US-09-540-213-52685
: Sequence 52685, Application US/09540213
: GENERAL INFORMATION:
: APPLICANT: Seilhamer, Jeffrey J.
: APPLICANT: Delegeane, Angelo M.
: APPLICANT: Stuart, Susan G.
: APPLICANT: Stuve, Laura L.
: APPLICANT: Mullahy, Sara J.
: APPLICANT: Naughton, Rebecca E.
: TITLE OF INVENTION: POLYNUCLEOTIDES OF LIVER AND PANCREAS
: FILE REFERENCE: PD-1031 CIP
: CURRENT APPLICATION NUMBER: US/09/540, 213
: CURRENT FILING DATE: 2000-03-31
: Prior application data removed - consult PALM or file wrapper
: NUMBER OF SEQ ID NOS: 53844
: SEQ ID NO 52685
: LENGTH: 241
: TYPE: DNA
: ORGANISM: Rattus norvegicus
: FEATURE:
: NAME/KEY: misc-feature

```

```
; OTHER INFORMATION: Incyte ID No: rat00171041
US-09-540-213-52685

Query Match
Best Local Similarity 1.7%; Score 17; DB 7; Length 241;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 aacagcagccagccaa 129
|||||
Db 71 aacagcagccagccaa 87

RESULT 39
US-60-253-457-26897/c
; Sequence 26897, Application US/60253457
; GENERAL INFORMATION:
; APPLICANT: Havukala, Ilkka J
; TITLE OF INVENTION: Polynucleotides, isolated from plants
; TITLE OF INVENTION: and methods for their use.
; FILE REFERENCE: 1054p2
; CURRENT APPLICATION NUMBER: US/60/253,457
; CURRENT FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 48893
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26897
; LENGTH: 250
; TYPE: DNA
; ORGANISM: Pinus radiata
US-60-253-457-26897

Query Match
Best Local Similarity 1.7%; Score 17; DB 8; Length 250;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 842 cgcacacacagcagaga 858
|||||
Db 91 CGCAACACACAGCCGAGA 75

RESULT 40
US-09-864-761-27318
; Sequence 27318, Application US/09864761
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Acomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
```

```
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 27318
; LENGTH: 262
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC004707.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.78
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.82
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.84
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.97
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.73
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.88
; OTHER INFORMATION: NT HIT: g111434402, EVALUE 1.00e-91
; OTHER INFORMATION: EST_HUMAN HIT: BE891148.1, EVALUE 2.00e-91
; OTHER INFORMATION: SWISSPROT HIT: P16815, EVALUE 4.20e+00
US-09-864-761-27318

Query Match
Best Local Similarity 1.7%; Score 17; DB 7; Length 262;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 812 tgacagagctgcagcag 828
|||||
Db 127 tgacagagctgcagcag 143

RESULT 41
US-09-540-213-44587
; Sequence 44587, Application US/09540213
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullaby, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES OF LIVER AND PANCREAS
; FILE REFERENCE: PD-1031 CIP
; CURRENT APPLICATION NUMBER: US/09/540,213
; CURRENT FILING DATE: 2000-03-31
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 53844
; SEQ ID NO 44587
; LENGTH: 264
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: rat00163047
US-09-540-213-44587

Query Match
Best Local Similarity 1.7%; Score 17; DB 7; Length 264;
```

Best Local Similarity 100.0%; Pred. No. 93;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 113 aacagcagccagcgccaa 129  
|||||  
Db 71 aacagcagccagcgccaa 87

RESULT 42  
US-60-253-456-17545/C  
; Sequence 17545, Application US/60253456  
; GENERAL INFORMATION:  
; APPLICANT: Havukkaia, Ilkka J  
; TITLE OF INVENTION: Polynucleotides, isolated from  
; FILE REFERENCE: 1054p1  
; CURRENT APPLICATION NUMBER: US/60/253,456  
; NUMBER OF SEQ ID NOS: 37096  
; SOFTWARE: fastseq for Windows Version 4.0  
; SEQ ID NO 17545  
; LENGTH: 268  
; TYPE: DNA  
; ORGANISM: Pinus radiata  
US-60-253-456-17545

Query Match 1.7%; Score 17; DB 8; Length 268;  
Best Local Similarity 100.0%; Pred. No. 93;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 842 cgcacaacagccgaga 858  
|||||  
Db 122 CCACAACACAGCCGAGA 106

RESULT 43  
US-09-912-292-45542  
; Sequence 45542, Application US/09912292  
; GENERAL INFORMATION:  
; APPLICANT: Rosen, et. al.  
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 101  
; FILE REFERENCE: PO-101  
; CURRENT APPLICATION NUMBER: US/09/912,292  
; CURRENT FILING DATE: 2001-07-26  
; PRIOR APPLICATION NUMBER: 08/103,746  
; PRIOR FILING DATE: 1993-08-09  
; PRIOR APPLICATION NUMBER: 09/859,417  
; PRIOR FILING DATE: 2001-05-18  
; PRIOR APPLICATION NUMBER: 08/103,743  
; PRIOR FILING DATE: 1993-08-09  
; PRIOR APPLICATION NUMBER: 09/741,827  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 09/813,154  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 08/196,482  
; PRIOR FILING DATE: 1994-02-15  
; PRIOR APPLICATION NUMBER: 09/783,587  
; PRIOR FILING DATE: 2001-02-15  
; PRIOR APPLICATION NUMBER: 08/196,481  
; PRIOR FILING DATE: 1994-02-15  
; PRIOR APPLICATION NUMBER: 08/220,662  
; PRIOR FILING DATE: 1994-03-31  
; PRIOR APPLICATION NUMBER: 08/220,661  
; PRIOR FILING DATE: 1994-03-31  
; PRIOR APPLICATION NUMBER: 08/275,627  
; PRIOR FILING DATE: 1994-07-15  
; PRIOR APPLICATION NUMBER: 08/345,704  
; PRIOR FILING DATE: 1994-11-21  
; PRIOR APPLICATION NUMBER: 09/859,662  
; PRIOR FILING DATE: 2001-05-18  
; PRIOR APPLICATION NUMBER: 08/401,881  
; PRIOR FILING DATE: 1995-03-10

; PRIOR APPLICATION NUMBER: 09/782,161  
; PRIOR FILING DATE: 2001-02-14  
; PRIOR APPLICATION NUMBER: 08/790,776  
; PRIOR FILING DATE: 1997-01-30  
; PRIOR APPLICATION NUMBER: 60/010,803  
; PRIOR FILING DATE: 1996-01-30  
; PRIOR APPLICATION NUMBER: 08/799,180  
; PRIOR FILING DATE: 1997-02-12  
; PRIOR APPLICATION NUMBER: 60/011,618  
; PRIOR FILING DATE: 1996-02-13  
; PRIOR APPLICATION NUMBER: 08/803,609  
; PRIOR FILING DATE: 1997-02-21  
; PRIOR APPLICATION NUMBER: 60/011,985  
; PRIOR FILING DATE: 1996-02-21  
; PRIOR APPLICATION NUMBER: 08/971,050  
; PRIOR FILING DATE: 1997-11-14  
; PRIOR APPLICATION NUMBER: 60/031,038  
; PRIOR FILING DATE: 1996-11-18  
; PRIOR APPLICATION NUMBER: 08/975,985  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: 60/031,221  
; PRIOR FILING DATE: 1996-11-25  
; PRIOR APPLICATION NUMBER: 08/985,366  
; PRIOR FILING DATE: 1997-12-04  
; PRIOR APPLICATION NUMBER: 09/842,827  
; PRIOR FILING DATE: 2001-04-27  
; PRIOR APPLICATION NUMBER: 60/032,782  
; PRIOR FILING DATE: 1996-12-06  
; PRIOR APPLICATION NUMBER: 09/076,898  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/047,004  
; PRIOR FILING DATE: 1997-05-13  
; PRIOR APPLICATION NUMBER: 09/078,614  
; PRIOR FILING DATE: 1998-05-14  
; PRIOR APPLICATION NUMBER: 60/046,498  
; PRIOR FILING DATE: 1997-05-14  
; PRIOR APPLICATION NUMBER: 09/189,834  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: 60/065,454  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 09/366,690  
; PRIOR FILING DATE: 1999-08-04  
; PRIOR APPLICATION NUMBER: 60/095,484  
; PRIOR FILING DATE: 1998-08-05  
; PRIOR APPLICATION NUMBER: 09/342,216  
; PRIOR FILING DATE: 1999-06-29  
; PRIOR APPLICATION NUMBER: 60/091,170  
; PRIOR FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: 09/487,572  
; PRIOR FILING DATE: 2000-01-19  
; PRIOR APPLICATION NUMBER: 60/116,678  
; PRIOR FILING DATE: 1999-01-21  
; PRIOR APPLICATION NUMBER: 09/497,772  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: 60/118,784  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: 09/504,577  
; PRIOR FILING DATE: 2000-02-15  
; PRIOR APPLICATION NUMBER: 60/120,434  
; PRIOR FILING DATE: 1999-02-16  
; PRIOR APPLICATION NUMBER: 09/517,011  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: 60/122,447  
; PRIOR FILING DATE: 1999-03-02  
; PRIOR APPLICATION NUMBER: 09/628,857  
; PRIOR FILING DATE: 2000-07-27  
; PRIOR APPLICATION NUMBER: 60/145,956  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: 09/628,858



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PRIORITY FILING DATE: 2000-07-27
PRIORITY APPLICATION NUMBER: 60/145,955
PRIORITY FILING DATE: 1999-07-28
PRIORITY APPLICATION NUMBER: 09/741,033
PRIORITY FILING DATE: 2000-12-21
PRIORITY APPLICATION NUMBER: 09/773,518
PRIORITY FILING DATE: 2001-02-02
PRIORITY APPLICATION NUMBER: 60/171,621
PRIORITY FILING DATE: 1999-12-23
PRIORITY APPLICATION NUMBER: 09/796,765
PRIORITY FILING DATE: 2001-03-02
PRIORITY APPLICATION NUMBER: 09/867,682
PRIORITY FILING DATE: 2001-05-31
PRIORITY APPLICATION NUMBER: 60/187,016
PRIORITY FILING DATE: 2000-03-06
PRIORITY APPLICATION NUMBER: 60/225,269
PRIORITY FILING DATE: 2000-08-14
PRIORITY APPLICATION NUMBER: 60/225,629
PRIORITY FILING DATE: 2000-08-15
NUMBER OF SEQ ID NOS: 55553
SEQ ID NO 45542
LENGTH: 273
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (28)..(28)
OTHER INFORMATION: n is equal to a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (43)..(43)
OTHER INFORMATION: n is equal to a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (52)..(53)
OTHER INFORMATION: n is equal to a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (59)..(59)
OTHER INFORMATION: n is equal to a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (105)..(105)
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NAME/KEY: misc_feature
LOCATION: (122)..(123)
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NAME/KEY: misc_feature
LOCATION: (150)..(151)
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NAME/KEY: misc_feature
LOCATION: (153)..(154)
OTHER INFORMATION: n is equal to a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (157)..(158)
OTHER INFORMATION: n is equal to a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (170)..(171)
OTHER INFORMATION: n is equal to a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (230)..(230)
OTHER INFORMATION: n is equal to a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (257)..(257)
OTHER INFORMATION: n is equal to a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (261)..(261)
OTHER INFORMATION: n is equal to a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (264)..(264)
OTHER INFORMATION: n is equal to a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (273)..(273)
OTHER INFORMATION: n is equal to a,t,g, or c
US-09-912-292-45542

```

```

Query Match      1.7%; Score 17; DB 7; Length 273;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 812 tgcacagactgcagcag 828
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Db 10 tgcacagactgcagcag 26

```

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RESULT 44
US-60-253-378-16751/c
Sequence 16751, Application US/60253378
GENERAL INFORMATION:
APPLICANT: Chaavukala, Ilkka J
TITLE OF INVENTION: Polynucleotides isolated from plants
FILE REFERENCE: 1054P3
CURRENT APPLICATION NUMBER: US/60/253,378
CURRENT FILING DATE: 2000-11-27
NUMBER OF SEQ ID NOS: 40367
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16751
LENGTH: 276
TYPE: DNA
ORGANISM: Pinus radiata
US-60-253-378-16751

```

```

Query Match      1.7%; Score 17; DB 8; Length 276;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 842 cgcacaacacagccgaga 858
|||||
Db 104 CGCAACACAGCCGAGA 88

```

```

RESULT 45
US-60-253-457-27422/c
Sequence 27422, Application US/60253457
GENERAL INFORMATION:
APPLICANT: Havukala, Ilkka J
TITLE OF INVENTION: Polynucleotides, isolated from plants
FILE REFERENCE: 1054P2
CURRENT APPLICATION NUMBER: US/60/253,457
CURRENT FILING DATE: 2000-11-27
NUMBER OF SEQ ID NOS: 48893
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 27422
LENGTH: 278
TYPE: DNA
ORGANISM: Pinus radiata
US-60-253-457-27422

```

```

Query Match      1.7%; Score 17; DB 8; Length 278;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 842 cgcacaacacagccgaga 858
|||||
Db 115 CGCAACACAGCCGAGA 99

```

```

RESULT 46
US-60-253-457-35043/c
Sequence 35043, Application US/60253457
GENERAL INFORMATION:
APPLICANT: Havukala, Ilkka J
TITLE OF INVENTION: Polynucleotides, isolated from plants
FILE REFERENCE: 1054P2

```

```

; CURRENT APPLICATION NUMBER: US/60/253,457
; CURRENT FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 48893
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35043
; LENGTH: 279
; TYPE: DNA
; ORGANISM: Pinus radiata
US-60-253-457-35043
```

```

Query Match          1.7%: Score 17; DB 8; Length 279;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 842 cgcgaacacagccgaga 858
    |||
Db 122 CGCAACACAGCCGAGA 106
```

```

RESULT 47
US-09-724-750-1826/C
; Sequence 1826, Application US/09724750
; GENERAL INFORMATION:
; APPLICANT: Havukkala, Ilkka
; TITLE OF INVENTION: Polynucleotide, Materials Incorporating
; FILE REFERENCE: 11000.1049AU
; CURRENT APPLICATION NUMBER: US/09/724,750
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/171,431
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 25199
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1826
; LENGTH: 280
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-724-750-1826
```

```

Query Match          1.7%: Score 17; DB 7; Length 280;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 842 cgcgaacacagccgaga 858
    |||
Db 130 CGCAACACAGCCGAGA 114
```

```

RESULT 48
US-09-863-524-1238
; Sequence 1238, Application US/09863524
; GENERAL INFORMATION:
; APPLICANT: Ito, Laura Y.
; APPLICANT: Gooding, Douglas H.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN ROOTS
; FILE REFERENCE: PL-0003 US
; CURRENT APPLICATION NUMBER: US/09/863,524
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 60/077,831
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 6814
; SOFTWARE: PERL Program
; SEQ ID NO 1238
; LENGTH: 289
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 700027505H1
; NAME/KEY: unsure
```

```

; LOCATION: 118-146, 183
; OTHER INFORMATION: a, t, c, g, or other
US-09-863-524-1238
```

```

Query Match          1.7%: Score 17; DB 7; Length 289;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 698 cgcgtgagcgcgtgag 714
    |||
Db 50 cgcgtgagcgcgtgag 66
```

```

RESULT 49
US-60-253-457-35140/C
; Sequence 35140, Application US/60253457
; GENERAL INFORMATION:
; APPLICANT: Havukkala, Ilkka J
; TITLE OF INVENTION: Polynucleotides, Isolated from plants
; FILE REFERENCE: 1054P2
; CURRENT APPLICATION NUMBER: US/60/253,457
; CURRENT FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 48893
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35140
; LENGTH: 291
; TYPE: DNA
; ORGANISM: Pinus radiata
US-60-253-457-35140
```

```

Query Match          1.7%: Score 17; DB 8; Length 291;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 842 cgcgaacacagccgaga 858
    |||
Db 122 CGCAACACAGCCGAGA 106
```

```

RESULT 50
US-09-540-213-33702
; Sequence 33702, Application US/09540213
; GENERAL INFORMATION:
; APPLICANT: Selbameer, Jeffrey J.
; APPLICANT: Deleagane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES OF LIVER AND PANCREAS
; FILE REFERENCE: PD-1031 CIP
; CURRENT APPLICATION NUMBER: US/09/540,213
; CURRENT FILING DATE: 2000-03-31
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 53844
; SEQ ID NO 33702
; LENGTH: 300
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: rat00076798
US-09-540-213-33702
```

```

Query Match          1.7%: Score 17; DB 7; Length 300;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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QY 113 aacagcagccagccaa 129
```

Mon Sep 24 09:36:18 2001

us-09-138-735-1\_copy\_1232\_2207.oli5.rnpn

Page 25

Db 76 aacagcagccagccaa 92

Search completed: September 21, 2001, 13:39:08  
job time: 909 sec

**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 21, 2001, 00:36:20 : Search time 3479.37 Seconds  
(without alignments)  
93.357 Million cell updates/sec

Title: US-09-138-735-12  
Perfect score: 21  
Sequence: 1 cgaagagaccatgaacaactt 21

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:\*

- 1: gb\_ba1:\*
- 2: gb\_ba2:\*
- 3: gb\_ba3:\*
- 4: gb\_in1:\*
- 5: gb\_in2:\*
- 6: gb\_in3:\*
- 7: gb\_om:\*
- 8: gb\_ov:\*
- 9: gb\_pat1:\*
- 10: gb\_pat2:\*
- 11: gb\_ph:\*
- 12: gb\_p11:\*
- 13: gb\_p12:\*
- 14: gb\_p13:\*
- 15: gb\_p14:\*
- 16: gb\_ba1:\*
- 17: gb\_ba2:\*
- 18: gb\_fun:\*
- 19: gb\_htg\_hum:\*
- 20: gb\_htg\_inv:\*
- 21: gb\_htg\_rod:\*
- 22: gb\_htg\_hum1:\*
- 23: gb\_htg\_hum2:\*
- 24: gb\_htg\_hum3:\*
- 25: gb\_htg\_hum4:\*
- 26: gb\_htg\_hum5:\*
- 27: gb\_htg\_hum6:\*
- 28: gb\_htg\_hum7:\*
- 29: gb\_htg\_hum8:\*
- 30: gb\_htg\_inv1:\*
- 31: gb\_htg\_inv2:\*
- 32: gb\_htg\_other:\*
- 33: gb\_htg\_rod:\*
- 34: gb\_hum1:\*
- 35: gb\_hum2:\*
- 36: gb\_hum3:\*
- 37: gb\_hum4:\*
- 38: gb\_hum5:\*
- 39: gb\_hum6:\*
- 40: gb\_hum7:\*
- 41: gb\_in:\*
- 42: gb\_om:\*
- 43: gb\_or:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID       | Description          |
|------------|-------|-------------|--------|-------------|----------------------|
| 1          | 21    | 100.0       | 21     | 9 A48921    | A48921 Sequence 12   |
| 2          | 21    | 100.0       | 21     | 9 AR047930  | AR047930 Sequence 12 |
| 3          | 21    | 100.0       | 3402   | 9 A48910    | A48910 Sequence 1    |
| 4          | 21    | 100.0       | 3402   | 9 AR047920  | AR047920 Sequence 1  |
| 5          | 21    | 100.0       | 3402   | 96 TC024190 | TC024190 Sequence 1  |
| 6          | 19    | 90.5        | 67442  | 63 AC015691 | AC015691 Homo sapi   |
| 7          | 18.4  | 87.6        | 64744  | 78 AC090694 | AC090694 Homo sapi   |
| 8          | 18.4  | 87.6        | 215798 | 79 AL161719 | AL161719 Homo sapi   |

|   |    |      |      |        |    |           |                    |
|---|----|------|------|--------|----|-----------|--------------------|
| C | 9  | 18   | 85.7 | 147042 | 62 | AC011647  | AC011647 Homo sapi |
| C | 10 | 18   | 85.7 | 199958 | 69 | AC026083  | AC026083 Homo sapi |
| C | 11 | 17.8 | 84.8 | 2984   | 3  | PST012352 | AI012352 Pseudomon |
| C | 12 | 17.8 | 84.8 | 6052   | 1  | AF121970  | AF121970 Pseudomon |
| C | 13 | 17.8 | 84.8 | 6921   | 1  | AF027768  | AF027768 Serratia  |
| C | 14 | 17.8 | 84.8 | 174376 | 64 | AC016562  | AC016562 Homo sapi |
| C | 15 | 17.8 | 84.8 | 205638 | 71 | AC040697  | AC040697 Homo sapi |
| C | 16 | 17.8 | 84.8 | 228434 | 62 | AC012205  | AC040927 Mus muscu |
| C | 17 | 17.4 | 82.9 | 313    | 54 | HS355TH1  | AC012205 Homo sapi |
| C | 18 | 17.4 | 82.9 | 128235 | 93 | HS3995C14 | Z51526 H.sapiens ( |
| C | 19 | 17.4 | 82.9 | 135983 | 93 | HS3595K12 | AL050340 Human DNA |
| C | 20 | 17.4 | 82.9 | 146431 | 75 | AC079098  | AL096828 Human DNA |
| C | 21 | 17.4 | 82.9 | 148030 | 78 | AL137803  | AC079098 Homo sap  |
| C | 22 | 17.4 | 82.9 | 155356 | 73 | AC068308  | AL137803 Homo sap  |
| C | 23 | 17.4 | 82.9 | 170887 | 79 | AL161910  | AC068308 Homo sap  |
| C | 24 | 17.4 | 82.9 | 173381 | 71 | AC040918  | AL161910 Homo sap  |
| C | 25 | 17.4 | 82.9 | 196941 | 64 | AC070662  | AC040918 Homo sap  |
| C | 26 | 17.4 | 82.9 | 312420 | 82 | AL509023  | AC070662 Homo sap  |
| C | 27 | 17   | 81.0 | 165443 | 76 | AC079939  | AL509023 Homo sap  |
| C | 28 | 17   | 81.0 | 191352 | 74 | AC073565  | AC079939 Mus muscu |
| C | 29 | 16.8 | 80.0 | 1590   | 6  | CEU25632  | AC073565 Mus muscu |
| C | 30 | 16.8 | 80.0 | 2141   | 89 | AK001946  | U25632 Caenorhabdi |
| C | 31 | 16.8 | 80.0 | 2158   | 93 | HSM601650 | AK001946 Homo sap  |
| C | 32 | 16.8 | 80.0 | 2163   | 9  | AX056419  | AL136682 Homo sap  |
| C | 33 | 16.8 | 80.0 | 2163   | 89 | AF113249  | AX056419 Sequence  |
| C | 34 | 16.8 | 80.0 | 2197   | 91 | BC001221  | AF113249 Homo sap  |
| C | 35 | 16.8 | 80.0 | 15033  | 63 | AC012888  | BC001221 Homo sap  |
| C | 36 | 16.8 | 80.0 | 31800  | 6  | CET21B10  | AC012888 Drosophi  |
| C | 37 | 16.8 | 80.0 | 50550  | 11 | AF271693  | Z68313 Caenorhabdi |
| C | 38 | 16.8 | 80.0 | 63409  | 67 | AC032982  | AF271693 mycobacte |
| C | 39 | 16.8 | 80.0 | 65843  | 69 | AC025903  | AC032982 Homo sap  |
| C | 40 | 16.8 | 80.0 | 85560  | 65 | AC019835  | AC025903 Homo sap  |
| C | 41 | 16.8 | 80.0 | 86719  | 91 | AP0000885 | AC019835 Drosophi  |
| C | 42 | 16.8 | 80.0 | 94378  | 13 | ATF15B8   | AP0000885 Homo sap |
| C | 43 | 16.8 | 80.0 | 100834 | 90 | AL160411  | AL049660 Arabidops |
| C | 44 | 16.8 | 80.0 | 104087 | 87 | AC008926  | AL160411 Human DNA |
| C | 45 | 16.8 | 80.0 | 104549 | 62 | AC011384  | AC008926 Homo sap  |
| C | 45 | 16.8 | 80.0 | 104549 | 62 | AC011384  | AC011384 Homo sap  |

|                       |                                                                                                        |                        |                  |
|-----------------------|--------------------------------------------------------------------------------------------------------|------------------------|------------------|
| Oy                    | 1                                                                                                      | CGAAGAGACCATgaacacctt  | 21               |
|                       |                                                                                                        |                        |                  |
| Dd                    | 1                                                                                                      | CGAAGAGACCATGAACAACCTT | 21               |
| RESULT                | 2                                                                                                      |                        |                  |
| LOCUS                 | AR047930                                                                                               |                        | PAT              |
| DEFINITION            | AR047930                                                                                               | 21 bp                  | 29-SEP-1999      |
| ACCESION              | Sequence 12 from patent US 5820864.                                                                    |                        |                  |
| VERSION               | AR047930                                                                                               |                        |                  |
| KEYWORDS              | AR047930.1 GI:5970273                                                                                  |                        |                  |
| SOURCE                | .                                                                                                      |                        |                  |
| ORGANISM              | Unknown.                                                                                               |                        |                  |
| REFERENCE             | Unknown.                                                                                               |                        |                  |
| AUTHORS               | Unclassified.                                                                                          |                        |                  |
| TITLE                 | 1 (bases 1 to 21)                                                                                      |                        |                  |
| JOURNAL               | Paranhos-Baccala,G., Iesenechal,M. and Jollivet,M.                                                     |                        |                  |
| FEATURES              | Trypanosoma cruzi antigen, gene encoding therefor and methods of detecting and treating chagas disease |                        |                  |
|                       | Patent: US 5820864-A 12 13-OCT-1998;                                                                   |                        |                  |
|                       | Location/Qualifiers                                                                                    |                        |                  |
|                       | 1..21                                                                                                  |                        |                  |
| BASE COUNT            | 9 a                                                                                                    | 5 c                    | 4 g              |
| ORIGIN                | /organism="unknown"                                                                                    | 3 t                    |                  |
| Query Match           | 100.0%;                                                                                                | Score 21;              | DB 9; Length 21; |
| Best Local Similarity | 100.0%;                                                                                                | Pred. NO. 2;           |                  |
| Matches 21;           | Conservative 0;                                                                                        | Mismatches 0;          | Indels 0;        |
| Gaps 0;               |                                                                                                        |                        |                  |
| OY                    | 1                                                                                                      | cgaagagaccatgaacaactt  | 21               |
|                       |                                                                                                        |                        |                  |
| Dd                    | 1                                                                                                      | CGAAGAGACCATGAACAACCTT | 21               |
| RESULT                | 3                                                                                                      |                        |                  |

| ALIGNMENTS            |          |                                                                                                                  |               |           |            |  |  |  |  |
|-----------------------|----------|------------------------------------------------------------------------------------------------------------------|---------------|-----------|------------|--|--|--|--|
| RESULT                | 1        |                                                                                                                  |               |           |            |  |  |  |  |
| LOCUS                 | A48921   |                                                                                                                  |               |           |            |  |  |  |  |
| DEFINITION            | A48921   | 21 bp                                                                                                            | DNA           |           |            |  |  |  |  |
| ACCESSION             | A48921   | Sequence 12 from Patent WO9605312.                                                                               |               |           |            |  |  |  |  |
| VERSION               | A48921.1 | GI:2302580                                                                                                       |               |           |            |  |  |  |  |
| KEYWORDS              |          |                                                                                                                  |               |           |            |  |  |  |  |
| SOURCE                |          | unidentified.                                                                                                    |               |           |            |  |  |  |  |
| ORGANISM              |          | unidentified.                                                                                                    |               |           |            |  |  |  |  |
| REFERENCE             |          | unclassified.                                                                                                    |               |           |            |  |  |  |  |
| AUTHORS               |          | 1 (bases 1 to 21)                                                                                                |               |           |            |  |  |  |  |
| TITLE                 |          | Paranos-Paccali,G., Lesenechal,M. and Jolivet,M.                                                                 |               |           |            |  |  |  |  |
| JOURNAL               |          | NOVEL TRYPANOSOMA CRUZI ANTIGEN, AND GENE CODING THEREFOR; THEIR APPLICATION TO THE DETECTION OF CHAGAS' DISEASE |               |           |            |  |  |  |  |
| COMMENT               |          | Patent: WO 9605312-A 12 22-FEB-1996;                                                                             |               |           |            |  |  |  |  |
| FEATURES              |          | BIO MERIEUX (FR)                                                                                                 |               |           |            |  |  |  |  |
| SOURCE                |          | Other publication CA 2173957 960222                                                                              |               |           |            |  |  |  |  |
|                       |          | Other publication AU 3169195 960307                                                                              |               |           |            |  |  |  |  |
|                       |          | Other publication FR 2723589 960216.                                                                             |               |           |            |  |  |  |  |
|                       |          | location/Qualifiers                                                                                              |               |           |            |  |  |  |  |
|                       |          | 1..21                                                                                                            |               |           |            |  |  |  |  |
|                       |          | /organism="unidentified"                                                                                         |               |           |            |  |  |  |  |
|                       |          | /db_xref="taxon:32644"                                                                                           |               |           |            |  |  |  |  |
| BASE COUNT            | 9 a      | 5 c                                                                                                              | 4 g           | 3 t       |            |  |  |  |  |
| ORIGIN                |          |                                                                                                                  |               |           |            |  |  |  |  |
| Query Match           |          | 100.0%                                                                                                           | Score 21;     | DB 9;     | Length 21; |  |  |  |  |
| Best Local Similarity |          | 100.0%                                                                                                           | Pred. No. 2;  |           |            |  |  |  |  |
| Matches 21;           |          | Conservative 0;                                                                                                  | Mismatches 0; | Indels 0; | Gaps 0;    |  |  |  |  |

[illegible]

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RESULT 4
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DEFINITION Sequence 1 from patent US 5820864.
ACCESSION AR047920
VERSION AR047920.1 GI:5970263
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
AUTHORS 1 (bases 1 to 3402)
TITLE Trypanosoma cruzi antigen, gene encoding therefor and methods of
JOURNAL detecting and treating chagas disease
FEATURES
source
BASE COUNT 888 a 821 c 956 g 737 t
ORIGIN
Query Match 100.0%; Score 21; DB 9; Length 3402;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 cgaagagaccatgacaactt 21
Db 1997 CGAGAGACCAGTACCACTT 2017

RESULT 5
LOCUS TC024190 3402 bp mRNA INV 04-AUG-1997
DEFINITION Trypanosoma cruzi Tc40 antigen (Tc40) mRNA, complete cds.
ACCESSION U24190
VERSION U24190.1 GI:790645
KEYWORDS
SOURCE Trypanosoma cruzi.
ORGANISM Trypanosoma cruzi
Eukaryota; Euzoenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.
REFERENCE
AUTHORS 1 (bases 1 to 3402)
TITLE Lesenechal, M., Duret, L., Cano, M.I., Mortara, R.A., Jolivet, M.,
JOURNAL Camargo, M.E., da Silveira, J.F. and Paranhos-Baccala, G.
DEFINITION Cloning and characterization of a gene encoding a novel
ACCESSION immunodominant antigen of Trypanosoma cruzi
VERSION Mo1. Biochem. Parasitol. 87 (2), 193-204 (1997)
KEYWORDS 97391123
SOURCE 2 (bases 1 to 3402)
JOURNAL Lesenechal, M., Franco Da Silveira, J., Mortara, R.A., Duret, L.,
AUTHORS Camargo, M.E., Jolivet, M. and Paranhos-Baccala, G.
TITLE Direct Submission
JOURNAL Submitted (06-APR-1995) Mylene Lesenechal, Biomerieux, 22 rue Saint
FEATURES
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1. 3402
/gene="Tc40"
266. 3013
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/codon_start=1
/product="Tc40 antigen"
/protein_id="AAC47657.1"

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SSLLERDVSLRATIORNCTTLRTLPVSESLCSVSGGWFPTTEPTVAACT
LNRSTPSMACCEGEVPAALHLDATVEENVSLVAATSTGVOMLTLTGAEPMLRK
FVIGDSIVAMESRETFVAFDDRKQALVNNHSPNFCYHAMPCCVORNGFCFNRT
ADGSCVLDAMDSNRLTIFHLRSSRREDOOPGCKTSVATAPKGCVSGDVASSHNT
TSAASAASPPVAPAPAKAAPPAARSAEPHVSKITIANLVNOLGIVORSVSTG
APATRTSTAVSTTTAPORTSPYCHNGRPVTAQIVANSGASAASSPTAAKPTGEEK
ASACETSVAINATRPALHNASLPQAFPDGVLAAAYOSFGEVHOSLERLEVYTN
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TOFTALTOVEENVLYRELAVLSINGSLVYENASLOKELNINSISGVLDEMR
MRELCITRESVAKRKATMPDSILHATSSPFGSRAPETTLATALSWREOQYRGL
YMLAOCPSLLRLRLSTITRENENASSELINVERPNDWCSVLIQLEAATYAEKE
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S"

BASE COUNT 889 a 818 c 958 g 737 t
ORIGIN
Query Match 100.0%; Score 21; DB 96; Length 3402;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 cgaagagaccatgacaactt 21
Db 1997 CGAGAGACCAGTACCACTT 2017

RESULT 6
LOCUS AC015691 67442 bp DNA HTG 17-NOV-1999
DEFINITION Homo sapiens chromosome 11 clone RP11-54F1 map 11, LOW-PASS
SEQUENCE SAMPLING.
ACCESSION AC015691
VERSION AC015691.1 GI:6446996
KEYWORDS HTG: HTGS_PHASE0; NULL.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 67442)
TITLE Birren, B., Linton, L., Nusbaum, C. and Lander, E.
JOURNAL Unpublished
AUTHORS 2* (bases 1 to 67442)
JOURNAL Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
AUTHORS Baldwin, J., Barna, N., Beckerly, R., Boguslavsky, L., Bouckhalter, B.,
Brown, A., Castle, A., Colangelo, M., Collins, S., Collamore, A.,
Cooke, P., Dearellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,
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Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Lehoczky, J., Liu, C., Locke, K., Macdonald, P., Marquis, N.,
McEwan, P., Mckernan, K., McLaughlin, J., Meldrum, J.,
Morrow, J., Naylor, J., Norman, C., O'Connor, T., O'Donnell, P.,
Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Testaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,
Wyman, D., Ye, W., J., Zimmer, A. and Zody, M.
TITLE Direct Submission
JOURNAL Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome
RESEARCH, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT All repeats were identified using RepeatMasker:
http://ftp.genome.washington.edu/RM/RepeatMasker.html
Project Information
Center project name: L1351
Center clone name: 54_F_1
* NOTE: This record contains 78 individual

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\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

1 867: contig of 867 bp in length  
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\* 868 1672: gap of unknown length  
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\* 1673 2513: gap of unknown length  
\* gap of 841 bp in length  
\*  
\* 2514 3397: contig of 884 bp in length  
\* gap of unknown length  
\*  
\* 3398 4293: contig of 896 bp in length  
\* gap of unknown length  
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\* 4294 5163: contig of 870 bp in length  
\* gap of unknown length  
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\* 5164 6023: contig of 860 bp in length  
\* gap of unknown length  
\*  
\* 6024 6934: gap of unknown length  
\* contig of 911 bp in length  
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\* gap of unknown length  
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* gap of unknown length

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```

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Best Local Similarity 100.0%; Pred. No.-44;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 2 gaagagaccatgaacaact 20
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RESULT 7
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LOCUS Homo sapiens chromosome 15 clone RP11-41P8 map 15, LOW-PASS
DEFINITION AC090694.2 GI:13487984
ACCESSION AC090694
VERSION AC090694.2 GI:13487984
KEYWORDS HTG: HTGS_PHASE0.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

```

```

REFERENCE
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,
TITLE Homo sapiens chromosome 15, clone RP11-41P8
JOURNAL (bases 1 to 64744)
REFERENCE
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens chromosome 15, clone RP11-41P8
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 64744)

```

```

Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Boguslavsky,L., Boukhalter,B., Brown,A.,
Camara,J., Campopiano,A., Choepel,Y., Colangelo,M., Collins,S.,
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O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,
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Travers,M., Travis,N., Triggillo,J., Vassiliev,R., Viel,R., Vo,A.,
Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.

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TITLE
JOURNAL
COMMENT
Submitted (08-MAR-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 29, 2001 this sequence version replaced g1:13249456.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

```

```

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu

```

```

Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L11882
Center clone name: 41_P8

```

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* NOTE: This record contains 80 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

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* 2392 3114: contig of 723 bp in length
* 3115 3214: gap of 100 bp
* 3215 3913: contig of 699 bp in length
* 3914 4013: gap of 100 bp
* 4014 4726: contig of 713 bp in length
* 4727 4826: gap of 100 bp
* 4827 5539: contig of 713 bp in length
* 5540 5639: gap of 100 bp
* 5640 6353: contig of 714 bp in length
* 6354 6453: gap of 100 bp
* 6454 7147: contig of 694 bp in length
* 7148 7247: gap of 100 bp
* 7248 7951: contig of 704 bp in length
* 7952 8051: gap of 100 bp
* 8052 8780: contig of 729 bp in length
* 8781 8880: gap of 100 bp
* 8881 9585: contig of 705 bp in length
* 9586 9685: gap of 100 bp
* 9686 10401: contig of 716 bp in length
* 10402 10501: gap of 100 bp
* 10502 11221: contig of 720 bp in length
* 11222 11321: gap of 100 bp
* 11322 12040: contig of 719 bp in length
* 12041 12140: gap of 100 bp
* 12141 12869: contig of 729 bp in length
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* 14469 14568: gap of 100 bp
* 14569 15301: contig of 733 bp in length
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* 15402 16116: contig of 715 bp in length
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* 16929 17028: gap of 100 bp
* 17029 17744: contig of 716 bp in length
* 17745 17844: gap of 100 bp
* 17845 18557: contig of 713 bp in length
* 18558 18657: gap of 100 bp
* 18659 19339: contig of 682 bp in length
* 19340 19439: gap of 100 bp
* 19440 20141: contig of 702 bp in length
* 20142 20241: gap of 100 bp
* 20242 20960: contig of 719 bp in length
* 20961 21060: gap of 100 bp
* 21061 21767: contig of 707 bp in length
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* 21868 22608: contig of 741 bp in length
* 22609 22708: gap of 100 bp
* 22709 23432: contig of 724 bp in length

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* 24248 24347: gap of 100 bp
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* 25053 25152: gap of 100 bp
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* 25863 25962: gap of 100 bp
* 25963 26777: contig of 715 bp in length
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* 27506 27605: gap of 100 bp
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* 29897 29996: gap of 100 bp
* 29997 30720: contig of 724 bp in length
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* 34065 34788: contig of 724 bp in length
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* 35600 35699: gap of 100 bp
* 35700 36407: contig of 708 bp in length
* 36408 36507: gap of 100 bp
* 36508 37225: contig of 718 bp in length
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* 37326 38046: contig of 721 bp in length
* 38047 38146: gap of 100 bp
* 38147 38868: contig of 723 bp in length
* 38870 38969: gap of 100 bp
* 38970 39519: contig of 550 bp in length
* 39520 39619: gap of 100 bp
* 39620 40331: contig of 712 bp in length
* 40332 40431: gap of 100 bp
* 40432 41144: contig of 713 bp in length
* 41145 41244: gap of 100 bp
* 41245 41946: contig of 702 bp in length
* 41947 42046: gap of 100 bp
* 42047 42746: contig of 700 bp in length
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* 42847 43553: contig of 707 bp in length
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* 50920 51019: gap of 100 bp
* 51020 51735: contig of 716 bp in length
* 51736 51835: gap of 100 bp
* 51836 52529: contig of 694 bp in length
* 52530 52629: gap of 100 bp

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* 52630 53344: contig of 715 bp in length
* 53345 53444: gap of 100 bp
* 53445 54150: contig of 706 bp in length
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* 54251 54955: contig of 705 bp in length
* 54956 55055: gap of 100 bp
* 55056 55779: contig of 724 bp in length

Query Match      87.6% Score 18.4; DB 78; Length 64744;
Best Local Similarity 95.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      2 gaagagaccatgaacaactt 21
Db      22249 GAAGATACCATGACAACTT 22268

RESULT      8
AL161719
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 215798)
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
----- Project Information
Center project name: ba3712
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: Plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 205502 bases at least Q40
Consensus quality: 211835 bases at least Q20
Insert size: 214196; sum-of-ctrls
Quality coverage: 6.59x in Q20 bases; sum-of-ctrls Quality
coverage: 11.54x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 17 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 20373 20372: contig of 20372 bp in length
* 20373 20472: gap of 100 bp
* 20473 35049: contig of 14577 bp in length
* 35050 35149: gap of 100 bp
* 35150 126259: contig of 91110 bp in length
* 126260 126359: gap of 100 bp
* 126360 134145: contig of 7786 bp in length
* 134146 134245: gap of 100 bp
* 134246 175683: contig of 41438 bp in length
* 175684 175783: gap of 100 bp

```

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* 175784 184379: contig of 8596 bp in length
* 184380 184479: gap of 100 bp
* 184480 188090: contig of 3611 bp in length
* 188091 188190: gap of 100 bp
* 188191 190453: contig of 2263 bp in length
* 190454 190553: gap of 100 bp
* 190554 193125: contig of 2572 bp in length
* 193126 193225: gap of 100 bp
* 193226 196254: contig of 3029 bp in length
* 196255 196354: gap of 100 bp
* 196355 198827: contig of 2473 bp in length
* 198828 198927: gap of 100 bp
* 198928 201913: contig of 2986 bp in length
* 201914 202013: gap of 100 bp
* 202014 204132: contig of 2119 bp in length
* 204133 204232: gap of 100 bp
* 204233 206775: contig of 2543 bp in length
* 206776 206875: gap of 100 bp
* 206876 209075: contig of 2200 bp in length
* 209076 209175: gap of 100 bp
* 209176 213317: contig of 4142 bp in length
* 213318 213417: gap of 100 bp
* 213418 215798: contig of 2381 bp in length.
location/Qualifiers
1. 215798
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="13"
/clone_RP11-37L2"
/clone_id="RP11-11.1"
1. 20372
/note="assembly-fragment:05293
fragment_chain:1"
misc_feature
20473. 35049
/note="assembly-fragment:02239
fragment_chain:1"
misc_feature
35150. 126259
/note="assembly-fragment:02452
fragment_chain:1"
misc_feature
126360. 134145
/note="assembly-fragment:01565
fragment_chain:1"
misc_feature
134246. 175683
/note="assembly-fragment:04916
fragment_chain:2"
misc_feature
175784. 184379
/note="assembly-fragment:04426
fragment_chain:2"
misc_feature
184480. 188090
/note="assembly-fragment:02922
fragment_chain:2"
misc_feature
188191. 190453
/note="assembly-fragment:00003"
misc_feature
190554. 193125
/note="assembly-fragment:00981"
misc_feature
193226. 196254
/note="assembly-fragment:00991"
misc_feature
196355. 198827
/note="assembly-fragment:01410"
misc_feature
198928. 201913
/note="assembly-fragment:01589"
misc_feature
202014. 204132
/note="assembly-fragment:02468"
misc_feature
204233. 206775
/note="assembly-fragment:04019"
misc_feature
206876. 209075
/note="assembly-fragment:04248"
misc_feature
209176. 213317
/note="assembly-fragment:04549"
misc_feature
213418. 215798
/note="assembly-fragment:04886"
BASE COUNT 65362 a 41441 c 41249 g 66128 t 1618 others
ORIGIN

```

```

Query Match      87.6%; Score 18.4; DB 79; Length 215798;
Best Local Similarity 95.0%; Pred. No. 1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 gaagagaccatgaacactt 21
Db 27622 GAAGAGACCATGACACTT 27641
|||||

```

```

RESULT 9
AC011647/c
LOCUS
DEFINITION
AC011647 147042 bp DNA HTG 20-SEP-2000
Homo sapiens clone RP11-15D18, WORKING DRAFT SEQUENCE, 7 unordered
pieces.
AC011647.5 GI:10198437
VERSION
HTG; HRGS_PHASE1; HRGS_DRAFT.
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 147042)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-15D18
Unpublished
2 (bases 1 to 147042)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Boukhalter,B.,
Brown,P., Castle,A., Colangelo,M., Collins,S., Collamore,A.,
Cooke,P., Deatellano,K., Dewar,K., Domingo,M., Donelan,L., Doyle,M.,
Ferreira,P., Fitzhugh,W., Forrest,C., Funke,R., Gage,D.,
Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Lehoczky,J., Lieu,C., Locke,K., MacDonald,P., Marquis,N.,
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrum,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Strange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Testaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (08-Oct-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Sep 20, 2000 this sequence version replaced gi:8096945.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: 13446
Center clone name: 15_D_18
----- Summary Statistics
Sequencing vector: M13; M77815; 97% of reads
Sequencing vector: Plasmid; n/a; 3% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 143564 bases at least Q40
Consensus quality: 145167 bases at least Q30
Consensus quality: 145878 bases at least Q20
Insert size: 143000; agarose-fp
Insert size: 146442; sum-of-contigs
Quality coverage: 7.6 in Q20 bases; agarose-fp
Quality coverage: 7.5 in Q20 bas.

```

```

* NOTE: This is a "working draft" sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as

```

\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 13561: contig of 13561 bp in length  
\* 13562 13661: gap of 100 bp  
\* 13662 14788: contig of 1127 bp in length  
\* 14789 14888: gap of 100 bp  
\* 14889 15930: contig of 1042 bp in length  
\* 15931 16030: gap of 100 bp  
\* 16031 39058: contig of 23029 bp in length  
\* 39060 39159: gap of 100 bp  
\* 39160 90776: contig of 51617 bp in length  
\* 90777 90876: gap of 100 bp  
\* 90877 119109: contig of 28233 bp in length  
\* 119110 119209: gap of 100 bp  
\* 119210 147042: contig of 27833 bp in length.  
Location/Qualifiers

## FEATURES

source

1.147042  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="RP11-15D18"  
/clone\_1fb="RPC1-11 Human Male BAC"  
1. 13561  
/note="assembly\_fragment"  
clone\_end:SP6  
vector\_side:left"

misc\_feature  
13662..14788  
/note="assembly\_fragment"  
misc\_feature  
14889..15930  
/note="assembly\_fragment"  
misc\_feature  
16031..39059  
/note="assembly\_fragment"  
misc\_feature  
39160..90776  
/note="assembly\_fragment"  
misc\_feature  
90877..119109  
/note="assembly\_fragment"  
misc\_feature  
119210..147042  
/note="assembly\_fragment"  
clone\_end:T7  
vector\_side:right"

BASE COUNT 42217 a 29871 c 30225 g 44129 t 600 others  
ORIGIN

Query Match 85.7%; Score 18; DB 62; Length 147042;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 aagagaccatgaacaact 20  
|||||  
Db 62098 AACGACCATGACACT 62081

RESULT 10  
AC026083/c DNA HTG 01-SEP-2000  
DEFINITION Homo sapiens chromosome 11 clone RP11-454022, WORKING DRAFT  
SEQUENCE: 19 unordered pieces.  
AC026083  
VERSION AC026083.3 GI:7658481  
KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 199958)  
AUTHORS Waterston,R.H.  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 199958)  
AUTHORS Waterston,R.H.  
TITLE Direct Submission

## JOURNAL

## COMMENT

Submitted (19-MAR-2000) Genome Sequencing Center, Washington  
University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA  
On Apr 28, 2000 this sequence version replaced gi:7644580.

----- Genome Center -----  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: <http://genome.wustl.edu/gsc/index.shtml>  
Project Information  
Center project name: H\_NH0454022  
----- Summary Statistics -----  
Sequencing vector: M13; 1008  
Sequencing vector: plasmid; 0%  
Chemistry: Dye-Primer ET; 100% of reads  
Chemistry: Dye-terminator Big Dye; 0% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 191185 bases at least Q40  
Consensus quality: 194042 bases at least Q30  
Consensus quality: 195420 bases at least Q20  
Insert size: 187000; agarose-fp  
Insert size: 198158; sum-of-contigs  
Quality coverage: 4.82 in Q20 bases; agarose-fp  
Quality coverage: 4.59 in Q20 bases; sum-of-contigs

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 19 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 1132: contig of 1132 bp in length  
\* 1133 1232: gap of unknown length  
\* 1233 2672: contig of 1440 bp in length  
\* 2673 2772: gap of unknown length  
\* 2773 3949: contig of 1177 bp in length  
\* 3950 4049: gap of unknown length  
\* 4050 6635: contig of 2586 bp in length  
\* 6636 6735: gap of unknown length  
\* 6736 9879: contig of 3144 bp in length  
\* 9880 9979: gap of unknown length  
\* 9980 12888: contig of 2909 bp in length  
\* 12889 12988: gap of unknown length  
\* 12989 16296: contig of 3308 bp in length  
\* 16297 16396: gap of unknown length  
\* 16397 20943: contig of 4547 bp in length  
\* 20944 21043: gap of unknown length  
\* 21044 27627: contig of 6584 bp in length  
\* 27628 27727: gap of unknown length  
\* 27728 35099: contig of 7372 bp in length  
\* 35100 35199: gap of unknown length  
\* 35200 44586: contig of 9387 bp in length  
\* 44587 44687: gap of unknown length  
\* 44688 52818: contig of 8132 bp in length  
\* 52819 52918: gap of unknown length  
\* 52919 63177: contig of 10259 bp in length  
\* 63178 63277: gap of unknown length  
\* 63278 74392: contig of 11115 bp in length  
\* 74393 74492: gap of unknown length  
\* 74493 90083: contig of 15591 bp in length  
\* 90084 90183: gap of unknown length  
\* 90184 108313: contig of 18130 bp in length  
\* 108314 132945: contig of 24532 bp in length  
\* 132946 133045: gap of unknown length  
\* 133046 161124: contig of 28079 bp in length  
\* 161125 161224: gap of unknown length  
\* 161225 199958: contig of 38734 bp in length.  
Location/Qualifiers  
1. 199958  
/organism="Homo sapiens"

## FEATURES

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/db\_xref="taxon:9606"  
/chromosome="11"  
/clone="RP11-454022"  
1. 1132  
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/note="assembly\_name:Contig11"  
1233. 2672  
misc\_feature  
/note="assembly\_name:Contig12"  
2773. 3949  
misc\_feature  
/note="assembly\_name:Contig13"  
4050. 6635  
misc\_feature  
/note="assembly\_name:Contig14  
clone\_end:r7  
vector\_side:right"  
6736. 9879  
misc\_feature  
/note="assembly\_name:Contig15"  
9980. 12888  
misc\_feature  
/note="assembly\_name:Contig16"  
12989. 16296  
misc\_feature  
/note="assembly\_name:Contig17"  
16397. 20943  
misc\_feature  
/note="assembly\_name:Contig18"  
21044. 27627  
misc\_feature  
/note="assembly\_name:Contig19"  
27728. 35099  
misc\_feature  
/note="assembly\_name:Contig20"  
35200. 44586  
misc\_feature  
/note="assembly\_name:Contig21  
clone\_end:SP6  
vector\_side:left"  
44687. 52818  
misc\_feature  
/note="assembly\_name:Contig22"  
52919. 63177  
misc\_feature  
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63278. 74392  
misc\_feature  
/note="assembly\_name:Contig24"  
74493. 90083  
misc\_feature  
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90184. 108313  
misc\_feature  
/note="assembly\_name:Contig26"  
108414. 132945  
misc\_feature  
/note="assembly\_name:Contig27"  
133046. 161124  
misc\_feature  
/note="assembly\_name:Contig28"  
161225. 199958  
misc\_feature  
/note="assembly\_name:Contig29"  
BASE COUNT 59966 a 39366 c 39871 g 58925 t 1810 others  
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Query Match 85.7% Score 18: DB 69: Length 199958;  
Best Local Similarity 100.0% Pred. No. 1.6e+02;  
Matches 18: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 3 aagagacatgacaact 20  
|||||  
Db 163010 AAGAGACATGACACT 162993

RESULT 11  
PST012352 2984 bp DNA BCT 10-MAY-1999  
DEFINITION Pseudomonas stutzeri insertion sequence ISp1.  
ACCESSION AJ012352  
VERSION AJ012352.1 GI:4803706  
KEYWORDS insertion sequence ISp1; ISL3 family; ORF1; ORF2; transposase.  
SOURCE Pseudomonas stutzeri.  
ORGANISM Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
Pseudomonas.  
1 (bases 1 to 2984)  
REFERENCE Bolognese,F., di Lecce,C., Galli,E. and Barbieri,P.  
AUTHORS Activation and inactivation of pseudomonas stutzeri methylbenzene  
TITLE catabolism pathways mediated by a transposable element

JOURNAL Appl. Environ. Microbiol. 65 (5), 1876-1882 (1999)  
MEDLINE 99240403  
REFERENCE 2 (bases 1 to 2984)  
AUTHORS Barbieri,P.  
TITLE Direct Submission  
JOURNAL Submitted (29-OCT-1998) Barbieri P., Dept. Genetica e Biologia del  
Microorganismi, University of Milan, Via Celoria 26, 20133 Milano,  
ITALY  
FEATURES  
source  
Location/Qualifiers  
1. 2984  
/organism="Pseudomonas stutzeri"  
/insertion\_seq="ISL3 family"  
/strain="M1"  
/db\_xref="taxon:316"  
/note="proposed name ISp1, inactivates catabolic genes"  
complement(94. 492)  
/note="ORF1"  
/codon\_start=1  
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/protein\_id="CAB42635.1"  
/db\_xref="GI:4803707"  
/translation="MDHEKVAASIAELGNSHRLSVRFVAKGHDGASVCDIQKGLI  
PASTLSHLARMAKVGILROEKHSRTVICIPEYGHLENLIGFLQECAGARIAPHEPE  
TALTIAQSLSSLSVSIAMKTOAKVETENMQ"  
1649. 2926  
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/protein\_id="CAB42636.1"  
/db\_xref="GI:4803708"  
/translation="MINSLSLPGVLYDSDONEDIHRLTAPFPVACGGCGVEFY  
RFGKRDVYRDLPHGKRVTLVAVRRITAGAPARHSCQPLPEWVGRRMLPLHEIV  
EKESFNHPYTFVAQTGDEKTVRFIFNARAEFLGRWRFETPRILGIDELYLNKRYR  
CILTNIERTLIDLATRRQDVYVNYLMLKLDROKVEIVSDMMNPYAAVAVLPQA  
RIYVVKFHVVRMANDALERVKRGLEKPSQSRFLKCDRKILKRAHEVSDRELLIM  
ETWGAFPQLAAYEYKRRFYGIMVATRILOAEALDMMIATIPGQKEWSDLYRAV  
GNWRREMTYFETDMPYVNNATYESINRLAKNRGRGTSFVMAKRLYTTKKHKKK  
PFAKSPYKTKITGIGLPFAELNMGVLSIT"  
2961. 2984  
/note="imperfect inverted repeats, 4 bp mismatch"  
/rpt\_unit=2961. 2984  
/rpt\_type=INVERTED  
BASE COUNT 669 a 811 c 823 g 681 t  
ORIGIN  
Query Match 84.8% Score 17.8: DB 3: Length 2984;  
Best Local Similarity 90.5% Pred. No. 1.4e+02;  
Matches 19: Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Oy 1 cgaagagacatgacaact 21  
|||||  
Db 2662 CGAAGAGACATGACCTACTT 2682

RESULT 12  
AF121970 6052 bp DNA BCT 07-MAY-1999  
LOCUS AF121970/C  
DEFINITION Pseudomonas aeruginosa topoisomerase (top), putative  
transcriptional regulatory protein OhbR (ohbR), ortho-halobenzoate  
1,2-dioxygenase beta-1S protein OhbA (ohbA), OhbC (ohbC),  
ortho-halobenzoate 1,2-dioxygenase alpha-1S protein OhbB (ohbB),  
and putative transposase A (tnpA) genes, complete cds.  
ACCESSION AF121970  
VERSION AF121970.1 GI:4406503  
KEYWORDS  
SOURCE Pseudomonas aeruginosa.  
ORGANISM Pseudomonas aeruginosa  
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
Pseudomonas.  
1 (bases 1 to 6052)



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ACCESSION      AF027768.1  GI:2688956
VERSION
KEYWORDS
SOURCE
ORGANISM       Serratia marcescens.
                Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                Serratia.
REFERENCE      1 (bases 1 to 6921)
AUTHORS        Hodges,R.W., Rodriguez-Lemoine,V. and Datta,N.
TITLE          R factors from Serratia marcescens
JOURNAL        J. Gen. Microbiol. 86 (1), 88-92 (1975)
MEDLINE        75096689
REFERENCE      2 (bases 1 to 6921)
AUTHORS        Ho,C., Kulaeva,O.I., Levine,A.S. and Woodgate,R.
TITLE          A rapid method for cloning mutagenic DNA repair genes: isolation of
                umu-complementing genes from multidrug resistance plasmids R391,
                R446b, and R471a
JOURNAL        J. Bacteriol. 175 (17), 5411-5419 (1993)
MEDLINE        93374835
REFERENCE      3 (bases 1 to 6921)
AUTHORS        Kulaeva,O.I., Koonin,E.V., Wootton,J.C., Levine,A.S. and
                Woodgate,R.
TITLE          Unusual insertion element polymorphisms in the promoter and
                terminator regions of the mucAB-like genes of R471a and R446b
JOURNAL        Mutat. Res. 397 (2), 247-262 (1998)
MEDLINE        98202731
REFERENCE      4 (bases 1 to 6921)
AUTHORS        Woodgate,R.
TITLE          Direct Submission
                Submitted (02-OCT-1997) SDRM, NICHD/NIH, 9000 Rockville Pike,
                Bethesda, MD 20892-2725, USA
                On Dec 16, 1997 this sequence version replaced gi:940364.
COMMENT        Location/Qualifiers
FEATURES
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                /db_xref="taxon:615"
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                /note="Incl/M R-plasmid"
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                /note="hypothetical protein; similar to an hypothetical
                ort in R446b encoded by Genbank Accession Number AF027767"
                /codon_start=2
                /transl_table=1
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                /db_xref="GI:2688958"
                /translation="KNTLFTHGAVLYLVCFLVYRWRVAPLPVYGQLRNVCAPMLV
                GALAVYVGEFLGKVLDDPAEPMTLFPADKSLPDTTLTLLAFLIAPLNEETLFGS
                IMLNPFERSRYSWTMMLGALITSLFVAHSOYONMLTLAEFLVGLITSARIRSGGL
                LPLVILHMEATAGLLFG"
                complement(715..2202)
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                /translation="MMYGEKSSDLIVAAQNNPKGAESVERRSGAKNAEQPHMR
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                MDYAGNMKNNTILHRLHOGSRYAQRGRHYIPKADGKORPLGIASLEIKVQYALV
                KILNAVYENDMGESYGFRRGSHODALDGLVNTNMVLDADISOEDRVSHH
                WLIRFPHRTGDRRVIRLIRKMLJAGSECGMATEEGTPQCAVISPILANILHY
                FDIAMHWRRRRYKATGNVYRVYADDIVIGDKRYDARFRFAKORLREFGLVHPERK
                TLMEFRFAENRAIRKGPKEFENLGLFTTHSGKRNRFMLIRTRHDMATATK
                AIKDGLRRRWHSIPDEGKMLRVVOGYLNVHSVGPMPMOKFRTHVTNIMRRALRR
                RSQKDDTTWKANKLAAMLPRVFLHPMEVERPTAHPRQEPGA"
                2539..2544
                2539..2568
                2566..2583
                /bound_molecy="LexA"
                /product="LexA"
                2588..2592
                /gene="mucA"

-35-signal
-10-signal
misc_binding
RBS

2588..3034
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2600..3034
/gene="mucA"
/note="similar to MucA from plasmid R446b, Genbank
Accession Number AF027767; also similar to Escherichia
coli Umud, Swiss-Prot Accession Number P04153, and to
Salmonella typhimurium Umud, Swiss-Prot Accession Number
P22493, Samh, Swiss-Prot Accession Number P23831, MucA,
Swiss-Prot Accession Number P07376, and ImpA, Swiss-Prot
Accession Number P18641"
/codon_start=1
/transl_table=1
/product="MucA"
/protein_id="AAC82521.1"
/db_xref="GI:2688959"
/translation="MALDLYVRPSVEGDALPFFAEPYAGFPSPAGYEANELNLD
YCVHPATYFLRVGSDSMRDARIHGDVLVLADEEPRHSIYIASIDNEFTVKQLQ
LRPPLCMPLNPAFPPIREFDEALQIMGVVFVYMRHRCPT"
3022..4287
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/note="similar to Muc from plasmid R446b, Genbank
Accession Number AF027767; also similar to Escherichia
coli Umuc, Swiss-Prot Accession Number P04152, and to
Salmonella typhimurium Umuc, Swiss-Prot Accession Number
P22494, Samh, Swiss-Prot Accession Number P23832, MucB,
Swiss-Prot Accession Number P14303, and ImpB, Swiss-Prot
Accession Number P18642"
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/transl_table=1
/product="MucB"
/protein_id="AAC82522.1"
/db_xref="GI:2688960"
/translation="MYALIDVNSMYSCSEAFRPDLGRPVVYLNNDGALVAVNRRA
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LFADASHMEGVSPQARQGLRAEVLRTITLTCGVYAPPTLAKICNHAKTPTAG
GVVALSDPVRKLRLMSLYSAGDVWGVGRTREKGLATMGIKTALAEMDITLARLIG
VTLERTIRELNGEACFALBEGTGAKQDLVSRSGSRVTOAQMOQAVTKYATRAGEK
LRQENRLAKVAVTVFIRSSVADGVAPYSNQTLYLVSPSOTRDIITAAOGLSRIMR
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IDPEYAMRREMLSPAYTTQWKDIPAAFR"
4315..6097
/organism="Serratia marcescens"
/db_xref="taxon:615"
/insertion_seq="IS1396"
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/codon_start=1
/transl_table=1
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/db_xref="GI:2688961"
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WVRRKYTCRACKTTFRQVLEWVDGFRMTLRLHEYVEKSFNRPYFVAOGLDEK
TVRDIYFNARAEFLRMRHFEETPRLIGIDELINKRYCIIITNIEERTLDDLATRRD
TIVTDLKAKIKROKVEIYSMDMMYRAVAVAPORIVYDKRHVYBMANDALERYR
KGLRKEKLPQSRLTKGDKRILKRAHVSQREILINMETWNGAPOLLAYEHKERY
GIDWATRLQAEALDIEATIPRGQEWMSDVLRAVGNREETWTFETDMPVTNAY
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complement(6141..6653)
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/transl_table=1
/product="lspsa"
/protein_id="AAC82524.1"
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TITLE  
JOURNAL  
COMMENT

Direct Submission  
Submitted (11-APR-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Dec 22, 2000 this sequence version replaced gi:8139533.  
All repeats were identified using RepeatMasker:  
Smt, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: W1BR

Web site: http://www-seq.wi.mit.edu

Contact: sequence\_submissions@genome.wi.mit.edu

Project information

Center project name: L8872

Center clone name: 186.A.21

Summary statistics

Sequencing vector: M13; M77815; 54% of reads

Sequencing vector: Plasmid; n/a; 46% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 200951 bases at least Q40

Consensus quality: 204253 bases at least Q30

Insert size: 198000; agarose-fp

Insert size: 204638; sum-of-contigs

Quality coverage: 6.7 in Q20 bases; agarose-fp

Quality coverage: 6.5 in Q20 b.

NOTE: This is a 'working draft' sequence. It currently

consists of 11 contigs. The true order of the pieces

is not known and their order in this sequence record is

arbitrary. Gaps between the contigs are represented as

runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence

as soon as it is available and the accession number will

be preserved.

1 4471: contig of 4471 bp in length  
4472 4571: gap of 100 bp  
4572 4645: contig of 74 bp in length  
4646 4745: gap of 100 bp  
4746 10308: contig of 5563 bp in length  
10309 10408: gap of 100 bp  
10409 64985: contig of 54577 bp in length  
64986 65085: gap of 100 bp  
65086 78435: contig of 13350 bp in length  
78436 78535: gap of 100 bp  
78536 93848: contig of 15313 bp in length  
93849 93948: gap of 100 bp  
93949 109475: contig of 15527 bp in length  
109476 109575: gap of 100 bp  
109576 130155: contig of 20580 bp in length  
130156 130255: gap of 100 bp  
130256 158585: contig of 28330 bp in length  
158586 158685: gap of 100 bp  
158686 201676: contig of 42991 bp in length  
201677 201776: gap of 100 bp  
201777 205638: contig of 3862 bp in length.

Location/Qualifiers

1. 205638

/organism="Mus musculus"

/db\_xref="taxon:10090"

/chromosome="5"

/map="5"

/clone="RP23-186A21"

/clone.lib="RPC1-23 Female Mouse BAC"

1. 4471

/note="assembly\_fragment"

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clone\_end:SP6

vector\_side:left

4572. 4645

/note="assembly\_fragment"

4746. 10308

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10409. 64985

misc\_feature

/note="assembly\_fragment"

65086. 78435

/note="assembly\_fragment"

78536. 93848

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93949. 109475

/note="assembly\_fragment"

109576. 130155

/note="assembly\_fragment"

130256. 158585

/note="assembly\_fragment"

158686. 201676

/note="assembly\_fragment"

201777. 205638

/note="assembly\_fragment"

clone\_end:T7

vector\_side:right

BASE COUNT 64156 a 38300 c 37657 g 64521 t 1004 others

ORIGIN

Query Match 84.8%; Score 17.8; DB 71; Length 205638;

Best Local Similarity 90.5%; Pred. No. 2.1e+02;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 cgaagagaccatgacacactt 21

|||||

DB 133856 CGACGACCATGAATAACAT 133836

Search completed: September 21, 2001, 00:36:50

Job time: 29665 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 21, 2001, 02:42:46 : Search time 330.77 Seconds  
(without alignments)  
39.864 Million cell updates/sec

Title: US-09-138-735-12

Perfect score: 21  
Sequence: 1 cgaagagaccatgaacaactt 21

Scoring table:

IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N\_Geneseq\_0601:\*

1: /cgnl\_9/gcgdata/geneseq/geneseqn/NA1980.DAT:\*  
2: /cgnl\_9/gcgdata/geneseq/geneseqn/NA1981.DAT:\*  
3: /cgnl\_9/gcgdata/geneseq/geneseqn/NA1982.DAT:\*  
4: /cgnl\_9/gcgdata/geneseq/geneseqn/NA1983.DAT:\*  
5: /cgnl\_9/gcgdata/geneseq/geneseqn/NA1984.DAT:\*  
6: /cgnl\_9/gcgdata/geneseq/geneseqn/NA1985.DAT:\*  
7: /cgnl\_9/gcgdata/geneseq/geneseqn/NA1986.DAT:\*  
8: /cgnl\_9/gcgdata/geneseq/geneseqn/NA1987.DAT:\*  
9: /cgnl\_9/gcgdata/geneseq/geneseqn/NA1988.DAT:\*  
10: /cgnl\_9/gcgdata/geneseq/geneseqn/NA1989.DAT:\*  
11: /cgnl\_9/gcgdata/geneseq/geneseqn/NA1990.DAT:\*  
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19: /cgnl\_9/gcgdata/geneseq/geneseqn/NA1998.DAT:\*  
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21: /cgnl\_9/gcgdata/geneseq/geneseqn/NA2000.DAT:\*  
22: /cgnl\_9/gcgdata/geneseq/geneseqn/NA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 21    | 100.0       | 21     | 17    | AAT27315    |
| 2          | 21    | 100.0       | 21     | 20    | AAK84097    |
| 3          | 21    | 100.0       | 3402   | 17    | AAT27310    |
| 4          | 21    | 100.0       | 3402   | 20    | AAK84092    |
| 5          | 16.8  | 80.0        | 747    | 21    | AAAO1873    |
| 6          | 16.8  | 80.0        | 1606   | 22    | AAAC64747   |
| 7          | 16.8  | 80.0        | 1931   | 21    | AAAC98922   |
| 8          | 16.8  | 80.0        | 2163   | 22    | AAAF44684   |
| 9          | 16.8  | 80.0        | 2241   | 19    | AAVS9121    |
| 10         | 15.8  | 75.2        | 1815   | 14    | AAQ42168    |
| 11         | 15.8  | 75.2        | 1958   | 21    | AAFI8267    |

|    |      |      |      |    |           |                     |
|----|------|------|------|----|-----------|---------------------|
| 12 | 15.8 | 75.2 | 2265 | 21 | AAZ44288  | Human brain PABP3   |
| 13 | 15.8 | 75.2 | 2265 | 21 | AAZ44289  | Human uterus type   |
| 14 | 15.4 | 73.3 | 1913 | 21 | AAAC64441 | Human secreted pro  |
| 15 | 15.4 | 73.3 | 1913 | 11 | AAQ04775  | Fragment contig. Ch |
| 16 | 15.4 | 73.3 | 1980 | 18 | AAT59454  | H-Delta-1 contig c  |
| 17 | 15.4 | 73.3 | 2135 | 21 | AAAC65395 | Human carbohydrate  |
| 18 | 15.4 | 73.3 | 2533 | 19 | AAT96031  | Mouse gamma II ada  |
| 19 | 15.4 | 73.3 | 2663 | 18 | AAT70174  | Proliferation and   |
| 20 | 15.4 | 73.3 | 2663 | 20 | AAK16300  | Human delta-1 prot  |
| 21 | 15.4 | 73.3 | 2663 | 20 | AAK16817  | Human delta-1 gene  |
| 22 | 15.4 | 73.3 | 2883 | 18 | AAT58898  | C-Delta-1 gene (al  |
| 23 | 15.4 | 73.3 | 2933 | 21 | AAAS4105  | PRO172 cDNA. Homo   |
| 24 | 15.4 | 73.3 | 2933 | 21 | AAAC58587 | Human PRO172 prote  |
| 25 | 15.4 | 73.3 | 2933 | 21 | AAAT7512  | Human PRO172 cDNA   |
| 26 | 15.4 | 73.3 | 2933 | 21 | AAZ93703  | PRO172 DNA35916-11  |
| 27 | 15.4 | 73.3 | 2933 | 22 | AAAC97368 | Human angiotensin   |
| 28 | 15.4 | 73.3 | 3162 | 21 | AAZ98677  | Human delta protei  |
| 29 | 15.2 | 72.4 | 359  | 21 | AAAT2677  | PCR primer PEMYC2   |
| 30 | 15.2 | 72.4 | 408  | 22 | AAAF66202 | Human colon cancer  |
| 31 | 15.2 | 72.4 | 504  | 20 | AAZ25115  | Novel human polynu  |
| 32 | 15.2 | 72.4 | 504  | 20 | AAZ25115  | wheat anthranilate  |
| 33 | 15.2 | 72.4 | 675  | 21 | AAAC43972 | Arabidopsis thalia  |
| 34 | 15.2 | 72.4 | 915  | 13 | AAQ31798  | PRP4 gene. Nicoti   |
| 35 | 15.2 | 72.4 | 1029 | 21 | AAAC75875 | Human ORFX ORF1430  |
| 36 | 15.2 | 72.4 | 1046 | 12 | AAO10377  | Plasmid PMG3C9 use  |
| 37 | 15.2 | 72.4 | 1056 | 21 | AAAC55832 | S. lavendulae Mmcr  |
| 38 | 15.2 | 72.4 | 1221 | 21 | AAAC49196 | Arabidopsis thalia  |
| 39 | 15.2 | 72.4 | 1221 | 21 | AAAC40196 | Arabidopsis thalia  |
| 40 | 15.2 | 72.4 | 1274 | 21 | AAAC45280 | Arabidopsis thalia  |
| 41 | 15.2 | 72.4 | 1371 | 21 | AAAC44690 | Arabidopsis thalia  |
| 42 | 15.2 | 72.4 | 1393 | 21 | AAAC46421 | Arabidopsis thalia  |
| 43 | 15.2 | 72.4 | 1395 | 21 | AAAC36574 | Arabidopsis thalia  |
| 44 | 15.2 | 72.4 | 1614 | 21 | AAAC45832 | Arabidopsis thalia  |
| 45 | 15.2 | 72.4 | 1624 | 21 | AAZ65339  | Human secreted pro  |

# ALIGNMENTS

|          |                                                                          |                        |
|----------|--------------------------------------------------------------------------|------------------------|
| RESULT 1 |                                                                          |                        |
| ID       | AAT27315                                                                 | standard; cDNA; 21 BP. |
| XX       |                                                                          |                        |
| AC       | AAT27315;                                                                |                        |
| XX       |                                                                          |                        |
| DT       | 26-NOV-1996                                                              | (first entry)          |
| XX       |                                                                          |                        |
| DE       | T.cruzi Epimastigotic PTC100t antigen primer corresp. to bases 1997-2017 |                        |
| XX       |                                                                          |                        |
| KW       | Antigen; Trypanosoma cruzi; epimastigote; serum; Chagas disease; probe;  |                        |
| KW       | Primer; PCR; polymerase chain reaction; amplification; antibody; ss.     |                        |
| XX       |                                                                          |                        |
| OS       | Synthetic.                                                               |                        |
| XX       |                                                                          |                        |
| PN       | FR2723589-A1.                                                            |                        |
| XX       |                                                                          |                        |
| PD       | 16-FEB-1996.                                                             |                        |
| XX       |                                                                          |                        |
| PF       | 12-AUG-1994;                                                             | 94FR-0010132.          |
| XX       |                                                                          |                        |
| PR       | 12-AUG-1994;                                                             | 94FR-0010132.          |
| XX       |                                                                          |                        |
| PA       | (IMMR ) BIO MERIEUX.                                                     |                        |
| XX       |                                                                          |                        |
| PI       | Jollivet M, Lesenechal M, Paranhos-Baccala G;                            |                        |
| XX       |                                                                          |                        |
| DR       | WPI; 1996-190287/20.                                                     |                        |
| XX       |                                                                          |                        |
| PT       | New nucleic acid encoding Trypanosoma cruzi epimastigotic antigen -      |                        |
| PT       | useful for diagnosis, monitoring and therapy of Chagas disease           |                        |
| XX       |                                                                          |                        |
| PS       | Claim 29; Page 40; 55pp; French.                                         |                        |
| XX       |                                                                          |                        |

CC The primers AAT27311-5 were used to PCR amplify the sequence encoding a  
 CC novel isolated antigenic protein from Trypanosoma cruzi epimastigotes,  
 CC designated PTC100t (AAT27310). The primers, derived from the sequences  
 CC of a 594 and 1041 bp fragment of PTC100t, amplified the gene as 3  
 CC fragments. This primer corresponds to nucleotides 1997-2017 of the PTC100t  
 CC sequence, derived from the 1041 bp fragment. The 594 bp fragment was  
 CC isolated from a T. cruzi genomic expression library in lambda gt11, using  
 CC a mixture of sera from patients with Chagas disease. It corresponds to  
 CC nucleotides 1232-1825 of PTC100t. The 1041 bp fragment was isolated from  
 CC a lambda gt10 library using the 594 bp fragment as a probe. The protein,  
 CC or antibodies raised against it, can be used in the detection and  
 CC monitoring of T. cruzi infection i.e. Chagas disease.  
 XX

SO Sequence 21 BP; 9 A; 5 C; 4 G; 3 T; 0 other;

Query Match 100.0%; Score 21; DB 17; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 0.3;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cgaagagaccatgaacacctt 21  
 ||||||||||||||||  
 Db 1 cgaagagaccatgaacacctt 21

## RESULT 2

AAX84097  
 ID AAX84097 standard; DNA; 21 BP.

AC AAX84097;

XX 27-AUG-1999 (first entry)

DE PCR primer for T. cruzi PTC40 coding sequence.

XX PTC40: Tc40; infection; diagnosis; immune complex; antigenic determinant;  
 KM therapy; antibody; PCR primer; ss.

OS Synthetic.

OS Trypanosoma cruzi.

XX WO929867-A1.

XX 17-JUN-1999.

XX 10-DEC-1998; 98WO-IB01987.

XX 10-DEC-1997; 97US-0988242.

XX (INMR ) BIO MERIEUX.

XX Jolivet M, Lesenechal M, Mandrand B, Paranhos-Baccala G;

XX WPI; 1999-394978/33.

XX New Trypanosoma cruzi antigen

PS Disclosure; Page 22; 65pp; English.

XX This sequence is a PCR primer for DNA encoding the Trypanosoma cruzi  
 CC PTC40 protein of the invention. The PTC40 antigenic determinant is  
 CC useful as a reagent for detection and/or monitoring of Trypanosoma cruzi  
 CC infection from samples including blood serum or plasma, urine, saliva, or  
 CC tears, by contacting with the sample and detecting an immune complex. The  
 CC PTC40 antigenic determinant, the vector, expression cassette, cell or  
 CC antibody are useful for treatment or prevention (vaccine) of a  
 CC Trypanosoma cruzi infection in a man or animal. Current Trypanosoma cruzi  
 CC antigens are obtained from protein fractions of the noninfectious stage  
 CC of the parasite, and these do not allow sufficient production of antigens  
 CC for use in reliable serological diagnostic tests. The strain to strain  
 CC polymorphism reduces reliability of the tests.  
 XX Sequence 21 BP; 9 A; 5 C; 4 G; 3 T; 0 other;

Query Match 100.0%; Score 21; DB 20; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 0.3;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cgaagagaccatgaacacctt 21  
 ||||||||||||||||  
 Db 1 cgaagagaccatgaacacctt 21

## RESULT 3

AAT27310  
 ID AAT27310 standard; cDNA; 3402 BP.

AC AAT27310;

XX 26-NOV-1996 (first entry)

DE Trypanosoma cruzi epimastigotic PTC100t antigen gene.

XX Antigen; Trypanosoma cruzi; epimastigote; serum; Chagas disease; probe;  
 KM Primer; PCR; polymerase chain reaction; amplification; antibody; ds.

XX Trypanosoma cruzi.

XX Key Location/Qualifiers

FT CDS 266..3013

FT /tag= a

FT /product= PTC100t epimastigotic antigen

XX FR273589-A1.

XX 16-FEB-1996.

XX 12-AUG-1994; 94FR-0010132.

XX 12-AUG-1994; 94FR-0010132.

XX (INMR ) BIO MERIEUX.

XX Jolivet M, Lesenechal M, Paranhos-Baccala G;

XX WPI; 1996-190287/20.

XX P-PsDB; AAR91615.

XX New nucleic acid encoding Trypanosoma cruzi epimastigotic antigen -  
 PS useful for diagnosis, monitoring and therapy of Chagas disease

XX Claim 1; Page 24-26; 55pp; French.

XX This is the nucleotide sequence encoding a novel isolated antigenic  
 CC protein from Trypanosoma cruzi epimastigotes, designated PTC100t.  
 CC The clone Tc50 was isolated from a T. cruzi genomic expression library in  
 CC lambda gt11, using a mixture of sera from patients with Chagas disease.  
 CC Clone Tc50 contained an 594 bp insert corresp. to nucleotides 1232-1825  
 CC of this sequence. The Tc50 sequence was subsequently used to probe a  
 CC Southern blot of restriction enzyme digested T. cruzi DNA and also screen  
 CC a lambda gt10 library to isolate a 1041 bp EcoRI fragment corresp. to  
 CC nucleotides 1403-2443 of PTC100t. Primers (AAT27311-5) were synthesised  
 CC based on the sequences of the 594 and 1041 bp fragments and used to  
 CC amplify the PTC100t clone as 3 fragments from cDNA derived from mRNA  
 CC purified from T. cruzi epimastigotes. The protein or antibodies raised  
 CC against it can be used in the detection and monitoring of T. cruzi  
 CC infection i.e. Chagas disease.  
 XX

SO Sequence 3402 BP; 889 A; 818 C; 958 G; 737 T; 0 other;

Query Match 100.0%; Score 21; DB 17; Length 3402;  
 Best Local Similarity 100.0%; Pred. No. 0.61;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY      1 cgaagagacatgaacaact 21
        |||||||
DB      1997 cgaagagacatgaacaact 2017

RESULT  4
ID      AAX84092
        AAX84092 standard; cDNA; 3402 BP.
XX
AC      AAX84092;
XX
DT      27-AUG-1999 (first entry)
XX
DE      T. cruzi PTc40 coding sequence.
XX
KW      PTc40; Tc40; infection; diagnosis; immune complex; antigenic determinant;
KW      therapy; antibody; ds.
XX
OS      Trypanosoma cruzi.
XX
PN      WO9929867-A1.
XX
PD      17-JUN-1999.
XX
PF      10-DEC-1998; 98WO-IB01987.
XX
PR      10-DEC-1997; 97US-0988242.
XX
PA      (IMMR ) BIO MERIEUX.
XX
PI      Jolivet M, Leseuechal M, Mandrand B, Paranhos-Baccala G;
XX
DR      WPI: 1999-394978/33.
XX
PT      P-PSDB; AAY22124.
XX
PS      New Trypanosoma cruzi antigen
XX
XX      Claim 1; Page 52-56; 65pp; English.
XX
CC      This sequence encodes the Trypanosoma cruzi PTc40 protein of the
CC      invention, and is designated Tc40. The PTc40 antigenic determinant is
CC      useful as a reagent for detection and/or monitoring of Trypanosoma cruzi
CC      infection from samples including blood serum or plasma, urine, saliva, or
CC      tears, by contacting with the sample and detecting an immune complex. The
CC      PTc40 antigenic determinant, the vector, expression cassette, cell or
CC      antibody are useful for treatment or prevention (vaccine) of a
CC      Trypanosoma cruzi infection in a man or animal. Current Trypanosoma cruzi
CC      antigens are obtained from protein fractions of the noninfectious stage
CC      of the parasite, and these do not allow sufficient production of antigens
CC      for use in reliable serological diagnostic tests. The strain to strain
CC      polymorphism reduces reliability of the tests.
XX
SQ      Sequence 3402 BP; 888 A; 821 C; 956 G; 737 T; 0 other.

Query Match      100.0%; Score 21; DB 20; Length 3402;
Best Local Similarity 100.0%; Pred. NO. 0.61;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 cgaagagacatgaacaact 21
        |||||||
DB      1997 cgaagagacatgaacaact 2017

RESULT  5
ID      AAA01873
        AAA01873 standard; cDNA; 747 BP.
XX
AC      AAA01873;
XX
DT      19-MAY-2000 (first entry)
XX
DE      Human colon cancer cell line polynucleotide sequence SEQ ID NO:1864.
```

```
XX
KW      Human; colon cancer; tumour; diagnosis; gene expression product;
KW      probe; detection; cancerous state; metastasis; identification;
KW      breast cancer; oestrogen receptor-positive breast cancer; therapy;
KW      oestrogen receptor-negative breast cancer; lung cancer; ss.
XX
OS      Homo sapiens.
XX
PN      WO9958675-A2.
XX
PD      18-NOV-1999.
XX
PF      13-MAY-1999; 99WO-US10602.
XX
PR      14-MAY-1998; 98US-0085426.
PR      15-MAY-1998; 98US-0085537.
PR      15-MAY-1998; 98US-0085696.
PR      21-OCT-1998; 98US-0105234.
PR      27-OCT-1998; 98US-0105877.
XX
PA      (CHIR ) CHIRON CORP.
PA      (HRSE-) HRSEQ INC.
XX
PI      Williams LT, Escobedo J, Innis MA, Garcia PD, Sudduth-Klinger J;
PI      Reinhard C, Giese K, Randazzo F, Kennedy GC, Pot D, Kassam A;
PI      Lanson G, Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;
PI      Leshkowitz D, Kita D, Garcia V, Jones LW, Stache-Crain B;
XX
DR      WPI: 2000-126369/11.
XX
PT      Polynucleotide library used to determine cancerous states of mammalian
XX      cells.
XX
PS      Claim 1; Page 697-698; 1097pp; English.
XX
CC      AAA00010 to AAA02716 represent polynucleotides isolated from cDNA
CC      libraries constructed from human colon cancer cell lines. The present
CC      invention also describes a method of detecting differentially expressed
CC      genes correlated with a cancerous state of a mammalian cell, comprising
CC      detecting at least one differentially expressed gene product in a test
CC      sample derived from a cell suspected of being cancerous, where detection
CC      of the differentially expressed gene product is correlated with a
CC      cancerous state of the cell from which the test sample was derived.
CC      The polynucleotide sequences can be used in a method for detecting
CC      differentially expressed genes correlated with a cancerous state of a
CC      mammalian cell. The polynucleotides can also be used as probes for
CC      detecting and mapping related genes. They can be used in diagnosis and
CC      prognosis of diseases and disorders (e.g. identification of
CC      pre-metastatic or metastatic cancerous states, stages of cancer, or
CC      responsiveness of cancer to therapy). This is particularly for breast
CC      cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-
CC      negative breast cancer, lung cancer, and colon cancer.
XX
SQ      Sequence 747 BP; 136 A; 227 C; 193 G; 179 T; 12 other.

Query Match      80.0%; Score 16.8; DB 21; Length 747;
Best Local Similarity 90.0%; Pred. NO. 50;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      2 gaagagacatgaacaact 21
        |||||||
DB      341 gaagagacatgaacaact 360

RESULT  6
ID      AAC64747
        AAC64747 standard; cDNA; 1606 BP.
XX
AC      AAC64747;
XX
DT      28-FEB-2001 (first entry)
XX
```

|                                                                       |                                                                              |
|-----------------------------------------------------------------------|------------------------------------------------------------------------------|
| DE                                                                    | Secreted protein K139_11 encoding cDNA SEQ ID NO:3.                          |
| XX                                                                    |                                                                              |
| KW                                                                    | Secreted protein; AM179_11; BG221_11; K139_11; K511_11; N154_11;             |
| KM                                                                    | immunomodulator; antiinflammatory; immunosuppressive; cytosolic; *           |
| KV                                                                    | vulnerary; osteopathic; antiatherosclerotic; neuroprotective; antirheumatic; |
| KW                                                                    | antiparkinsonian; nootropic; antitumor; vasotrophic; cerebroprotective;      |
| KX                                                                    | contraceptive; haemostatic; thrombolytic; antibacterial; nutritional;        |
| KY                                                                    | cytokine; cell proliferation; cell differentiation; immunomodulatory;        |
| KZ                                                                    | immune disorder; proliferative disorder; regulation; haematopoiesis; ss.     |
| XX                                                                    |                                                                              |
| OS                                                                    | Mus musculus.                                                                |
| PN                                                                    | WO20066148-A1.                                                               |
| PD                                                                    | 09-NOV-2000.                                                                 |
| XX                                                                    |                                                                              |
| PE                                                                    | 29-APR-2000; 2000WO-US11818.                                                 |
| XX                                                                    |                                                                              |
| PR                                                                    | 29-APR-1999; 99US-0131596.                                                   |
| XX                                                                    |                                                                              |
| PA                                                                    | (GEMV ) GENETICS INST INC.                                                   |
| PI                                                                    | Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;                  |
| PT                                                                    | Merberg D;                                                                   |
| DR                                                                    | WPI: 2001-015913/02.                                                         |
| DR                                                                    | P-PSTDB; AAB36408.                                                           |
| XX                                                                    |                                                                              |
| PT                                                                    | Novel AM17911, BG22111, K13911, K5111 and N15411 secreted proteins,          |
| PT                                                                    | their fragments and polynucleotides, useful in diagnostic and research       |
| PT                                                                    | assays and for treating, e.g., immune and proliferative disorders and        |
| PT                                                                    | for regulating hematopoiesis -                                               |
| XX                                                                    |                                                                              |
| XX                                                                    | Claim 9; Page 60; 67p; English.                                              |
| XX                                                                    |                                                                              |
| CC                                                                    | The present invention describes secreted proteins designated AM179_11,       |
| CC                                                                    | BG221_11, K139_11, K511_11 and N154_11. The secreted proteins can have       |
| CC                                                                    | immunomodulator, antiinflammatory, immunosuppressive, cytosolic,             |
| CC                                                                    | vulnerary, osteopathic, antiatherosclerotic, neuroprotective, antirheumatic, |
| CC                                                                    | antiparkinsonian, nootropic, antitumor, vasotrophic, cerebroprotective,      |
| CC                                                                    | contraceptive, haemostatic, thrombolytic and antibacterial activities.       |
| CC                                                                    | The proteins can be used in assays to determine biological activity and      |
| CC                                                                    | as markers for tissues in which the corresponding protein is                 |
| CC                                                                    | preferentially expressed (either constitutively or at a particular stage     |
| CC                                                                    | of tissue differentiation or development or in a disease state). The         |
| CC                                                                    | proteins can be used as nutritional sources or supplements and may           |
| CC                                                                    | exhibit cytokine, cell proliferation, cell differentiation and               |
| CC                                                                    | immunomodulatory activities. They may be useful in the treatment of          |
| CC                                                                    | immune and proliferative disorders and for regulating haematopoiesis.        |
| CC                                                                    | The present sequence encodes the K139_11 secreted protein from the           |
| CC                                                                    | present invention.                                                           |
| XX                                                                    |                                                                              |
| XX                                                                    | Sequence 1606 BP; 389 A; 448 C; 412 G; 357 T; 0 other:                       |
| SQ                                                                    |                                                                              |
| Query Match                                                           | 80.0%; Score 16.8; DB 22; Length 1606;                                       |
| Best Local Similarity                                                 | 90.0%; Pred. NO. 56;                                                         |
| Matches 18; Conservative                                              | 0; Mismatches 2; Indels 0; Gaps 0;                                           |
| OY                                                                    | 2 gaagagaccatgaacaactt 21<br>                                                |
| Db                                                                    | 1068 gaagagaccttgaaacaagt 1087                                               |
| RESULT 7                                                              |                                                                              |
| AAC98922                                                              |                                                                              |
| ID AAC98922 standard; CDNA: 1931 BP.                                  |                                                                              |
| XX                                                                    |                                                                              |
| AAC98922;                                                             |                                                                              |
| XX                                                                    |                                                                              |
| DT 09-MAR-2001 (first entry)                                          |                                                                              |
| XX                                                                    |                                                                              |
| DE Human pancreatic cancer antigen nucleotide sequence SEQ ID NO:150. |                                                                              |

|                          |                                                                           |                                                                |
|--------------------------|---------------------------------------------------------------------------|----------------------------------------------------------------|
| XX                       |                                                                           | Human; pancreas; pancreatic cancer; pancreatic cancer antigen; |
| KM                       | detection; diagnosis; identification; cytosolic; neuroprotective;         |                                                                |
| KM                       | nootropic; immunomodulatory; relaxant; contraceptive; gynaecological;     |                                                                |
| KM                       | antiinflammatory; cardiac; gene therapy; chromosome mapping;              |                                                                |
| KW                       | linkage analysis; tissue identification; tissue typing; forensic;         |                                                                |
| KM                       | neural; immune system; muscular; reproductive; gastrointestinal;          |                                                                |
| KM                       | pulmonary; cardiovascular; renal; proliferative; ss.                      |                                                                |
| OS                       | Homo sapiens.                                                             |                                                                |
| PX                       | WO20005320-A1.                                                            |                                                                |
| PN                       | 21-SEP-2000.                                                              |                                                                |
| PD                       |                                                                           |                                                                |
| XX                       |                                                                           |                                                                |
| XX                       | 08-MAR-2000; 2000WO-US05989.                                              |                                                                |
| PE                       |                                                                           |                                                                |
| PR                       | 12-MAR-1999; 99US-0124270.                                                |                                                                |
| PA                       | (HUMA-) HUMAN GENOME SCI INC.                                             |                                                                |
| XX                       |                                                                           |                                                                |
| PI                       | Rosen CA, Ruben SM;                                                       |                                                                |
| DR                       | WPT: 2000-579444/54.                                                      |                                                                |
| DR                       | P-BSDS: AAB54457.                                                         |                                                                |
| PT                       | New nucleic acid that is a pancreatic cancer antigen for preventing,      |                                                                |
| PT                       | treating, or ameliorating a medical condition, particular pancreatic      |                                                                |
| - PT                     | cancer, or for use in assays for diagnosing a pathological condition -    |                                                                |
| PS                       | Claim 1; Page 608-609; 1379pp; English.                                   |                                                                |
| XX                       |                                                                           |                                                                |
| CC                       | AAC98773 to AAC99231 encode the human pancreatic cancer associated        |                                                                |
| CC                       | proteins, called pancreatic cancer antigens, given in AAB54008 to         |                                                                |
| CC                       | AAB54466. The human pancreatic cancer antigens have cytostatic,           |                                                                |
| CC                       | neuroprotective, nootropic, immunomodulatory, relaxant, contraceptive,    |                                                                |
| CC                       | gynaecological, cardiac and antiinflammatory activities, and can be used  |                                                                |
| CC                       | in gene therapy. The polynucleotide and proteins can be used for          |                                                                |
| CC                       | preventing, treating, or ameliorating a medical condition or in assays    |                                                                |
| CC                       | for diagnosing a pathological condition or a susceptibility to one in a   |                                                                |
| CC                       | subject. Binding partners to the proteins and the activity of the         |                                                                |
| CC                       | proteins can be identified. The pancreatic cancer antigens can be used to |                                                                |
| CC                       | detect, treat or prevent pancreatic disorders, especially cancer.         |                                                                |
| CC                       | Agonists and antagonists to the antigens can be screened for. The         |                                                                |
| CC                       | pancreatic cancer antigen polynucleotides can be used to design nucleic   |                                                                |
| CC                       | acid hybridisation probes that can be used in chromosome mapping, linkage |                                                                |
| CC                       | analysis, tissue identification and/or typing and a variety of forensic   |                                                                |
| CC                       | and diagnostic methods. The proteins can be used to generate antibodies   |                                                                |
| CC                       | which are used to purify, detect and target the polypeptides, including   |                                                                |
| CC                       | both in vivo and in vitro diagnostic and therapeutic methods. The         |                                                                |
| CC                       | proteins can be used to treat or prevent neural, immune system, muscular, |                                                                |
| CC                       | reproductive, gastrointestinal, pulmonary, cardiovascular, renal or       |                                                                |
| CC                       | proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent      |                                                                |
| CC                       | sequences used in the exemplification of the present invention.           |                                                                |
| SQ                       | Sequence 1931 BP; 496 A; 499 C; 517 G; 413 T; 6 other:                    |                                                                |
| Query Match              | 80.0%; Score 16.8; DB 21; Length 1931;                                    |                                                                |
| Best Local Similarity    | 90.0%; Pred. No. 57;                                                      |                                                                |
| Matches 18; Conservative | 0; Mismatches 2; Indels 0; Gaps 0.0;                                      |                                                                |
| OY                       | 2 gaagagacatgaacaactt 21<br>                                              |                                                                |
| Db                       | 1658 gaagagacctgaacaagt 1677                                              |                                                                |
| RESULT                   | 8                                                                         |                                                                |
| AAAF44684                |                                                                           |                                                                |
| ID                       | AAAF44684 standard; cDNA; 2163 BP.                                        |                                                                |
| AC                       |                                                                           |                                                                |
| XX                       | AAAF44684;                                                                |                                                                |
| XX                       |                                                                           |                                                                |

DT 27-MAR-2001 (first entry)  
XX  
XX Novel protein kinase cDNA, SEQ ID NO: 64.  
DE  
XX  
KW Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;  
KW immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic;  
KW dermatological; antidiabetic; antifertility; gene therapy; vaccine;  
KW immune disorder; cardiovascular disease; neurodegenerative disease;  
KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;  
KW inflammatory pelvic disease; multiple sclerosis; psoriasis; ss.  
XX  
XX Homo sapiens.  
OS  
XX WO200073469-A2.  
PN  
XX 07-DEC-2000.  
PD  
XX 26-MAY-2000; 2000WO-US14842.  
PF  
XX 28-MAY-1999; 99US-0136503.  
PR  
XX (SUGEN-) SUGEN INC.  
XX  
XX Plowman GD, Martinez R, Whyte D, Sudersanam S;  
PI WPI; 2001-032161/04.  
DR P-PSDB; AAB65657.  
XX  
XX Nucleic acids encoding kinase polypeptides, useful for diagnosing and  
PT treating immune-related diseases and disorders, cardiovascular disease,  
PT neurodegenerative diseases and/or cancers -  
XX  
XX Disclosure: Fig 2; 310pp; English.  
PS  
XX The present sequence encodes a novel protein kinase. The nucleic acids  
CC and the protein kinases they encode may be used in the treatment and  
CC diagnosis of diseases associated with inappropriate kinase expression  
CC such as immune-related diseases and disorders, cardiovascular disease,  
CC neurodegenerative diseases and/or cancers. The nucleic acids and  
CC complementary sequences may also be used as DNA probes in diagnostic  
CC assays. The kinase polypeptides may be used as antigens in the production  
CC of antibodies of kinase expression and activity. Anti-kinase antibodies  
CC and kinase antagonists may also be used to down regulate kinase  
CC expression and activity. Diseases related to kinase expression and  
CC activity include rheumatoid arthritis, atherosclerosis, autoimmune  
CC disorders, complications of organ transplantation, myocardial infarction,  
CC immune disorders, cardiomyopathies, strokes, renal failure,  
CC oxidative-stress related disorders, chronic inflammatory bowel disease,  
CC chronic inflammatory pelvic disease, multiple sclerosis, asthma,  
CC osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and  
CC reproductive disorders.  
XX  
XX Sequence 2163 BP; 520 A; 572 C; 589 G; 482 T; 0 other;  
SQ

Query Match 80.0%; Score 16.8; DB 22; Length 2163;  
Best Local Similarity 90.0%; Pred. No. 58;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 gaagagaccatgaacactt 21  
|||||  
Db 1646 gaagagacctgaacagt 1665

RESULT 9  
AAV59121  
ID AAV59121 standard; DNA; 2241 BP.  
XX  
AC AAV59121;  
XX  
DT 07-JAN-1999 (first entry)  
XX  
DE Nucleotide sequence of BCOM3, a kinase.

XX  
XX Serine protease; regulation; cell activity; viability; HELA2; ATC2;  
KW BCOM3; testisin; fertility; suppressor; testicular germ cell cancer;  
KW seminoma; testis-specific expression; antitumour; sperm development;  
KW infertility; ss.  
XX  
XX Homo sapiens.  
OS  
XX Key Location/Qualifiers  
FH CDS 166..1773  
FT /\*tag= a  
FT /product= BCOM3  
XX  
XX WO9836054-A1.  
PN  
XX 20-AUG-1998.  
PD  
XX 13-FEB-1998; 98WO-AU00085.  
PF  
XX 18-NOV-1997; 97AU-0000422.  
PR 13-FEB-1997; 97AU-0005101.  
XX  
XX (AMRA-) AMRAD OPERATIONS PTY LTD.  
XX  
XX Antalis TM, Hooper JD;  
PI WPI; 1998-480768/41.  
DR P-PSDB; AAM77299.  
XX  
XX New serine protease(s) and kinase involved in regulating cell  
PT activity and viability - particularly the testis-specific protease  
PT HELA2 used for modulation of fertility and as tumour suppressor  
XX  
XX Claim 30; Pages 70-73; 167pp; English.  
PS  
XX The present sequence represents the nucleotide sequence of BCOM3.  
CC cDNA generated from HeLa cells and PAI-2 expressing HeLa cells  
CC was amplified using PCR primers AAV48312-13. Three new sequences  
CC were detected in the 480 bp amplicon. These sequences are designated  
CC HELA2 and ATC2 which have high homology to serine proteases and BCOM3  
CC which has homology to a kinase. The proteins are involved in or  
CC associated with regulation of cell activity and/or viability.  
CC Administration of recombinant HELA2 (also called testisin) is used to  
CC increase fertility. Downregulation of HELA2 reduces fertility. HELA2 is  
CC also a suppressor of testicular germ cell cancers (seminoma) and is also  
CC expressed in some non-testicular cancers (of colon, pancreas, prostate  
CC and ovary), so is a marker/potential therapeutic target for cancer. The  
CC promoter from the HELA2 gene is useful for testis-specific expression of  
CC other genes, e.g. for gene therapy or modulation of fertility. Drugs  
CC that block activity of HELA2 should have antitumour activity (other than  
CC in testis) while in testis recombinant HELA2 should stop growth of  
CC tumours and normalise sperm development (eliminating the need for  
CC orchidectomy). Identification of mutant forms of HELA2 can be used to  
CC diagnose infertility.  
XX  
XX Sequence 2241 BP; 557 A; 583 C; 602 G; 499 T; 0 other;  
SQ

Query Match 80.0%; Score 16.8; DB 19; Length 2241;  
Best Local Similarity 90.0%; Pred. No. 58;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 gaagagaccatgaacactt 21  
|||||  
Db 1699 gaagagacctgaacagt 1718

RESULT 10  
AAQ42188  
ID AAQ42188 standard; DNA; 1815 BP.  
XX  
AC AAQ42188;  
XX

DT 14-SEP-1993 (first entry)  
 XX ODC CDNA.  
 XX  
 XX Polymerase chain reaction: primer; amplify; PCR: protein A; rabbit;  
 KM ODC; hyaloma; ornithine decarboxylase; human; kidney; cDNA library;  
 KM fusion protein; E. coli; antibody; detect; cancer; immunostaining; ss.  
 XX  
 XX Synthetic.  
 OS  
 FH Key Location/Qualifiers  
 FT CDS 88..1473  
 FT /\*tag= a  
 XX  
 XX EP542287-A.  
 XX  
 PD 19-MAY-1993.  
 XX  
 PF 13-NOV-1992; 92EP-0119416.  
 XX  
 PR 14-NOV-1991; 91JP-0327041.  
 PR 10-AUG-1992; 92JP-0234278.  
 XX  
 PA (IDEX ) IDEMITSU KOSAN CO LTD.  
 XX  
 PI Irie S, Nakayama K, Wadama K;  
 DR WPI: 1993-160785/20.  
 DR P-PSDB: AAR37270.  
 XX  
 PT Antibodies specific for human ornithine decarboxylase - useful  
 PT for diagnosis of cancer  
 XX  
 PS Disclosure: Fig 7; 23pp; English.  
 XX  
 CC This sequence represents the ornithine decarboxylase (ODC) cDNA. The  
 CC ODC cDNA was isolated using the primers given in AA042186-87. These  
 CC primers introduced a BamHI site to the 5' end, and an EcoRI site to  
 CC the 3' end of the ODC cDNA to facilitate cloning. A human kidney cDNA  
 CC library was used as the template and the ODC cDNA was isolated as a  
 CC BamHI-EcoRI fragment. This fragment was expressed in a protein A  
 CC fusion gene vector. The vector was cloned in to E. coli and a protein  
 CC A-ODC fusion protein was produced. The ODC was separated from the  
 CC fusion protein and the N-terminus of the ODC was sequenced, and the  
 CC compared to a reference N-terminal peptide to ensure that the protein  
 CC A had been cleaved. The isolated ODC protein was used to raise  
 CC antibodies in rabbits. The antibodies may be used to detect cancer  
 CC cells producing ODC by immunostaining.  
 CC  
 SO Sequence 1815 BP; 485 A; 364 C; 449 G; 517 T; 0 other;

Query Match 75.2%; Score 15.8; DB 14; Length 1815;  
 Best Local Similarity 89.5%; Pred. No. 1.7e+02;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 aagagaccatgaacaactt 21  
 ||||| | ||||| |||||  
 DB 80 aagaatacatgaacaactt 98

RESULT 11  
 AAF18267  
 ID AAF18267 standard; DNA; 1958 BP.  
 XX  
 AC AAF18267;  
 XX  
 DT 14-MAR-2001 (first entry)  
 XX  
 DE Lung cancer associated, polynucleotide sequence SEQ ID 286.  
 XX  
 KM Human: lung cancer associated protein; neuroprotective; cytostatic;  
 KM cardioactive; immunomodulatory; muscular active; vulnery;

KM gastrointestinal; nephrotropic; antineoplastic; gynecological;  
 KM antibacterial; diagnosis; neural disorder; immune disorder; reproductive;  
 KM proliferative disorder; wound healing; infectious disease; ds.  
 XX  
 XX Homo sapiens.  
 OS  
 PN WO200055180-A2.  
 XX  
 PD 21-SEP-2000.  
 XX  
 PF 08-MAR-2000; 2000MO-US05918.  
 XX  
 PR 12-MAR-1999; 99US-0124270.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (ROSE/) ROSEN C A.  
 XX  
 PI Ruben SM.  
 XX  
 DR WPI: 2000-587514/55.  
 DR P-PSDB: AAB58391.  
 XX  
 PT Lung cancer associated gene sequences, referred to as lung cancer  
 PT antigens, useful for treatment, prevention, and diagnosis of disorders  
 PT such as lung cancer -  
 XX  
 PS Claim 1; Page 744-745; 1425pp; English.  
 XX  
 CC Polynucleotide sequences AAF1982 - AAF18424 encode human lung cancer  
 CC associated proteins represented in AAB58106 - AAB58548. Lung cancer  
 CC associated proteins and polynucleotide sequences, their agonists, and  
 CC antagonists may have neuroprotective; cytostatic; cardioactive;  
 CC immunomodulatory; muscular active general; vulnery; gastrointestinal  
 CC general; nephrotropic; antineoplastic; gynecological; or antibacterial  
 CC activity. The invention also includes antibodies specific for the  
 CC protein or polynucleotide sequences. The lung cancer associated  
 CC polynucleotide sequences may be used for detection of lung cancer,  
 CC chromosome identification, as chromosome markers, and for numerous other  
 CC diagnostic or research purposes. The proteins may be used to treat  
 CC disorders such as neural, immune, muscular, reproductive,  
 CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative  
 CC disorders. The proteins may also be used in the treatment of wounds and  
 CC infectious diseases. Polynucleotide sequences AAF18425 - AAF18433 and  
 CC peptide AAB58549 are used in the course of the invention for the  
 CC identification and characterization of the polynucleotide and protein  
 CC sequences.  
 XX  
 SO Sequence 1958 BP; 520 A; 402 C; 497 G; 538 T; 1 other;

Query Match 75.2%; Score 15.8; DB 21; Length 1958;  
 Best Local Similarity 89.5%; Pred. No. 1.7e+02;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 aagagaccatgaacaactt 21  
 ||||| | ||||| |||||  
 DB 171 aagaatacatgaacaactt 189

RESULT 12  
 AA244288  
 ID AA244288 standard; cDNA; 2265 BP.  
 XX  
 AC AA244288;  
 XX  
 DT 31-MAR-2000 (first entry)  
 XX  
 DE Human brain PARP3 CDNA.  
 XX  
 KM PARP: poly(ADP-ribose) polymerase; human; murine; detection; sepsis;  
 KM diagnosis; therapy; necrosis; apoptosis; neurodegenerative illness;  
 KM ischemic tissue damage; PARP3; ss.  
 XX



|           |                                                                                                            |
|-----------|------------------------------------------------------------------------------------------------------------|
| OS        | Homo sapiens.                                                                                              |
| XX        |                                                                                                            |
| FH        | Key                                                                                                        |
| FT        | CDS                                                                                                        |
| FT        | Location/Qualifiers                                                                                        |
| FT        | 242..1843                                                                                                  |
| XX        | /tag= a                                                                                                    |
| XX        | /product= "PARP3"                                                                                          |
| PN        |                                                                                                            |
| XX        | M0964572-A2.                                                                                               |
| XX        |                                                                                                            |
| PD        | 16-DEC-1999.                                                                                               |
| XX        |                                                                                                            |
| PE        | 04-JUN-1999; 99WO-EP03889.                                                                                 |
| XX        |                                                                                                            |
| PR        | 05-JUN-1998; 98DE-1025213.                                                                                 |
| PR        | 01-MAR-1999; 99DE-1008837.                                                                                 |
| XX        |                                                                                                            |
| PA        | (BADI ) BASF AG.                                                                                           |
| XX        |                                                                                                            |
| PI        | Kock M, Hoeger T, Kroegeer B, Otterbach B, Lubisch W, Lemaire H,                                           |
| DR        | WPI: 2000-087218/07.                                                                                       |
| P-PSDB:   | AAY51175.                                                                                                  |
| XX        |                                                                                                            |
| PT        | Novel genes and proteins, antibodies and binding partners useful in                                        |
| PT        | diagnosis and therapy of energy deficiency associated disease                                              |
| PT        | conditions -                                                                                               |
| XX        |                                                                                                            |
| PS        | Claim 7b; Page 54-57; 96pp; German.                                                                        |
| XX        |                                                                                                            |
| CC        | This invention describes novel human and murine poly(ADP-ribose)                                           |
| CC        | polymerase (PARP) homologues, which are characterised by an amino acid                                     |
| CC        | sequence with a functional NAD <sup>+</sup> -binding site and no zinc finger                               |
| CC        | sequence motif, of general formula CX <sub>2</sub> CX <sub>2</sub> MX <sub>2</sub> C (1). The nucleic acid |
| CC        | sequences, PARP homologues and antibodies are useful for analytic                                          |
| CC        | detection of PARP homologues and for identifying PARP effectors or                                         |
| CC        | binding partners, as well as for determining their effectiveness.                                          |
| CC        | PARP-binding partners are useful for the diagnosis or therapy of a                                         |
| CC        | disease condition, which is the result of a PARP protein, especially an                                    |
| CC        | energy deficiency, which may comprise tissue damage from cell death                                        |
| CC        | following necrosis or apoptosis. The disease condition may be chosen                                       |
| CC        | from a neurodegenerative illness, or sepsis or ischemic tissue damage,                                     |
| CC        | in particular neurotoxic disturbances, etc. This sequence encodes the                                      |
| CC        | human PARP3 protein used in the method of the invention.                                                   |
| SQ        |                                                                                                            |
|           | Sequence 2265 BP; 570 A; 662 C; 587 G; 446 T; 0 other;                                                     |
|           |                                                                                                            |
|           | Query Match 75.2%; Score 15.8; DB 21; Length 2265;                                                         |
|           | Best Local Similarity 89.5%; Pred. No. 1.8e+02;                                                            |
|           | Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0.                                                |
| OY        | 2 gaagagacatgaacaact 20                                                                                    |
|           |                                                                                                            |
| Ddb       | 632 gaaaagaccagaacaact 650                                                                                 |
|           |                                                                                                            |
| RESULT 13 |                                                                                                            |
| AAZ44289  |                                                                                                            |
| ID        | AAZ44289 standard; CDNA; 2265 BP.                                                                          |
| AC        | AAZ44289;                                                                                                  |
| XX        |                                                                                                            |
| DT        | 31-MAR-2000 (first entry)                                                                                  |
| XX        |                                                                                                            |
| DE        | Human uterus type 2 PARP3 CDNA.                                                                            |
| XX        |                                                                                                            |
| KM        | PARP; poly(ADP-ribose) polymerase; human; murine; detection; sepsis;                                       |
| KW        | diagnosis; therapy; necrosis; apoptosis; neurodegenerative illness;                                        |
| KW        | ischemic tissue damage; PARP3; ss.                                                                         |
| XX        |                                                                                                            |
| OS        | Homo sapiens.                                                                                              |
| XX        |                                                                                                            |
| FH        | Key                                                                                                        |
|           | Location/Qualifiers                                                                                        |

|           |                                                                            |                                                                                                             |               |  |
|-----------|----------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------|---------------|--|
| FT        | CDS                                                                        |                                                                                                             | 221..1843     |  |
| FT        |                                                                            | /**tag=                                                                                                     | a             |  |
| FT        |                                                                            | /product=                                                                                                   | "PARP3"       |  |
| XX        |                                                                            |                                                                                                             |               |  |
| XX        | PN                                                                         | W09964572-A2.                                                                                               |               |  |
| XX        |                                                                            |                                                                                                             |               |  |
| XX        | PD                                                                         | 16-DEC-1999.                                                                                                |               |  |
| XX        |                                                                            |                                                                                                             |               |  |
| XX        | PF                                                                         | 04-JUN-1999;                                                                                                | 99WO-EP03889. |  |
| XX        | PR                                                                         | 05-JUN-1998;                                                                                                | 98DE-1025213. |  |
| XX        | PR                                                                         | 01-MAR-1999;                                                                                                | 99DE-1008837. |  |
| XX        | PA                                                                         | (BADI ) <BASF AG.                                                                                           |               |  |
| XX        | PI                                                                         | Kock M., Hoeger T., Kroeger B., Otterbach B., Lubisch W., Lemaire H,                                        |               |  |
| XX        | DR                                                                         | WPI: 2000-087218/07.                                                                                        |               |  |
| XX        | DR                                                                         | P-PSDB: AAY51176.                                                                                           |               |  |
| XX        | PT                                                                         | Novel genes and proteins, antibodies and binding partners useful in                                         |               |  |
| XX        | PT                                                                         | diagnosis and therapy of energy deficiency associated disease                                               |               |  |
| XX        | PT                                                                         | conditions -                                                                                                |               |  |
| XX        |                                                                            |                                                                                                             |               |  |
| XX        | PS                                                                         | Claim 7c; Page 59-62; 96pp; German.                                                                         |               |  |
| XX        |                                                                            |                                                                                                             |               |  |
| CC        |                                                                            | This invention describes novel human and murine poly(ADP-ribose)                                            |               |  |
| CC        |                                                                            | sequence (PARP) homologues, which are characterised by an amino acid                                        |               |  |
| CC        |                                                                            | polymerase with a functional NAD <sup>+</sup> -binding site and no zinc finger                              |               |  |
| CC        |                                                                            | sequence motif, of general formula CX <sub>2</sub> CX <sub>2</sub> MHX <sub>2</sub> C (1). The nucleic acid |               |  |
| CC        |                                                                            | sequences, PARP homologues and antibodies are useful for analytic                                           |               |  |
| CC        |                                                                            | detection of PARP homologues and for identifying PARP effectors or                                          |               |  |
| CC        |                                                                            | binding partners, as well as for determining their effectiveness.                                           |               |  |
| CC        |                                                                            | PARP-binding partners are useful for the diagnosis or therapy of a                                          |               |  |
| CC        |                                                                            | disease condition, which is the result of a PARP protein, especially an                                     |               |  |
| CC        |                                                                            | energy deficiency, which may comprise tissue damage from cell death                                         |               |  |
| CC        |                                                                            | following necrosis or apoptosis. The disease condition may be chosen                                        |               |  |
| CC        |                                                                            | from a neurodegenerative illness, or sepsis or ischemic tissue damage,                                      |               |  |
| CC        |                                                                            | in particular neurotoxic disturbances, etc. This sequence encodes the                                       |               |  |
| CC        |                                                                            | human PARP3 protein used in the method of the invention.                                                    |               |  |
| XX        |                                                                            |                                                                                                             |               |  |
| SQ        |                                                                            | Sequence 2265 BP; 570 A; 662 C; 587 G; 446 T; 0 other;                                                      |               |  |
|           |                                                                            |                                                                                                             |               |  |
|           | Query Match                                                                | 75.2%; Score 15.8; DB 21; Length 2265;                                                                      |               |  |
|           | Best Local Similarity                                                      | 89.5%; Pred. No. 1.8e+02;                                                                                   |               |  |
|           | Matches 17; Conservative                                                   | 0; Mismatches 2; Indels 0; Gaps 0;                                                                          |               |  |
| OY        | 2 gaagagaccatgaacaact 20                                                   |                                                                                                             |               |  |
|           |                                                                            |                                                                                                             |               |  |
| Db        | 632 gaaagaccaagaacaact 650                                                 |                                                                                                             |               |  |
|           |                                                                            |                                                                                                             |               |  |
| RESULT 14 |                                                                            |                                                                                                             |               |  |
| ID        | AAC63441/c                                                                 |                                                                                                             |               |  |
| XX        | AAC63441 standard; cDNA; 1913 BP.                                          |                                                                                                             |               |  |
| XX        |                                                                            |                                                                                                             |               |  |
| XX        | AAC63441;                                                                  |                                                                                                             |               |  |
| XX        |                                                                            |                                                                                                             |               |  |
| XX        | 09-FEB-2001 (first entry)                                                  |                                                                                                             |               |  |
| XX        |                                                                            |                                                                                                             |               |  |
| DE        | Human secreted protein coding sequence SEQ ID NO: 42.                      |                                                                                                             |               |  |
| XX        |                                                                            |                                                                                                             |               |  |
| KW        | Cytostatic; immunosuppressive; neutrophic; neuroprotective; antiviral;     |                                                                                                             |               |  |
| KW        | antiallergic; hepatotoxic; antidiabetic; antiinflammatory; anticancer;     |                                                                                                             |               |  |
| KW        | vulnerary; anticoagulant; antibacterial; antifungal; antiparasitic;        |                                                                                                             |               |  |
| KW        | candidant; gene therapy; cancer; immune disorder; cardiovascular disorder; |                                                                                                             |               |  |
| KW        | neurological disease; infection; human; secreted protein; ss.              |                                                                                                             |               |  |
| OS        | Homo sapiens.                                                              |                                                                                                             |               |  |
| XX        |                                                                            |                                                                                                             |               |  |
| XX        | W0200061779-A1.                                                            |                                                                                                             |               |  |
| PN        |                                                                            |                                                                                                             |               |  |
| XX        |                                                                            |                                                                                                             |               |  |

```

PD 19-OCT-2000.
XX
XX 06-APR-2000; 2000MO-US09068.
XX
XX 09-APR-1999; 99US-0128699.
XX
XX 20-JAN-2000; 2000US-0177050.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM, Komatsoulis G;
XX
XX WPI; 2000-647424/62.
XX
XX P-PSDB; AAB29833.
XX
XX Isolated nucleic acid molecule encoding a human secreted protein is
XX PT used in preventing, treating or ameliorating a medical condition -
XX
XX
XX PS Claim 1; Page 414; 495pp; English.
XX
XX The invention relates to the isolation of genes AAGC3410-CG3458 encoding
XX CC 49 human secreted proteins AAB29802-B29850. The genes can be used to
XX CC generate fusion proteins by linking to the gene for the human
XX CC immunoglobulin G Fc portion (SEQID) for increasing the stability of
XX CC the fusion protein as compared to the human protein only. The genes and
XX CC proteins are useful for preventing, ameliorating or treating medical
XX CC conditions, e.g. by protein or gene therapy. The genes are isolated
XX CC from a range of human tissues disclosed in the specification. The
XX CC nucleic acids, proteins, antibodies and (ant)agonists are useful in
XX CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
XX CC and ovarian cancer, and other cancers of the adrenal gland, bone, bone
XX CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
XX CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
XX CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
XX CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
XX CC colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d)
XX CC wound healing; (e) neurological diseases e.g. cerebral anoxia and
XX CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
XX CC and parasitic infections.
XX
XX SQ Sequence 1913 BP; 601 A; 356 C; 375 G; 581 T; 0 other;

Query Match          73.3%; Score 15.4; DB 21; Length 1913;
Best Local Similarity 94.1%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 gaagagacatgaacaa 18
   |||||
Db 1112 GAAGAGACATGCACAA 1096

RESULT 15
AAQ04775/c
ID AAQ04775 standard; DNA; 1915 BP.
XX
XX AAQ04775;
AC
XX 18-OCT-1990 (first entry)
XX
XX Fragment contg. Chloramphenicol resistance gene.
DE
XX Chloramphenicol resistance; mutagenesis; ss.
XX
XX Key Location/Qualifiers
XX FT CDS 545..1714
XX FT /tag= a
XX FT /label=Chloramphenicol resistance gene
XX FT RBS 535..538
XX FT /tag= b
XX
XX DE3841454-A.
XX
XX 13-JUN-1990.

```

```

XX
XX 09-DEC-1988; 88DE-3841454.
XX
XX 09-DEC-1988; 88DE-3841454.
XX
XX (DEGS) DEGUSSA AG.
XX
XX Kassing F, Kalinowski J, Arnold W, Winterfeldt A, Puhler A;
XX PI Kautz P-S, Thierbach G;
XX
XX WPI; 1990-186465/25.
XX
XX P-PSDB; AAR05475.
XX
XX Site specific mutagenesis of DNA at restriction enzyme positions -
XX PT by treating corresp. restriction fragments with hydroxylamine,
XX PT and new mutated sequences and transformed microorganisms
XX
XX
XX PS Disclosure; ; P; German.
XX
XX This fragment when ligated into a plasmid and used to transform host
XX CC cells confers Chloramphenicol resistance on them.
XX
XX SQ Sequence 1915 BP; 353 A; 601 C; 567 G; 394 T; 0 other;

Query Match          73.3%; Score 15.4; DB 11; Length 1915;
Best Local Similarity 94.1%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 gagacatgaacaact 21
   |||||
Db 1826 GAGACATGAACATCTT 1810

Search completed: September 21, 2001, 02:42:51
Job time: 11467 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 20, 2001, 23:28:33 : Search time 4309.39 Seconds  
(without alignments)  
46.065 Million cell updates/sec

Title: US-09-138-735-12

Perfect score: 21  
Sequence: 1 cgaagagaccatgaacaactt 21

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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|------------|-------|-------------|--------|----------|--------------------|
| 1          | 18.4  | 87.6        | 504    | AA982948 | AA982948 ua22h06.r |
| 2          | 18.4  | 87.6        | 520    | AM585823 | EST317446          |
| 3          | 18.4  | 87.6        | 533    | BF932609 | BF932609 RC5-NT018 |
| 4          | 17.8  | 84.8        | 532    | BF760064 | BF760064 an-2069 A |
| 5          | 17.4  | 82.9        | 628    | BE856251 | BE856251 7191C06.x |
| 6          | 16.8  | 80.0        | 118    | AM805050 | QV1-UM009          |
| 7          | 16.8  | 80.0        | 209    | BF799621 | BF799621 CM0-C1009 |
| 8          | 16.8  | 80.0        | 277    | AA043840 | AA043840 zk6ia12.r |
| 9          | 16.8  | 80.0        | 282    | BF78704  | BF78704 PM4-KT004  |
| 10         | 16.8  | 80.0        | 298    | N78192   | N78192 yv74e05.r1  |
| 11         | 16.8  | 80.0        | 300    | AV177260 | AV177260 AV177260  |
| 12         | 16.8  | 80.0        | 300    | AV178859 | AV178859 AV178859  |
| 13         | 16.8  | 80.0        | 300    | AV184752 | AV184752 AV184752  |
| 14         | 16.8  | 80.0        | 300    | C29371   | C29371 C29371 Yuj1 |
| 15         | 16.8  | 80.0        | 300    | C37295   | C37295 C37295 Yuj1 |
| 16         | 16.8  | 80.0        | 300    | C37468   | C37468 C37468 Yuj1 |
| 17         | 16.8  | 80.0        | 300    | C38177   | C38177 C38177 Yuj1 |
| 18         | 16.8  | 80.0        | 300    | C38520   | C38520 C38520 Yuj1 |
| 19         | 16.8  | 80.0        | 300    | C55407   | C55407 C55407 Yuj1 |
| 20         | 16.8  | 80.0        | 309    | BF856629 | BF856629 PM1-FT020 |
| 21         | 16.8  | 80.0        | 323    | BF857651 | BF857651 PM1-FT020 |
| 22         | 16.8  | 80.0        | 325    | BF856627 | BF856627 PM1-FT020 |
| 23         | 16.8  | 80.0        | 331    | BF85438  | BF85438 RC6-TN007  |
| 24         | 16.8  | 80.0        | 347    | BE693578 | BE693578 RC3-BT033 |
| 25         | 16.8  | 80.0        | 347    | BF856628 | BF856628 PM1-FT020 |
| 26         | 16.8  | 80.0        | 354    | BF856609 | BF856609 PM1-FT020 |
| 27         | 16.8  | 80.0        | 357    | BF856632 | BF856632 PM1-FT020 |
| 28         | 16.8  | 80.0        | 359    | BF857646 | BF857646 PM1-FT020 |
| 29         | 16.8  | 80.0        | 360    | D67597   | D67597 CELK034E3F  |
| 30         | 16.8  | 80.0        | 361    | BF856634 | BF856634 PM1-FT020 |
| 31         | 16.8  | 80.0        | 367    | BF856611 | BF856611 PM1-FT020 |
| 32         | 16.8  | 80.0        | 368    | AM380268 | AM380268 OV3-HT026 |
| 33         | 16.8  | 80.0        | 372    | BE817820 | BE817820 CM0-BN026 |
| 34         | 16.8  | 80.0        | 373    | AM380277 | AM380277 OV3-HT026 |
| 35         | 16.8  | 80.0        | 378    | AM917829 | AM917829 EST349133 |
| 36         | 16.8  | 80.0        | 388    | BF857647 | BF857647 PM1-FT020 |
| 37         | 16.8  | 80.0        | 400    | BE830145 | BE830145 RC6-ET008 |
| 38         | 16.8  | 80.0        | 422    | AA587314 | AA587314 nt74q11.s |
| 39         | 16.8  | 80.0        | 433    | AA975653 | AA975653 c063e02.s |
| 40         | 16.8  | 80.0        | 434    | AM482284 | AM482284 41788 MAR |
| 41         | 16.8  | 80.0        | 444    | H79060   | H79060 yu24e03.r1  |
| 42         | 16.8  | 80.0        | 475    | W01185   | W01185 za59e08.r1  |
| 43         | 16.8  | 80.0        | 484    | AM984006 | AM984006 RC1-HN000 |
| 44         | 16.8  | 80.0        | 495    | AA196613 | AA196613 zq08a03.r |
| 45         | 16.8  | 80.0        | 495    | AM983992 | AM983992 RC1-HN000 |

## ALIGNMENTS

RESULT 1  
LOCUS AA982948 504 bp mRNA EST 27-MAY-1998  
DEFINITION ua22h06.r1 Soares\_mammary\_gland\_NBMNG Mus musculus cDNA clone  
IMAGE:1347515 5' similar to gb:X92346 M.musculus mRNA for CART1  
protein (MOUSE);, mRNA sequence.  
ACCESSION AA982948  
VERSION AA982948.1 GI:3160311  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 504)  
Matta,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,  
Giesel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,  
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

TITLE  
JOURNAL  
COMMENT

Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and  
Waterston,R.  
The Mashu-HIMI Mouse EST Project  
Unpublished (1996)  
Contact: Marra M/Mouse EST Project  
Mashu-HIMI Mouse EST Project  
Washington University School of Medicine  
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@wustl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@imgl.lnl.gov) for further information.  
MGI:696307  
Trace considered overall poor quality  
Seq primer: -28m13 rev2 ET from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers  
1..504  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone\_image="1347515"  
/clone\_lib="Soares\_mammary\_gland\_NBMNG"  
/sex="male"  
/tissue\_type="mammary gland"  
/dev\_stage="4 weeks"  
/lab\_host="DH10B"  
/note="Organ: mammary gland; Vector: pRT73D-Pac (Pharmacia)  
with a modified polylinker; Site\_1: Not I; Site\_2: Eco  
RI; 1st strand cDNA was primed with a Not I - oligo(dt)  
primer [5',  
TGTACCAATCGAATGCGCGCCGCGCAAGCTTTTCTTTTCTTTTCTTTT  
3'); double stranded cDNA was ligated to Eco RI  
adaptors (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of the modified pRT73 vector.  
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library  
constructed and normalized by Bento Soares and M.Fatima  
Bonaldo."

BASE COUNT  
ORIGIN

129 a 129 c 131 g 115 t

Query Match 87.6%; Score 18.4; DB 14; Length 504;  
Best Local Similarity 95.0%; Pred. No. 1.3e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 cgaagagaccatgaacact 20  
1 ||||||||||||||||  
DB 172 CTAGAGACGACGACACT 191

## RESULT 2

AM585823 520 bp mRNA EST 07-SEP-2000  
DEFINITION EST317446 MHAM Medicago truncatula/Gloms versiforme mixed EST  
library cDNA clone PMHAM-39L1, mRNA sequence.  
ACCESSION AM585823  
VERSION AM585823.1 GI:7265337  
KEYWORDS EST.  
SOURCE Medicago truncatula/Gloms versiforme mixed EST library.  
ORGANISM Medicago truncatula/Gloms versiforme mixed EST library.  
Eukaryota; mixed EST libraries.  
REFERENCE 1 (bases 1 to 520)  
Harrison,M.J., Liu,J., Peng,H., Gonzales,M., Ellis,L., Town,C.D.,  
Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and Fraser,C.M.  
ESTs from roots of Medicago truncatula after colonization with  
Gloms versiforme  
Unpublished (2000)  
Contact: Maria J. Harrison  
Plant Biology Division  
The Samuel Roberts Noble Foundation  
2510 Sam Noble Parkway, Ardmore, OK 73401, USA

Tel: 580-223-5810  
 Fax: 580-221-7380  
 Email: mjharrison@noble.org  
 Noble EST name: N254751e  
 TIGR sequence name: MTDAG617K  
 More information is available at:  
 'http://chryslie.tamu.edu/medicago/  
 Seq primer: SKmod (CTA gAA CTA gTg gAT CC).  
 Location/Qualifiers

## FEATURES

source

1. 520  
 /organism="Medicago truncatula/Glomsus versiforme mixed EST  
 library"  
 /cultivar="Medicago truncatula genotype A17"  
 /db\_xref="taxon:119092"  
 /clone\_lib="PMHAM-39L1"  
 /clone\_lib="MHAM"  
 /tissue\_type="roots colonized with Glomsus versiforme"  
 /dev\_stage="roots harvested at 10, 17, 22, 31 and 38 days  
 post-inoculation with Glomsus versiforme. The library was  
 made from a mixture of RNA from each of these stages."  
 /lab\_host="E. coli strain XL0LR"  
 /note="Vector: Bluescript SK-; Site 1: EcoRI; Site 2:  
 XhoI; cDNA was prepared from polyA+ enriched RNA from  
 roots harvested at 10, 17, 22, 31 and 38 days  
 post-inoculation with Glomsus versiforme. The cDNA was  
 directionally ligated into the Unizap XR vector from  
 StrataGene and packaged using Gigapack III Gold packaging  
 extracts. Plasmids containing cDNA inserts were excised  
 from the recombinant lambda-Zap phage using Ex-assist  
 helper phage and propagated in XL0LR cells."  
 BASE COUNT 178 a 96 c 95 g 151 t  
 ORIGIN

Query Match 87.6%; Score 18.4; DB 118; Length 520;  
 Best Local Similarity 95.0%; Pred. No. 1.4e+02;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 gaagagacatgaacactt 21  
 ||||||| |||||||  
 Db 48 GAAGAGACCTGAACACTT 67

RESULT 3  
 LOCUS BF932609 533 bp mRNA EST 22-JAN-2001  
 DEFINITION RC5-WT0181-201200-021-F10 WT0181 Homo sapiens cDNA, mRNA sequence.  
 ACCESSION BF932609  
 VERSION BF932609.1 GI:12349933  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 533)

AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,  
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.R.,  
 Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,  
 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
 Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 MEDLINE 20202663  
 COMMENT Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&cl=RC5-WT0181-  
 201200-021-F10&lt3=2000-12-20&cl=1)  
 Seq primer: puc 18 forward  
 high quality sequence start: 43  
 high quality sequence stop: 384.  
 Location/Qualifiers

## FEATURES

source

1. 533  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="WT0181"  
 /dev\_stage="Adult"  
 /note="Organ: nervous\_tumor; Vector: puc18; site\_1: SmaI;  
 site\_2: SmaI; A mini-library was made by cloning products  
 derived from ORESTES PCR (U.S. Letters Patent application  
 No. 196,716 - Ludwig Institute for Cancer Research)  
 profiles into the puc 18 vector. Reverse transcription of  
 tissue mRNA and cDNA amplification were performed under  
 low stringency conditions."  
 BASE COUNT 135 a 130 c 163 g 105 t  
 ORIGIN

Query Match 87.6%; Score 18.4; DB 171; Length 533;  
 Best Local Similarity 95.0%; Pred. No. 1.4e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 gaagagacatgaacactt 21  
 ||||||| |||||||  
 Db 322 GAAGAGACCTGAACACTT 303

RESULT 4  
 LOCUS BE760064 532 bp mRNA EST 24-OCT-2000  
 DEFINITION an\_2069 Aspergillus niger, pYES2 (XhoI-EcoRI) Aspergillus niger  
 cDNA clone 2069 5', mRNA sequence.  
 ACCESSION BE760064  
 VERSION BE760064.1 GI:10182701  
 KEYWORDS EST.  
 SOURCE Aspergillus niger.  
 ORGANISM Aspergillus niger

REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.  
 1 (bases 1 to 532)  
 AUTHORS Tsang, A. and Storms, R.  
 TITLE Aspergillus niger Expressed Sequence Tags  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Tsang, A.  
 Dept. of Biology  
 Concordia University  
 1455 de Maisonneuve Blvd. West, Montreal, Quebec CANADA, H3G 1M8  
 Tel: 514-848-3405  
 Fax: 514-848-4504  
 Email: tsang@vax2.concordia.ca  
 PCR PRIMERS  
 FORWARD: CGACATTATGCTGAGTATATCC  
 Insert Length: 532 Std Error: 0.00  
 POLYA=No.

## FEATURES

source

1. 532  
 /organism="Aspergillus niger"  
 /db\_xref="taxon:5061"  
 /clone\_lib="2069"  
 /clone\_lib="Aspergillus niger, pYES2 (XhoI-EcoRI)"  
 /lab\_host="E. coli"  
 /note="Vector: pYES2; Site 1: Xho-I; Site 2: EcoRI; cDNA  
 was synthesized with Zap kit (Stratagene) using poly(A)+  
 RNA isolated from Aspergillus niger grown in both complete  
 and minimal media. Synthesis was primed with oligo(dT)  
 primer/XhoI-linker. EcoRI adaptors were later ligated to  
 polished ends. EcoRI-XhoI-digested cDNA was ligated with



BASE COUNT 130 a 135 c 123 g 108 t 36 others  
 EcorI-XhoI-digested pYES2 (Invitrogen Corp). This vector permits expression of our library in Yeast. "

Query Match 84.8%; Score 17.8; DB 139; Length 532;  
 Best Local Similarity 90.5%; Pred. No. 2.7e+02;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 cgaagagaccatgaacaact 21  
 |||||  
 Db 44 CGAAGAGACATCATCAACTT 64

RESULT 5  
 BE856251/c 628 bp mRNA EST 29-SEP-2000  
 LOCUS 7191C06.X1 NCI\_CGAP\_Brn23 Homo sapiens cDNA clone IMAGE:3304330 3'  
 DEFINITION similar to TR:075377 075377 HISTONE MACROH2A1.1.; mRNA sequence.  
 ACCESSION BE856251  
 VERSION BE856251.1 GI:10369087  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 628)  
 NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute / National Institute of Neurological  
 Disorders and Stroke, Brain Tumor Genome Anatomy Project  
 (CGAP/BRGAP), Tumor Gene Index  
 Unpublished (1998)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs@mail.nih.gov  
 Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,  
 Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
 Bonaldo, Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA sequencing by: Washington University Genome Sequencing Center  
 cDNA distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/ILML, send email to:  
 info@image.llnl.gov  
 Seg primer: -40UP from GIBCO  
 High quality sequence stop: 478.  
 Location/Qualifiers

FEATURES  
 source  
 1..628  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3304330"  
 /clone\_1ib="NCI\_CGAP\_Brn23"  
 /tissue\_type="q1ioblastoma (pooled)"  
 /lab\_host="DH10B"  
 /note="Organ: brain; Vector: pTV73D-Pac (Pharmacia) with a  
 modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st  
 strand cDNA was primed with a Not I - oligo(dT) primer [5',  
 TGTACCAATCTGAAGTGGAGCGCGCATATCTTTTCTTTTCTTTTCTTTT  
 T 3']; double-stranded cDNA was ligated to Eco RI  
 adaptors (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of the modified pTV73 vector.  
 Library is normalized, and was constructed by Bento  
 Soares and M. Fatima Bonaldo."

BASE COUNT 138 a 160 c 173 g 136 t 1 others  
 ORIGIN

Query Match 82.9%; Score 17.4; DB 141; Length 628;  
 Best Local Similarity 94.7%; Pred. No. 4.2e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 2 gaagagaccatgaacaact 20  
 |||||

Db 565 GAAGAGACCATCAACT 547

RESULT 6  
 AM805050 118 bp mRNA EST 16-MAY-2000  
 LOCUS OVI-UM0098-300400-184-f02 UM0098 Homo sapiens cDNA, mRNA sequence.  
 DEFINITION AM805050  
 ACCESSION AM805050.1 GI:7856920  
 VERSION EST.  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 118)  
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,  
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,  
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,  
 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
 Simpson, A.J.  
 Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags  
 Sequence tags  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 20202663  
 Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-QV1-UM0098-300400-184-f02&lt3=2000-04-30&lt4=1>)  
 Seg primer: puc 18 forward  
 High quality sequence start: 29  
 High quality sequence stop: 118.  
 Location/Qualifiers

FEATURES

source  
 1..118  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_1ib="UM0098"  
 /dev\_stage="Adult"  
 /note="Organ: uterus; Vector: puc18; Site\_1: SmaI; Site\_2:  
 SmaI; A mini-library was made by cloning products derived  
 from ORESTES PCR (U.S. Letters Patent application No. 196  
 ,716 - Ludwig Institute for Cancer Research) profiles  
 into the pUC 18 vector. Reverse transcription of tissue  
 mRNA and cDNA amplification were performed under low  
 stringency conditions."  
 BASE COUNT 28 a 26 c 36 g 28 t  
 ORIGIN

Query Match 80.0%; Score 16.8; DB 120; Length 118;  
 Best Local Similarity 90.0%; Pred. No. 6.3e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 gaagagaccatgaacaact 21  
 |||||

Db 70 GAAGAGACCTTGAACAAGT 89

RESULT 7  
 BF799621/c 209 bp mRNA EST 12-JAN-2001  
 LOCUS BF799621  
 DEFINITION <C00-CT10096-101000-559-a10 CT10096 Homo sapiens cDNA, mRNA sequence.  
 ACCESSION BF799621  
 VERSION BF799621.1 GI:12128610  
 KEYWORDS EST.

SOURCE human.  
ORGANISM Homo sapiens  
COMMENT Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 209)  
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.  
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
MEDLINE 20202663  
COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=CM0&t2=CM0-CI0096-101000-599-a10&t3=2000-10-10&t4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 209.  
location/Qualifiers  
1..209  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="CI0096"  
/dev\_stage="Adult"  
/note="Organ: colon.ins; Vector: puc18; site.1: Sma1; site.2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."  
BASE COUNT 58 a 45 c 67 g 39 t  
ORIGIN  
Query Match 80.0%; Score 16.8; DB 169; Length 209;  
Best Local Similarity 90.0%; Pred. No. 6.9e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 gaagagacatgaacaact 21  
|||||  
Db 68 GAAGAGACCTTGAAACAGTT 49  
RESULT 8  
LOCUS AA043840 277 bp mRNA EST 04-SEP-1996  
DEFINITION zK61a12.r1 Soares\_pregnant\_uterus\_NbHPU Homo sapiens cDNA clone  
ACCESSION AA043840  
IMAGE:487294 5', mRNA sequence.  
VERSION AA043840.1 GI:1521697  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
COMMENT Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 277)  
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.  
TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)  
COMMENT Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: estewatson.wustl.edu  
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
Seq primer: -28M13 rev2 from Amersham  
High quality sequence stop: 247.  
location/Qualifiers  
1..277  
/organism="Homo sapiens"  
/db\_xref="GDB:376108"  
/db\_xref="taxon:9606"  
/clone\_lib="IMAGE:487294"  
/clone\_lib="Soares\_pregnant\_uterus\_NbHPU"  
/sex="Female"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/note="Organ: uterus; Vector: pRTT3-Pac; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' ACTGGAGAGATTTCGCGCCGCTTTTGTGTGTGTGT 3']  
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRTT3 vector. Library went through one round of normalization. Library constructed by M. Fatima Bonaldo."  
BASE COUNT 73 a 63 c 83 g 58 t  
ORIGIN  
Query Match 80.0%; Score 16.8; DB 1; Length 277;  
Best Local Similarity 90.0%; Pred. No. 7.2e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 gaagagacatgaacaact 21  
|||||  
Db 228 GAAGAGACCTTGAAACAGTT 247  
RESULT 9  
LOCUS BF738704 282 bp mRNA EST 10-JAN-2001  
DEFINITION PM4-KT0045-191200-005-a07 KT0045 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BF738704  
VERSION BF738704.1 GI:12065380  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
COMMENT Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 282)  
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.  
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
MEDLINE 20202663  
COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br



RESULT 12  
AV178859 300 bp mRNA EST 21-JUL-1999  
LOCUS AV178859 yuji kohara unpublished cDNA:Strain N2 hermaphrodite  
DEFINITION embryo Caenorhabditis elegans cDNA clone yk573a1 3', mRNA sequence.  
ACCESSION AV178859.1 GI:5556760  
VERSION AV178859.1 GI:5556760  
SOURCE EST.  
KEYWORDS Caenorhabditis elegans.  
ORGANISM Caenorhabditis elegans.  
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea  
; Rhabditidae; Pelodermidae; Caenorhabditis.  
REFERENCE 1 (bases 1 to 300)  
AUTHORS Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Mitsuiki,H.,  
Nishigaki,A., Mochizashi,T., Zeng,Q., Watanabe,H., Sugimoto,A., Sano  
M., Miyata,A., Mitani,Y., Iida,K., Uesugi,H., Sugiyama,Y. and  
Nomoto,H.  
Expressed genes in C.elegans  
TITLE Unpublished (1999)  
JOURNAL Contact: Yuji Kohara  
COMMENT Gene Library Lab  
National Institute of Genetics  
Yata 1111, Mishima, Shizuoka 411, Japan  
Tel: 81-559-81-6854  
Fax: 81-559-81-6855  
Email: ykohara@lab.nig.ac.jp.  
Location/Qualifiers  
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/db\_xref="taxon:6239"  
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BASE COUNT 107 a 56 c 65 g 67 t 5 others  
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Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gaagagaccatgaacaactt 21  
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Db 233 GAAGAAACCATGCACACTT 252

RESULT 13  
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LOCUS AV184752 yuji kohara unpublished cDNA:Strain N2 hermaphrodite  
DEFINITION embryo Caenorhabditis elegans cDNA clone yk669a12 3', mRNA  
sequence.  
ACCESSION AV184752.1 GI:5564653  
VERSION AV184752.1 GI:5564653  
SOURCE EST.  
KEYWORDS Caenorhabditis elegans.  
ORGANISM Caenorhabditis elegans.  
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea  
; Rhabditidae; Pelodermidae; Caenorhabditis.  
REFERENCE 1 (bases 1 to 300)  
AUTHORS Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Mitsuiki,H.,  
Nishigaki,A., Mochizashi,T., Zeng,Q., Watanabe,H., Sugimoto,A., Sano  
M., Miyata,A., Mitani,Y., Iida,K., Uesugi,H., Sugiyama,Y. and  
Nomoto,H.  
Expressed genes in C.elegans  
TITLE Unpublished (1999)  
JOURNAL Contact: Yuji Kohara  
COMMENT Gene Library Lab  
National Institute of Genetics

Yata 1111, Mishima, Shizuoka 411, Japan  
Tel: 81-559-81-6854  
Fax: 81-559-81-6855  
Email: ykohara@lab.nig.ac.jp.  
Location/Qualifiers  
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BASE COUNT 105 a 48 c 76 g 67 t 4 others  
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Best Local Similarity 90.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gaagagaccatgaacaactt 21  
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Db 278 GAAGAAACCATGCACACTT 297

RESULT 14  
C29371 300 bp mRNA EST 18-OCT-1999  
LOCUS C29371 yuji kohara unpublished cDNA:Strain N3 hermaphrodite embryo  
DEFINITION Caenorhabditis elegans cDNA clone yk201f1 3', mRNA sequence.  
ACCESSION C29371.1 GI:2361167  
VERSION C29371.1 GI:2361167  
SOURCE EST.  
KEYWORDS Caenorhabditis elegans.  
ORGANISM Caenorhabditis elegans.  
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea  
; Rhabditidae; Pelodermidae; Caenorhabditis.  
REFERENCE 1 (bases 1 to 300)  
AUTHORS Kohara,Y., Mochizashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano  
M., Miyata,A. and Nishigaki,A.  
Expression map of the C.elegans genome  
TITLE Unpublished (1996)  
JOURNAL Contact: Yuji Kohara  
COMMENT Gene Library Lab  
National Institute of Genetics  
Yata 1111, Mishima, Shizuoka 411, Japan  
Tel: 81-559-81-6854  
Fax: 81-559-81-6855  
Email: ykohara@lab.nig.ac.jp.  
Location/Qualifiers  
1. 300  
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hermaphrodite embryo"  
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/dev\_stage="embryo"  
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Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gaagagaccatgaacaactt 21  
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Db 279 GAAGAAACCATGCACACTT 298

## RESULT 15

## LOCUS

C37295 300 bp mRNA

EST 18-OCT-1999

## DEFINITION

C37295 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo  
Caenorhabditis elegans cDNA clone yk464a3 3', mRNA sequence.

## ACCESSION

C37295

## VERSION

C37295.1 GI:2373532

## KEYWORDS

EST.

## SOURCE

Caenorhabditis elegans.

## REFERENCE

## AUTHORS

Kohara,Y., Motobashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano  
M., Miyata,A. and Nishigaki,A.  
1 (bases 1 to 300)

Expression map of the C.elegans genome

## TITLE

Unpublished (1996)

## JOURNAL

Contact: Yuji Kohara

Gene Library Lab

National Institute of Genetics

Yata 1111 Mishima, Shizuoka 411, Japan

Tel: 81-559-81-6854

Fax: 81-559-81-6855

Email: ykohara@lab.nig.ac.jp.

## FEATURES

## Source

1. 300

Location/Qualifiers

/organism="Caenorhabditis elegans"

/strain="N2"

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/clone="yk464a3"

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hermaphrodite embryo"

/sex="hermaphrodite"

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BASE COUNT 107 a 50 c 74 g 66 t 3 others

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Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 gaagagaccatgaacactt 21

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Db 264 GAAGAACCATGCACACACTT 283

Search completed: September 20, 2001, 23:28:42  
Job time: 25582 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 21, 2001, 02:16:42 : Search time 164.23 Seconds  
(without alignments)  
24.207 Million cell updates/sec

Title: US-09-138-735-12

Perfect score: 21

Sequence: 1 cgaagagacatgacacactt 21

Scoring table: IDENTITY\_NUC

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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6: /cgn1\_7/ptodata/1/ina/Backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description       |
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| 4          | 16.8  | 80.0        | 2029   | 3     | US-09-234-613-69  |
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| 6          | 15.2  | 72.4        | 1046   | 1     | US-08-361-467B-4  |
| 7          | 15.2  | 72.4        | 1046   | 1     | US-08-484-332C-4  |
| 8          | 15.2  | 72.4        | 1610   | 4     | US-09-276-531-56  |
| 9          | 15.2  | 72.4        | 1685   | 1     | US-08-360-673-1   |
| 10         | 15.2  | 72.4        | 12492  | 6     | 5206163-2         |
| 11         | 15.2  | 71.4        | 8906   | 2     | US-08-826-267-1   |
| 12         | 14.8  | 70.5        | 69     | 5     | PCT-US92-01015-12 |
| 13         | 14.8  | 70.5        | 72     | 5     | PCT-US92-01015-3  |
| 14         | 14.8  | 70.5        | 81     | 1     | US-08-026-145-3   |
| 15         | 14.8  | 70.5        | 96     | 1     | US-07-872-673B-4  |
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| 17         | 14.8  | 70.5        | 6216   | 3     | US-09-213-053-1   |
| 18         | 14.8  | 70.5        | 7742   | 2     | US-08-882-704A-4  |
| 19         | 14.6  | 69.5        | 39     | 1     | US-08-411-727-9   |
| 20         | 14.6  | 69.5        | 39     | 1     | US-08-411-727-17  |
| 21         | 14.6  | 69.5        | 728    | 4     | US-08-411-727-19  |
| 22         | 14.6  | 69.5        | 728    | 4     | US-08-988-416-654 |
| 23         | 14.6  | 69.5        | 4049   | 1     | US-08-162-809-17  |
| 24         | 14.6  | 69.5        | 4097   | 1     | US-08-162-809-11  |
| 25         | 14.4  | 68.6        | 1146   | 2     | US-09-256-496-1   |
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| 32 | 14.4 | 68.6 | 2173  | 5 | PCT-US93-03942-1 | Sequence 1, Appli  |
| 33 | 14.4 | 68.6 | 3870  | 1 | US-08-138-641-1  | Sequence 1, Appli  |
| 34 | 14.4 | 68.6 | 3870  | 1 | US-08-138-133-1  | Sequence 1, Appli  |
| 35 | 14.4 | 68.6 | 3893  | 1 | US-08-138-641-3  | Sequence 1, Appli  |
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| 37 | 14.4 | 68.6 | 3844  | 4 | US-08-462-437-30 | Sequence 3, Appli  |
| 38 | 14.4 | 68.6 | 13104 | 4 | US-08-256-799-4  | Sequence 30, Appli |
| 39 | 14.4 | 68.6 | 13104 | 4 | US-08-462-437-4  | Sequence 4, Appli  |
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| 45 | 14.2 | 67.6 | 1042  | 3 | US-08-584-031-2  | Sequence 2, Appli  |

#### ALIGNMENTS

RESULT 1  
US-08-480-917-12  
; Sequence 12, Application US/08480917  
; Patent No. 5820864  
; GENERAL INFORMATION:  
; APPLICANT: PARANHOS-BACCALA, Glaucia  
; APPLICANT: LESENECHAL, Mylene  
; APPLICANT: JOLIVET, Michel  
; TITLE OF INVENTION: NEW TRYPAOSOMA CRUZI ANTIGEN, AND GENE  
; TITLE OF INVENTION: ENCODING THE LATTER, THEIR APPLICATION TO THE DETECTION OF  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Oliff & Berridge  
; STREET: 700 South Washington Street, Suite 300  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/480,917  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: A35  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Berridge, William P.  
; REGISTRATION NUMBER: 30,024  
; REFERENCE/DOCKET NUMBER: WPA 36400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-836-6400  
; TELEFAX: 703-836-2787  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 21 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; US-08-480-917-12  
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Best Local Similarity 100.0%; Pred. No. 0.076;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 cgaagagacatgacacactt 21

Db 1 CGAAGAGACCATGACCACTT 21  
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US-08-480-917-1  
Sequence 1, Application US/08480917  
Patent No. 5820864  
GENERAL INFORMATION:  
APPLICANT: PARANHOS-BACCALA, Glaucia  
APPLICANT: LESENECHAL, Mylene  
APPLICANT: JOUVET, Michel  
TITLE OF INVENTION: NEW TRYANOSOMA CRUZI ANTIGEN, AND GENE  
TITLE OF INVENTION: ENCODING THE LATTER; THEIR APPLICATION TO THE DETECTION OF  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Oliff & Berridge  
STREET: 700 South Washington Street, Suite 300  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22314  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,917  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Berridge, William P.  
REGISTRATION NUMBER: 30,024  
REFERENCE/DOCKET NUMBER: WPB 36400  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6400  
TELEFAX: 703-836-2787  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3402 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
US-08-480-917-1

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Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1997 CGAAGAGACCATGACCACTT 2017  
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RESULT 3  
US-08-933-750C-69  
Sequence 69, Application US/08933750C  
Patent No. 5932442  
GENERAL INFORMATION:  
APPLICANT: Lal, Preeti  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Bandman, Olga  
APPLICANT: Shah, Purvi  
APPLICANT: Au-Young, Janice  
APPLICANT: Yue, Henry  
APPLICANT: Guegler, Karl J.  
APPLICANT: Corley, Neil C.  
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES  
NUMBER OF SEQUENCES: 98

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/933,750C  
FILING DATE: September 23, 1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0356 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 69:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2029 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: BRAITTON03  
CLONE: 864683  
US-08-933-750C-69

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Best Local Similarity 90.0%; Pred. No. 15;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 2 gaagagacatgaacactt 21  
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US-09-234-613-69  
Sequence 69, Application US/09234613  
Patent No. 6132973  
GENERAL INFORMATION:  
APPLICANT: Lal, Preeti  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Bandman, Olga  
APPLICANT: Shah, Purvi  
APPLICANT: Au-Young, Janice  
APPLICANT: Yue, Henry  
APPLICANT: Guegler, Karl J.  
APPLICANT: Corley, Neil C.  
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES  
NUMBER OF SEQUENCES: 98  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible



OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/234.613  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/933.750  
FILING DATE: September 23, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0356 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 69:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2029 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: BRAINFUT03  
CLONE: 864683  
US-09-234-613-69

Query Match 80.0%; Score 16.8; DB 3; Length 2029;  
Best Local Similarity 90.0%; Pred. No. 15;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 1644 GAAGAGACCTTGACACACTT 1663

RESULT 5  
US-08-861-745B-2  
Sequence 2, Application US/08861745B  
Patent No. 6165733  
GENERAL INFORMATION:  
APPLICANT: Cen, Hui  
APPLICANT: Williams, Lewis  
TITLE OF INVENTION: Gamma II Adaptorin  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Banner & Witcoff  
STREET: 1001 G Street, NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/861.745B  
FILING DATE: 22-MAY-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Kagan, Sarah A  
REGISTRATION NUMBER: 32141  
REFERENCE/DOCKET NUMBER: 02441.05336  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-508-9100  
TELEFAX: 202-508-9299

TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2533 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-861-745B-2

Query Match 73.3%; Score 15.4; DB 4; Length 2533;  
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Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 gagaccatgaacaactt 21  
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DB 823 GAGACCATGACGACTT 839

RESULT 6  
US-08-361-467B-4/C  
Sequence 4, Application US/08361467B  
Patent No. 5633441  
GENERAL INFORMATION:  
APPLICANT: De Greef, Willy  
APPLICANT: Van Emmelo, John  
APPLICANT: De Oliveira, Dulce E.  
APPLICANT: De Souza, Maria-Helena  
TITLE OF INVENTION: PLANTS WITH MODIFIED FLOWERS, SEEDS OR  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/361.467B  
FILING DATE: 22-DEC-1994  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/681,492  
FILING DATE: 04-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/EP90/01275  
FILING DATE: 01-AUG-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 89 402 224.3  
FILING DATE: 04-AUG-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Schultman, Robert M.  
REGISTRATION NUMBER: 31,196  
REFERENCE/DOCKET NUMBER: 010830-027  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1046 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
IMMEDIATE SOURCE:  
CLONE: 3C9



; Sequence 1, Application US/08360673  
; Patent No. 5679544  
; GENERAL INFORMATION:  
; APPLICANT: Fleer, Reinhard  
; APPLICANT: Fournier, Alain  
; APPLICANT: Yeh, Patrice  
; TITLE OF INVENTION: MODIFIED KLUYVEROMYCES YEASTS, THEIR  
; TITLE OF INVENTION: PREPARATION AND USE  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rhone-Poulenc Rorer Inc.  
; STREET: 500 Arcola Rd. 3C43  
; CITY: Collegeville  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19002  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/360,673  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/FR93/00623  
; FILING DATE: 23-JUN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 92/07785  
; FILING DATE: 25-JUN-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, Julie K.  
; REGISTRATION NUMBER: 38,619  
; REFERENCE/DOCKET NUMBER: ST92040-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (610)454-3839  
; TELEFAX: (610)454-3808  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1685 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; ORIGINAL SOURCE:  
; ORGANISM: Kluveromyces lactis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1683  
; OTHER INFORMATION: /product="Protease B gene"  
; OTHER INFORMATION: /gene="Kl.PRB1"  
US-08-360-673-1

Query Match 72.4%; Score 15.2; DB 1; Length 1685;  
Best Local Similarity 85.0%; Pred. No. 86;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 gaagagaccatgaacaactt 21  
||||| ||| ||||| |||||  
Db 1486 GAAGATACCGTGAACACTT 1505

RESULT 10  
5206163-2  
; Patent No. 5206163  
; APPLICANT: RENARD, ANDRE;DINA, DINO;MARTIAL, JOSEPH  
; TITLE OF INVENTION: DNA ENCODING BOVINE DIARRHEA  
; VIRUS PROTEIN  
; NUMBER OF SEQUENCES: 3  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/550,816

; FILING DATE: 06-JUL-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 331,037  
; FILING DATE: 29-MAR-1989  
; APPLICATION NUMBER: 752,981  
; FILING DATE: 08-JUL-1985  
; SEQ ID NO: 2;  
; LENGTH: 12492  
5206163-2

Query Match 72.4%; Score 15.2; DB 6; Length 12492;  
Best Local Similarity 85.0%; Pred. No. 1,1e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 gaagagaccatgaacaactt 21  
||||| ||| ||||| |||||  
Db 12158 gaagagaccatgaacaactt 12177

RESULT 11  
US-08-826-267-1  
; Sequence 1, Application US/08826267  
; Patent No. 5994070  
; GENERAL INFORMATION:  
; APPLICANT: Streuli, Michel  
; TITLE OF INVENTION: No. 5994070e1 TRIO Molecules and Uses Related Thereto  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/826,267  
; FILING DATE: 1997  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/014,214  
; FILING DATE: 27 MARCH (1996)  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Amy E. Mandragouras  
; REGISTRATION NUMBER: 36,207  
; REFERENCE/DOCKET NUMBER: DFW-010  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8906 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 67..8647  
US-08-826-267-1

Query Match 71.4%; Score 15; DB 2; Length 8906;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 gaccatgaacaactt 21  
||||| ||||| ||||| |||||

Db 2397 GACCATGACACTT 2411

## RESULT 12

PCT-US92-01015-12/c  
Sequence 12, Application PC/TUS9201015

## GENERAL INFORMATION:

APPLICANT: Davis, Geneva R  
APPLICANT: Provow, Sally P  
TITLE OF INVENTION: Production of Human Serum Albumin in  
TITLE OF INVENTION: Methyloctrophic Yeast Cells  
NUMBER OF SEQUENCES: 26

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Fitch, Even, Tabin & Flannery  
STREET: 135 South LaSalle Street, Suite 900  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/01015  
FILING DATE: 19920204CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:APPLICATION NUMBER: US/07/650,040  
FILING DATE: 04-FEB-1991

ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 50857PCT  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (619)552-1311

TELEFAX: (619)552-0095

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 69 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

PCT-US92-01015-12

## Query Match

Best Local Similarity 70.5%; Score 14.8; DB 5; Length 69;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gaagagacatgaacaac 19

Db 26 GAAGAGACAAGAACAC 9

## RESULT 13

PCT-US92-01015-3/c  
Sequence 3, Application PC/TUS9201015

## GENERAL INFORMATION:

APPLICANT: Davis, Geneva R  
APPLICANT: Provow, Sally P  
TITLE OF INVENTION: Production of Human Serum Albumin in  
TITLE OF INVENTION: Methyloctrophic Yeast Cells  
NUMBER OF SEQUENCES: 26

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Fitch, Even, Tabin & Flannery  
STREET: 135 South LaSalle Street, Suite 900  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/01015

FILING DATE: 19920204

CLASSIFICATION: 435

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US/07/650,040

FILING DATE: 04-FEB-1991

ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 50857PCT  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (619)552-1311

TELEFAX: (619)552-0095

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 72 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..72

OTHER INFORMATION:

PCT-US92-01015-3

Query Match 70.5%; Score 14.8; DB 5; Length 72;  
Best Local Similarity 88.9%; Pred. No. 87;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gaagagacatgaacaac 19

Db 44 GAAGAGACAAGAACAC 27

## RESULT 14

US-08-026-145-3/c  
Sequence 3, Application US/08026145

Patent No. 5378614

## GENERAL INFORMATION:

APPLICANT: Petersen, Jens G. Litske  
APPLICANT: No. 5378614dfang, Ole Juul  
TITLE OF INVENTION: Method for Making TPPI Analogues  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 53786140 No. 5378614disk of No. 5378614th America, Inc.

STREET: 405 Lexington Avenue, Suite 6200

CITY: New York

STATE: N. Y.

COUNTRY: United States of America

ZIP: 10174-6201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/026,145

FILING DATE: 19930302

CLASSIFICATION: 435

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 07/828,920

FILING DATE: 27-JAN-1992

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: WO PCT/DK/90/00212

FILING DATE: 17-AUG-1990

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DK 4080/89  
FILING DATE: 18-AUG-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Agtis, Cheryl H.  
REGISTRATION NUMBER: 34086  
REFERENCE/DOCKET NUMBER: 3321.214-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212 867 0123  
TELEFAX: 212 867 0298  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 81 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Synthetic  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..81  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 1..54  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 55..72  
US-08-026-145-3

Query Match 70.5%; Score 14.8; DB 1; Length 81;  
Best Local Similarity 88.9%; Pred. No. 88;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gaagagaccatgaacaac 19  
||||| || |||||  
DB 44 GAAGAGACACAGACACAC 27

RESULT 15  
US-07-872-673B-4/C  
Sequence 4, Application US/07872673B  
Patent No. 5578466  
GENERAL INFORMATION:  
APPLICANT: Toshiya HAYANO, Setsuko KATO, No. 5578466uhiro TAKAHASHI, and Masanori  
TITLE OF INVENTION: Co-expression system of Protein Disulfide Isomerase Gene an  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DAVID G. CONLIN, DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
STREET: 130 WATER STREET  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: US  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Type 2DD, 3.50 inch, 720 KB  
COMPUTER: Apple Macintosh SE  
OPERATING SYSTEM: Apple DOS  
SOFTWARE: Microsoft Word Version 4.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/872,673B  
FILING DATE: 19920417  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: Japanese Patent Application No. 5578466, 114074/91 and 31160  
FILING DATE: 18-APR-1991 and 30-OCT-1991  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 96  
TYPE: NUCLEIC ACID

STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: Other nucleic acid  
US-07-872-673B-4

Query Match 70.5%; Score 14.8; DB 1; Length 96;  
Best Local Similarity 88.9%; Pred. No. 90;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gaagagaccatgaacaac 19  
||||| || |||||  
DB 44 GAAGAGACACAGACACAC 27

Search completed: September 21, 2001, 02:16:45  
Job time: 28238 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 21, 2001, 02:20:06 : Search time 6407.28 Seconds  
(without alignments)  
48.431 Million cell updates/sec

Title: US-09-138-735-12  
Perfect score: 21  
Sequence: 1 cgaagagacatgaacactt 21

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 14155048 seqs, 7388405095 residues

Total number of hits satisfying chosen parameters: 28310096

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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| 1          | 21    | 100.0       | 21     | 13    | US-08-988-242-7       |
| 2          | 21    | 100.0       | 21     | 15    | US-09-138-736-12      |
| 3          | 21    | 100.0       | 3402   | 13    | US-08-988-242-1       |
| 4          | 21    | 100.0       | 3402   | 15    | US-09-138-736-1       |
| 5          | 18    | 85.7        | 13837  | 56    | US-60-248-935-93      |
| 6          | 18    | 85.7        | 32768  | 54    | US-60-229-515-89      |
| 7          | 18    | 85.7        | 32768  | 54    | US-60-229-515-90      |
| 8          | 18    | 85.7        | 32768  | 54    | US-60-229-515-91      |
| 9          | 18    | 85.7        | 32768  | 54    | US-60-229-515-92      |
| 10         | 18    | 85.7        | 32768  | 54    | US-60-229-515-93      |
| 11         | 17.8  | 84.8        | 240    | 21    | US-08-917-047-472     |
| 12         | 17.8  | 84.8        | 240    | 21    | US-08-917-047-472     |
| 13         | 17.8  | 84.8        | 240    | 21    | US-08-917-047-472     |
| 14         | 17.8  | 84.8        | 240    | 21    | US-08-917-047-472     |
| 15         | 17.4  | 82.9        | 278    | 19    | US-09-521-640-66611   |
| 16         | 17.4  | 82.9        | 286    | 21    | US-09-540-229-150778  |
| 17         | 17.4  | 82.9        | 477    | 15    | US-09-107-532-323     |
| 18         | 17.4  | 82.9        | 524    | 40    | US-60-082-300-21418   |
| 19         | 17.4  | 82.9        | 687    | 18    | US-09-417-507-21543   |
| 20         | 17.4  | 82.9        | 969    | 15    | US-09-107-532-258     |
| 21         | 17.4  | 82.9        | 1044   | 16    | US-09-270-849B-149102 |
| 22         | 16.8  | 80.0        | 195    | 11    | US-08-734-050-589     |
| 23         | 16.8  | 80.0        | 195    | 13    | US-08-992-868-589     |
| 24         | 16.8  | 80.0        | 195    | 21    | US-09-540-764-27960   |
| 25         | 16.8  | 80.0        | 195    | 32    | US-60-006-111-589     |
| 26         | 16.8  | 80.0        | 196    | 12    | US-08-808-904-4845    |
| 27         | 16.8  | 80.0        | 196    | 12    | US-08-808-904A-4845   |
| 28         | 16.8  | 80.0        | 196    | 21    | US-09-540-212A-26524  |
| 29         | 16.8  | 80.0        | 233    | 14    | US-09-013-812-2028    |
| 30         | 16.8  | 80.0        | 233    | 21    | US-09-540-764-34474   |
| 31         | 16.8  | 80.0        | 233    | 35    | US-60-036-570-2028    |
| 32         | 16.8  | 80.0        | 233    | 11    | US-08-733-814-81      |
| 33         | 16.8  | 80.0        | 236    | 21    | US-09-540-764-16183   |
| 34         | 16.8  | 80.0        | 237    | 4     | US-08-008-542-490     |
| 35         | 16.8  | 80.0        | 237    | 12    | US-08-857-212-913     |
| 36         | 16.8  | 80.0        | 237    | 18    | US-09-480-902-5904    |
| 37         | 16.8  | 80.0        | 237    | 21    | US-09-540-208-29228   |
| 38         | 16.8  | 80.0        | 237    | 21    | US-09-540-229-88357   |
| 39         | 16.8  | 80.0        | 239    | 15    | US-09-107-910-5136    |
| 40         | 16.8  | 80.0        | 241    | 14    | US-09-540-229-68062   |
| 41         | 16.8  | 80.0        | 241    | 14    | US-09-074-999-1854    |
| 42         | 16.8  | 80.0        | 241    | 36    | US-60-048-431-1854    |
| 43         | 16.8  | 80.0        | 243    | 13    | US-08-903-474-1860    |
| 44         | 16.8  | 80.0        | 243    | 21    | US-09-540-208-1064    |
| 45         | 16.8  | 80.0        | 253    | 13    | US-08-901-904-3120    |

## ALIGNMENTS

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RESULT 1
US-08-988-242-7
; Sequence 7, Application US/08988242
; GENERAL INFORMATION:
; APPLICANT: PARANHOS-BACCALA, GLAUCIA
; APPLICANT: LESENECHAL, MYLENE
; APPLICANT: JOLIVET, MICHEL
; APPLICANT: MANDRAND, BERNARD
; TITLE OF INVENTION: NEW TRIPANOSOMA CRUZI ANTIGEN, GENE
; TITLE OF INVENTION: ENCODING THEREFOR, AND METHODS OF DETECTING AND TREATING
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OLIFF & BERRIDGE, PLC
; STREET: P.O. BOX 19928
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/988,242
; FILING DATE: 10-DEC-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: MPB 36400A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6400
; TELEFAX: 703-836-2787
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-988-242-7

Query Match          100.0%; Score 21; DB 13; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cgaagagaccatgaacaactt 21
DB 1 CGAAGAGACCATGACCACTT 21

RESULT 2
US-09-138-736-12
; Sequence 12, Application US/09138736
; GENERAL INFORMATION:
; APPLICANT: PARANHOS-BACCALA, GLAUCIA
; APPLICANT: LESENECHAL, MYLENE
; APPLICANT: JOLIVET, MICHEL
; TITLE OF INVENTION: NEW TRIPANOSOMA CRUZI ANTIGEN, AND GENE
; TITLE OF INVENTION: ENCODING THE LATTER, THEIR APPLICATION TO THE DETECTION OF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oliff & Berridge
; STREET: 700 South Washington Street, Suite 300
; CITY: Alexandria
```

```
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/138,736
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,917
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: MPB 36400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6400
; TELEFAX: 703-836-2787
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-138-736-12

Query Match          100.0%; Score 21; DB 15; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cgaagagaccatgaacaactt 21
DB 1 CGAAGAGACCATGACCACTT 21

RESULT 3
US-08-988-242-1
; Sequence 1, Application US/08988242
; GENERAL INFORMATION:
; APPLICANT: PARANHOS-BACCALA, GLAUCIA
; APPLICANT: LESENECHAL, MYLENE
; APPLICANT: JOLIVET, MICHEL
; APPLICANT: MANDRAND, BERNARD
; TITLE OF INVENTION: NEW TRIPANOSOMA CRUZI ANTIGEN, GENE
; TITLE OF INVENTION: ENCODING THEREFOR, AND METHODS OF DETECTING AND TREATING
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OLIFF & BERRIDGE, PLC
; STREET: P.O. BOX 19928
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/988,242
; FILING DATE: 10-DEC-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: MPB 36400A
```



TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-836-6400  
 TELEFAX: 703-836-2787  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3402 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: CDNA  
 US-09-988-242-1

Query Match 100.0%; Score 21; DB 13; Length 3402;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 cgaagagacatgaacaact 21  
 ||||||||||||||||  
 Db 1997 CGAAGACCATGAACTT 2017

RESULT 4  
 US-09-138-736-1

Sequence 1, Application US/09138736  
 GENERAL INFORMATION:  
 APPLICANT: PARANHOS-BACCALA, Glaucia  
 APPLICANT: LESENECHAL, Mylene  
 APPLICANT: JOLIVET, Michel  
 TITLE OF INVENTION: NEW TRYPANOSOMA CRUZI ANTIGEN, AND GENE  
 TITLE OF INVENTION: ENCODING THE LATTER, THEIR APPLICATION TO THE DETECTION OF  
 NUMBER OF SEQUENCES: 13  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Oliff & Berridge  
 STREET: 700 South Washington Street, Suite 300  
 CITY: Alexandria  
 STATE: Virginia  
 COUNTRY: U.S.A.  
 ZIP: 22314

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/138,736  
 FILING DATE:

CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/480,917  
 FILING DATE: 07-JUN-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Berridge, William P.  
 REGISTRATION NUMBER: 30,024  
 REFERENCE/DOCKET NUMBER: MPB 36400  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-836-6400  
 TELEFAX: 703-836-2787

INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3402 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: CDNA  
 US-09-138-736-1

Query Match 100.0%; Score 21; DB 15; Length 3402;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 cgaagagacatgaacaact 21  
 ||||||||||||||||  
 Db 1997 CGAAGACCATGAACTT 2017

RESULT 5  
 US-60-248-505-93

Sequence 93, Application US/60248505  
 GENERAL INFORMATION:  
 APPLICANT: Beasley, Ellen  
 TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED  
 TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR  
 FILE REFERENCE: C1000918  
 CURRENT APPLICATION NUMBER: US/60/248,505  
 CURRENT FILING DATE: 2000-11-15  
 NUMBER OF SEQ ID NOS: 1998  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 93  
 LENGTH: 13837  
 TYPE: DNA  
 ORGANISM: human  
 US-60-248-505-93

Query Match 85.7%; Score 18; DB 56; Length 13837;  
 Best Local Similarity 100.0%; Pred. No. 46+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 aagagacatgaacaact 20  
 ||||||||||||||||  
 Db 772 aagagacatgaacaact 789

RESULT 6  
 US-60-229-515-89/c

Sequence 89, Application US/60229515  
 GENERAL INFORMATION:  
 APPLICANT: Beasley, Ellen  
 TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED  
 TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR  
 FILE REFERENCE: C1000776  
 CURRENT APPLICATION NUMBER: US/60/229,515  
 CURRENT FILING DATE: 2000-09-05  
 NUMBER OF SEQ ID NOS: 2013  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 89  
 LENGTH: 32768  
 TYPE: DNA  
 ORGANISM: HUMAN  
 US-60-229-515-89

Query Match 85.7%; Score 18; DB 54; Length 32768;  
 Best Local Similarity 100.0%; Pred. No. 4.66+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 aagagacatgaacaact 20  
 ||||||||||||||||  
 Db 4732 AAGAGACCATGAACTT 4715

RESULT 7  
 US-60-229-515-90/c

Sequence 90, Application US/60229515  
 GENERAL INFORMATION:  
 APPLICANT: Beasley, Ellen  
 TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED  
 TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR  
 FILE REFERENCE: C1000776  
 CURRENT APPLICATION NUMBER: US/60/229,515

;; CURRENT FILING DATE: 2000-09-05  
;; NUMBER OF SEQ ID NOS: 2013  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 90  
;; LENGTH: 32768  
;; TYPE: DNA  
;; ORGANISM: HUMAN  
US-60-229-515-90

Query Match 85.7%; Score 18; DB 54; Length 32768;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 aagagaccatgaacaact 20  
|||||  
Db 4732 AAGAGACCATGACAACT 4715

RESULT 8  
US-60-229-515-91/C  
; Sequence 91, Application US/60229515  
; GENERAL INFORMATION:

;; APPLICANT: Beasley, Ellen  
;; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED  
;; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR  
;; FILE REFERENCE: CL000776  
;; CURRENT APPLICATION NUMBER: US/60/229,515  
;; CURRENT FILING DATE: 2000-09-05  
;; NUMBER OF SEQ ID NOS: 2013  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 91  
;; LENGTH: 32768  
;; TYPE: DNA  
;; ORGANISM: HUMAN  
US-60-229-515-91

Query Match 85.7%; Score 18; DB 54; Length 32768;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 aagagaccatgaacaact 20  
|||||  
Db 4732 AAGAGACCATGACAACT 4715

RESULT 9  
US-60-229-515-92/C  
; Sequence 92, Application US/60229515  
; GENERAL INFORMATION:

;; APPLICANT: Beasley, Ellen  
;; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED  
;; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR  
;; FILE REFERENCE: CL000776  
;; CURRENT APPLICATION NUMBER: US/60/229,515  
;; CURRENT FILING DATE: 2000-09-05  
;; NUMBER OF SEQ ID NOS: 2013  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 92  
;; LENGTH: 32768  
;; TYPE: DNA  
;; ORGANISM: HUMAN  
US-60-229-515-92

Query Match 85.7%; Score 18; DB 54; Length 32768;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 aagagaccatgaacaact 20

|||||  
Db 4732 AAGAGACCATGACAACT 4715

RESULT 10  
US-60-245-225-193  
; Sequence 193, Application US/60245225  
; GENERAL INFORMATION:

;; APPLICANT: Beasley, Ellen  
;; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED  
;; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR  
;; FILE REFERENCE: CL000885  
;; CURRENT APPLICATION NUMBER: US/60/245,225  
;; CURRENT FILING DATE: 2000-11-03  
;; NUMBER OF SEQ ID NOS: 705  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 193  
;; LENGTH: 34117  
;; TYPE: DNA  
;; ORGANISM: Human  
US-60-245-225-193

Query Match 85.7%; Score 18; DB 56; Length 34117;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 aagagaccatgaacaact 20  
|||||  
Db 773 aagagaccatgaacaact 790

RESULT 11  
US-08-917-047-472/C  
; Sequence 472, Application US/08917047  
; GENERAL INFORMATION:

;; APPLICANT: Gooding, Douglas H.  
;; APPLICANT: Stuve, Laura L.  
;; APPLICANT: Stuart, Susan G.  
;; APPLICANT: Ito, Laura Y.  
;; APPLICANT: Akerblom, Ingrid E.  
;; APPLICANT: Deleage, Angela M.  
;; APPLICANT: Naughton, Rebecca E.  
;; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM  
;; TITLE OF INVENTION: HUMAN FETAL LUNG  
;; NUMBER OF SEQUENCES: 2077  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
;; STREET: 3174 PORTER DRIVE  
;; CITY: PALO ALTO  
;; STATE: CALIFORNIA  
;; COUNTRY: USA  
;; ZIP: 94304

;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; OPERATING SYSTEM: IBM PC compatible  
;; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/917,047  
;; FILING DATE:  
;; CLASSIFICATION: 536  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: CERRONE, MICHAEL C., Ph.D.  
;; REGISTRATION NUMBER: 39132  
;; REFERENCE/DOCKET NUMBER: PD-0230P  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 855-0555  
;; TELEFAX: (415) 845-4166  
;; INFORMATION FOR SEQ ID NO: 472:  
;; SEQUENCE CHARACTERISTICS:

```

; LENGTH: 240 base pairs
;
; TYPE: nucleic acid
;
; STRANDEDNESS: single
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: cdna
;
; IMMEDIATE SOURCE:
;
; CLONE: 1849638
;
US-08-917-047-472

```

|                       |              |                    |               |             |
|-----------------------|--------------|--------------------|---------------|-------------|
| Query Match           | 84.8%        | Score 17.8;        | DB 13.        | Length 240; |
| Best Local Similarity | 90.5%        | Pred. No. 2.6e+02; |               |             |
| Matches 19;           | Conservative | 0;                 | Mismatches 2; | Indels 0;   |
|                       |              |                    |               | Gaps 0      |

|    |     |                       |    |
|----|-----|-----------------------|----|
| QY | 1   | cgaagagaccatgaacact   | 21 |
|    |     |                       |    |
| Db | 115 | CTAAGAGACCATGAGCAACTT | 95 |

```

RESULT 12
US-09-540-212A-32930/C
Sequence 32930, Application US/09540212A
GENERAL INFORMATION:
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
APPLICANT: Mullahy, Sara J.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES OF AIRWAY AND LUNG SYSTEM TISSUE
FILE REFERENCE: PD-1034 CIP
CURRENT APPLICATION NUMBER: US/09/540.212A
CURRENT FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 67551
SOFTWARE: PERL Program
SEQ ID NO 32930
LENGTH: 240
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc-feature
OTHER INFORMATION: Incyte ID No: hu00018466
US-09-540-212A-32930

```

|                       |                |                   |          |            |
|-----------------------|----------------|-------------------|----------|------------|
| Query Match           | 84.8%          | Score 17.8        | DB 21    | Length 240 |
| Best Local Similarity | 90.5%          | Pred. No. 2.6e+02 |          |            |
| Matches 19            | Conservative 0 | Mismatches 2      | Indels 0 | Gaps 0     |

```

QY      1  cgaagagaccatgaacaact 21
          | | | | | | | | | | | | |
Db      115 CTAAGAGACCATGAGCAACTT 95

```

RESULT 13  
US-60-025-203-472/C  
: Sequence 472. Application US/60025203  
: GENERAL INFORMATION:  
: APPLICANT: Gooding, Douglas H.  
: APPLICANT: Stuve, Laura L.  
: APPLICANT: Stuart, Susan G.  
: APPLICANT: Ito, Laura Y.  
: APPLICANT: Akherblom, Ingrid E.  
: APPLICANT: Delegeane, Angelo M.  
: APPLICANT: Naughton, Rebecca E.  
: APPLICANT: Klingler, Tod M.  
: TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM  
: TITLE OF INVENTION: HUMAN FETAL LUNG  
: NUMBER OF SEQUENCES: 2077  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
: STREET: 3174 PORTER DRIVE  
: CITY: PALO ALTO  
:

STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/60/025,203  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: CERRONE, MICHAEL C., Ph.D.  
REGISTRATION NUMBER: 39132  
REFERENCE/DOCKET NUMBER: PD-0230P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 855-0555  
TELEFAX: (415) 845-4166  
INFORMATION FOR SEQ ID NO: 472:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
IMMEDIATE SOURCE:  
CLONE: 1849638  
US-60-025-203-472

|                          |       |                    |           |             |
|--------------------------|-------|--------------------|-----------|-------------|
| Query Match              | 84.8% | Score 17.8;        | DB 34.    | Length 240; |
| Best Local Similarity    | 90.5% | Pred. No. 2.6e+02; |           |             |
| Matches 19; Conservative | 0;    | Mismatches 2;      | Indels 0; | Gaps 0;     |

```

QY      1 cgaagagaccatgaacaactt 21
        | | | | | | | | | | | | |
Db      115 cTAAGAGACCATGAGCAACTT 95

```

```

RESULT 14
US-60-268-380-121
; Sequence 121, Application US/60268380
; GENERAL INFORMATION:
; APPLICANT: Huel-Wei Chen
; TITLE OF INVENTION: GENES EXPRESSED IN SENSESCENCE
; FILE REFERENCE: PA-0043 P
; CURRENT APPLICATION NUMBER: US/60/268,380
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: PERL Program
; SEQ ID NO 121
; LENGTH: 2206
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: 474629.4
; NAME/KEY: unsure
; LOCATION: 486
; OTHER INFORMATION: a, t, c, g, or other
US-60-268-380-121

```

|                       |                 |                    |           |              |
|-----------------------|-----------------|--------------------|-----------|--------------|
| Query Match           | 84.8%           | Score 17.8:        | DB 58:    | Length 2206: |
| Best Local Similarity | 90.5%           | Pred. No. 3.7e+02: |           |              |
| Matches 19:           | Conservative 2: |                    | Indels 0: | Gaps 0:      |

```

QY      1  cgaagagaccatgtaacaatt 21
          ||||| | ||||| |||||
Db      345 cgaagaatcatgtaacaatt 365

```

```

RESULT 15
US-09-521-640-66611
; Sequence 66611, Application US/09521640
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Halling, Conrad H.
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15750)D
; CURRENT APPLICATION NUMBER: US/09/521,640
; CURRENT FILING DATE: 2000-03-10
; NUMBER OF SEQ. ID NOS: 304701
; SEQ. ID NO 66611
; LENGTH: 278
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: unsure at all n locations
US-09-521-640-66611
    
```

```

Query Match      82.9%; Score 17.4; DB 19; Length 278;
Best Local Similarity 94.7%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 gaagagacatgaacaact 20
   ||||||| |||||||
Db 245 gaagagacgtaacaact 263
    
```

Search completed: September 21, 2001, 02:20:15  
 Job time: 30487 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 21, 2001, 02:40:43 : Search time 1035.34 Seconds  
(without alignments)  
40,480 Million cell updates/sec

Title: US-09-138-735-12

Perfect score: 21

Sequence: 1 cgaagagaccatgaacaactt 21

Scoring table: IDENTITY\_NUC

Searched: 1741792 seqs, 997871973 residues

Total number of hits satisfying chosen parameters: 3483584

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_NA\_New : \*

- 1: /cgn1\_7/ptodata/2/pna/US06\_NEW\_COMB.seq:\*
- 2: /cgn1\_7/ptodata/2/pna/US07\_NEW\_COMB.seq:\*
- 3: /cgn1\_7/ptodata/2/pna/US08\_NEW\_COMB.seq:\*
- 4: /cgn1\_7/ptodata/2/pna/US09\_NEW\_COMB.seq:\*
- 5: /cgn1\_7/ptodata/2/pna/US09\_NEW\_COMB.seq:\*
- 6: /cgn1\_7/ptodata/2/pna/US09\_NEW\_COMB.seq:\*
- 7: /cgn1\_7/ptodata/2/pna/US09\_NEW\_COMB.seq:\*
- 8: /cgn1\_7/ptodata/2/pna/US60\_NEW\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID                | Description       |
|------------|-------|-------------|--------|----------------------|-------------------|
| 1          | 21    | 100.0       | 21     | US-09-138-735-12     | Sequence 12, Appl |
| 2          | 21    | 100.0       | 3402   | US-09-138-735-1      | Sequence 1, Appl  |
| 3          | 16.8  | 80.0        | 422    | US-09-866-555-6605   | Sequence 6005, Ap |
| 4          | 16.8  | 80.0        | 470    | US-09-904-809-7574   | Sequence 7574, Ap |
| 5          | 16.8  | 80.0        | 632    | US-09-691-918-480    | Sequence 490, App |
| 6          | 16.8  | 80.0        | 794    | US-09-861-478-6875   | Sequence 6875, Ap |
| 7          | 16.8  | 80.0        | 1107   | US-09-757-034-62     | Sequence 62, Appl |
| 8          | 16.8  | 80.0        | 1187   | US-09-898-888-12899  | Sequence 12899, A |
| 9          | 16.8  | 80.0        | 1931   | US-09-925-297-150    | Sequence 150, App |
| 10         | 16.8  | 80.0        | 2225   | US-09-764-875-151    | Sequence 151, App |
| 11         | 16.8  | 80.0        | 13630  | US-09-764-868-1369   | Sequence 1369, Ap |
| 12         | 16.8  | 80.0        | 13630  | US-09-764-875-1220   | Sequence 1220, Ap |
| 13         | 16.8  | 80.0        | 94378  | US-09-803-736-500    | Sequence 500, App |
| 14         | 16.8  | 80.0        | 105863 | US-09-803-736-1145   | Sequence 1145, Ap |
| 15         | 16.8  | 80.0        | 308503 | US-09-803-110-214    | Sequence 214, App |
| 16         | 16.4  | 78.1        | 369    | US-09-904-809-15595  | Sequence 12595, A |
| 17         | 16.4  | 78.1        | 405    | US-09-773-486-3347   | Sequence 3347, Ap |
| 18         | 16.4  | 78.1        | 852    | US-09-764-864-285    | Sequence 285, App |
| 19         | 16.4  | 78.1        | 852    | US-09-764-891-1407   | Sequence 1407, Ap |
| 20         | 16.4  | 78.1        | 2883   | PCR-US01-14827-2476  | Sequence 2476, Ap |
| 21         | 16.4  | 78.1        | 2883   | PCR-US01-08656-2635  | Sequence 2635, Ap |
| 22         | 16.4  | 78.1        | 2883   | PCR-US01-08631-17735 | Sequence 17735, A |
| 23         | 16.4  | 78.1        | 2883   | PCR-US01-08631-25966 | Sequence 25966, A |
| 24         | 16.4  | 78.1        | 3659   | US-09-764-864-1668   | Sequence 1668, Ap |
| 25         | 16.4  | 78.1        | 3659   | US-09-764-891-7820   | Sequence 7820, Ap |

|    |      |      |        |                     |                    |
|----|------|------|--------|---------------------|--------------------|
| 26 | 16.4 | 78.1 | 200576 | US-09-803-736-580   | Sequence 580, App  |
| 27 | 16.4 | 78.1 | 206606 | US-09-803-736-581   | Sequence 581, App  |
| 28 | 16.2 | 77.1 | 255    | US-60-253-457-6542  | Sequence 6542, App |
| 29 | 16.2 | 77.1 | 308    | US-60-253-833-10885 | Sequence 10885, A  |
| 30 | 16.2 | 77.1 | 316    | US-60-253-457-3359  | Sequence 3359, App |
| 31 | 16.2 | 77.1 | 354    | US-60-253-653-8211  | Sequence 8211, App |
| 32 | 16.2 | 77.1 | 430    | US-09-906-555-13496 | Sequence 13496, A  |
| 33 | 16.2 | 77.1 | 451    | US-09-864-761-5     | Sequence 5, Appl   |
| 34 | 16.2 | 77.1 | 496    | US-60-253-653-12425 | Sequence 12425, A  |
| 35 | 16.2 | 77.1 | 536    | US-60-253-653-5302  | Sequence 5302, App |
| 36 | 16.2 | 77.1 | 590    | US-60-253-653-6041  | Sequence 6041, App |
| 37 | 16.2 | 77.1 | 604    | US-60-253-653-4496  | Sequence 4496, App |
| 38 | 16.2 | 77.1 | 605    | US-60-253-653-4652  | Sequence 4652, App |
| 39 | 16.2 | 77.1 | 636    | US-60-253-833-10704 | Sequence 10704, A  |
| 40 | 16.2 | 77.1 | 668    | US-60-253-653-3848  | Sequence 3848, App |
| 41 | 16.2 | 77.1 | 999    | PCR-US01-08631-626  | Sequence 626, App  |
| 42 | 16.2 | 77.1 | 1218   | US-09-803-110-8105  | Sequence 8105, App |
| 43 | 16.2 | 77.1 | 67757  | US-09-803-736-1252  | Sequence 1252, App |
| 44 | 16.2 | 77.1 | 69506  | US-09-803-736-1258  | Sequence 1258, App |
| 45 | 16.2 | 77.1 | 110826 | US-09-803-736-547   | Sequence 547, App  |

## ALIGNMENTS

```

RESULT 1
US-09-138-735-12
Sequence 12, Application US/09138735
GENERAL INFORMATION:
APPLICANT: PARANHOS-BACCALA, Glaucia
APPLICANT: LESENECHAL, Mylene
TITLE OF INVENTION: TREPANOSOMA CRUZI ANTIGEN, GENE ENCODING THEREFOR AND METHODS
FILE REFERENCE: WPB 36400B
CURRENT FILING DATE: 1998-08-24
PRIOR APPLICATION NUMBER: US/09/138,735
PRIOR FILING DATE: 1994-08-12
PRIOR APPLICATION NUMBER: FR 94/10132
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.0
SEQ ID NO 12
LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: probe/primer
US-09-138-735-12

Query Match 100.0%; Score 21; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgaagagaccatgaacaactt 21
Db 1 cgaagagaccatgaacaactt 21

RESULT 2
US-09-138-735-1
Sequence 1, Application US/09138735
GENERAL INFORMATION:
APPLICANT: PARANHOS-BACCALA, Glaucia
APPLICANT: LESENECHAL, Mylene
TITLE OF INVENTION: TREPANOSOMA CRUZI ANTIGEN, GENE ENCODING THEREFOR AND METHODS
FILE REFERENCE: WPB 36400B
CURRENT APPLICATION NUMBER: US/09/138,735
CURRENT FILING DATE: 1998-08-24

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;; PRIOR APPLICATION NUMBER: US 08/480,917  
;; PRIOR FILING DATE: 1995-06-07  
;; PRIOR APPLICATION NUMBER: FR 94/10132  
;; PRIOR FILING DATE: 1994-08-12  
;; NUMBER OF SEQ ID NOS: 13  
;; SOFTWARE: PatentIn version 3.0  
;; SEQ ID NO 1  
;; LENGTH: 3402  
;; TYPE: DNA  
;; ORGANISM: Trypanosoma cruzi  
;; US-09-138-735-1

Query Match 100.0%; Score 21; DB 6; Length 3402;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgaagagaccatgaacaactt 21  
DB 1997 cgaagagaccatgaacaactt 2017

RESULT 3  
US-09-866-555-6005/C  
;; Sequence 6005, Application US/09866555  
;; GENERAL INFORMATION:  
;; APPLICANT: Harlocker, Susan L.  
;; APPLICANT: Wang, Tongtong  
;; APPLICANT: Bangur, Chaltanya S.  
;; APPLICANT: Algate, Paul A.  
;; APPLICANT: Jones, Robert  
;; APPLICANT: Klee, Jennifer  
;; TITLE OF INVENTION: LUNG TUMOR-ASSOCIATED SEQUENCES AND METHODS OF USE  
;; FILE REFERENCE: 210121.580  
;; CURRENT APPLICATION NUMBER: US/09/866,555  
;; CURRENT FILING DATE: 2001-05-25  
;; NUMBER OF SEQ ID NOS: 20487  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 6005  
;; LENGTH: 422  
;; TYPE: DNA  
;; ORGANISM: Homo sapien  
;; US-09-866-555-6005

Query Match 80.0%; Score 16.8; DB 6; Length 422;  
Best Local Similarity 90.0%; Pred. No. 98;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gaagagaccatgaacaactt 21  
DB 316 GAAGGACCATGAACAACGT 297

RESULT 4  
US-09-904-809-7574/C  
;; Sequence 7574, Application US/09904809  
;; GENERAL INFORMATION:  
;; APPLICANT: Hyseq, Inc.  
;; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
;; FILE REFERENCE: 20411-757  
;; CURRENT APPLICATION NUMBER: US/09/904,809  
;; CURRENT FILING DATE: 2001-07-12  
;; PRIOR APPLICATION NUMBER: 09/234,611  
;; PRIOR FILING DATE: 1999-01-22  
;; NUMBER OF SEQ ID NOS: 21025  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 7574  
;; LENGTH: 470  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:

;; NAME/KEY: misc\_feature  
;; LOCATION: (1)...(470)  
;; OTHER INFORMATION: n = A,T,C or G  
;; US-09-904-809-7574

Query Match 80.0%; Score 16.8; DB 6; Length 470;  
Best Local Similarity 90.0%; Pred. No. 1e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gaagagaccatgaacaactt 21  
DB 329 GAAGAGACCTTGAAACAACGT 310

RESULT 5  
US-09-691-918-490/C  
;; Sequence 490, Application US/09691918  
;; GENERAL INFORMATION:  
;; APPLICANT: Guegler, Karl J.  
;; APPLICANT: Doyle, Martin  
;; APPLICANT: Leader, David  
;; APPLICANT: Momiyama, Monika G.  
;; APPLICANT: Mooney, Mark  
;; APPLICANT: Schuch, Wolfgang  
;; APPLICANT: Didier, Thomas  
;; TITLE OF INVENTION: WHEAT METABOLIC PROTEINS  
;; FILE REFERENCE: PL-0034 P  
;; CURRENT APPLICATION NUMBER: US/09/691,918  
;; CURRENT FILING DATE: 1999-09-16  
;; NUMBER OF SEQ ID NOS: 910  
;; SOFTWARE: PERL Program  
;; SEQ ID NO 490  
;; LENGTH: 632  
;; TYPE: DNA  
;; ORGANISM: Triticum aestivum  
;; FEATURE:  
;; NAME/KEY: unsure  
;; LOCATION: 23, 53, 72  
;; OTHER INFORMATION: a or g or c or t, unknown, or other  
;; NAME/KEY: misc\_feature  
;; OTHER INFORMATION: incyte template ID No: 014558.1c  
;; US-09-691-918-490

Query Match 80.0%; Score 16.8; DB 6; Length 632;  
Best Local Similarity 90.0%; Pred. No. 1e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gaagagaccatgaacaactt 21  
DB 539 GAAGAAACGATGAACAACCTT 520

RESULT 6  
US-09-861-478-6875/C  
;; Sequence 6875, Application US/09861478  
;; GENERAL INFORMATION:  
;; APPLICANT: Bush, David F.  
;; APPLICANT: Chasalow, Scott D.  
;; APPLICANT: Epp, J. Andrew  
;; APPLICANT: Hauge, Brian M.  
;; APPLICANT: Lai, Chao-Qiang  
;; APPLICANT: Laurie, Cathy C.  
;; APPLICANT: McCarroll, Robert M.  
;; TITLE OF INVENTION: Maize Polymorphisms and Methods of Genotyping  
;; FILE REFERENCE: 38-10(52018)A  
;; CURRENT APPLICATION NUMBER: US/09/861,478  
;; CURRENT FILING DATE: 2001-05-18  
;; NUMBER OF SEQ ID NOS: 10380  
;; SEQ ID NO 6875  
;; LENGTH: 794

TYPE: DNA  
ORGANISM: Zea mays  
US-09-861-478-6875

Query Match 80.0%; Score 16.8; DB 7; Length 794;  
Best Local Similarity 90.0%; Pred. No. 1.1e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 cgaagagaccatgaacaact 20  
||||| ||| ||||| |||  
DB 358 CGAAGATACCTTGACAACT 339

RESULT 7  
US-09-757-034-62  
Sequence 62, Application US/09757034  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: PM002  
CURRENT APPLICATION NUMBER: US/09/757,034  
CURRENT FILING DATE: 2001-01-09  
PRIOR APPLICATION NUMBER: 60/179,065  
PRIOR FILING DATE: 2000-01-31  
PRIOR APPLICATION NUMBER: 60/180,628  
PRIOR FILING DATE: 2000-02-04  
NUMBER OF SEQ ID NOS: 1440  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 62  
LENGTH: 1107  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-757-034-62

Query Match 80.0%; Score 16.8; DB 6; Length 1107;  
Best Local Similarity 90.0%; Pred. No. 1.2e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gaagagaccatgaacaact 21  
||||| ||| ||||| |||  
DB 556 gaagagaccctgaacaact 575

RESULT 8  
US-09-898-888-12899/c  
Sequence 12899, Application US/09898888  
GENERAL INFORMATION:  
APPLICANT: HySeq, Inc.  
TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA  
FILE REFERENCE: 20411-748CON1  
CURRENT APPLICATION NUMBER: US/09/898,888  
CURRENT FILING DATE: 2001-07-03  
PRIOR APPLICATION NUMBER: 09/340,623  
PRIOR FILING DATE: 1999-06-28  
NUMBER OF SEQ ID NOS: 45207  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 12899  
LENGTH: 1187  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-898-888-12899

Query Match 80.0%; Score 16.8; DB 6; Length 1187;  
Best Local Similarity 90.0%; Pred. No. 1.2e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gaagagaccatgaacaact 21  
||||| ||| ||||| |||  
DB 529 GAAGAGACCTTGACAACT 510

RESULT 9  
US-09-925-297-150  
Sequence 150, Application US/09925297  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
FILE REFERENCE: PA105  
CURRENT APPLICATION NUMBER: US/09/925,297  
CURRENT FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: PCT/US00/05989  
PRIOR FILING DATE: 2000-03-08  
PRIOR APPLICATION NUMBER: 60/124,270  
PRIOR FILING DATE: 1998-03-12  
NUMBER OF SEQ ID NOS: 928  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 150  
LENGTH: 1931  
TYPE: DNA  
ORGANISM: Homo sapiens

FEATURE:  
NAME/KEY: misc feature  
LOCATION: (311)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (314)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (1897)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (1923)  
OTHER INFORMATION: n equals a,t,g, or c  
US-09-925-297-150

Query Match 80.0%; Score 16.8; DB 5; Length 1931;  
Best Local Similarity 90.0%; Pred. No. 1.3e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gaagagaccatgaacaact 21  
||||| ||| ||||| |||  
DB 1658 gaagagaccctgaacaact 1677

RESULT 10  
US-09-764-875-151  
Sequence 151, Application US/09764875  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: PJ202  
CURRENT APPLICATION NUMBER: US/09/764,875  
CURRENT FILING DATE: 2001-01-17  
Prior application data removed - consult PALM or file wrapper  
NUMBER OF SEQ ID NOS: 1249  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 151  
LENGTH: 2225  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-764-875-151

Query Match 80.0%; Score 16.8; DB 6; Length 2225;  
Best Local Similarity 90.0%; Pred. No. 1.3e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gaagagaccatgaacaact 21

Db 1674 gaagagacctgaacaagct 1693

RESULT 11

US-09-764-868-1369  
; Sequence 1369, Application US/09764868  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: P7232  
; CURRENT APPLICATION NUMBER: US/09/764,868  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - refer to PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 1510  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 1369  
; LENGTH: 13630  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (2408)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (2615)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (2616)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (2635)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (2636)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (2639)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (2642)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (2643)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (2649)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (2650)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (2652)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (2653)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (9943)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-764-868-1369

Query Match 80.0%; Score 16.8; DB 6; Length 13630;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gaagagacctgaacaact 21

Db 13109 gaagagacctgaacaagct 13128

RESULT 12

US-09-764-875-1220  
; Sequence 1220, Application US/09764875  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: P7202  
; CURRENT APPLICATION NUMBER: US/09/764,875  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 1249  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 1220  
; LENGTH: 13630  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (2408)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (2615)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (2616)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (2635)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (2636)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (2639)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (2642)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (2643)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (2649)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (2650)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (2652)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (2653)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (9943)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-764-875-1220

Query Match 80.0%; Score 16.8; DB 6; Length 13630;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gaagagacctgaacaact 21

Db 13109 gaagagacctgaacaagct 13128

RESULT 13

US-09-803-736-500/c  
; Sequence 500, Application US/09803736  
; GENERAL INFORMATION:  
; APPLICANT: Bush, David F.  
; APPLICANT: Levin, Irena M.



APPLICANT: Norris, Susan R.  
APPLICANT: Rounsley, Steven D.  
APPLICANT: Wiegand, Roger C.  
TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof  
FILE REFERENCE: 38-10(115493)D  
CURRENT FILING DATE: 2001-03-12  
PRIOR APPLICATION NUMBER: US 09/803,736  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: Identified by Attorney Docket number 04983.0206CPUS01 38-10  
PRIOR FILING DATE: 2000-10-20  
NUMBER OF SEQ ID NOS: 1582  
SEQ ID NO 500  
LENGTH: 94378  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
US-09-803-736-500

Query Match 80.0%; Score 16.8; DB 6; Length 94378;  
Best Local Similarity 90.0%; Pred. No. 2.4e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gaagagaccatgaacaact 21  
||||| ||||||| ||  
DB 8941 GAAGAGACCATGACCAATT 8922

RESULT 14  
US-09-803-736-1145/c  
Sequence 1145, Application US/09803736  
GENERAL INFORMATION:  
APPLICANT: Bush, David F.  
APPLICANT: Levin, Irena M.  
APPLICANT: Norris, Susan R.  
APPLICANT: Rounsley, Steven D.  
TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof  
FILE REFERENCE: 38-10(115493)D  
CURRENT FILING DATE: 2001-03-12  
PRIOR APPLICATION NUMBER: US 09/803,736  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: Identified by Attorney Docket number 04983.0206CPUS01 38-10  
PRIOR FILING DATE: 2000-10-20  
NUMBER OF SEQ ID NOS: 1582  
SEQ ID NO 1145  
LENGTH: 105863  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
US-09-803-736-1145

Query Match 80.0%; Score 16.8; DB 6; Length 105863;  
Best Local Similarity 90.0%; Pred. No. 2.5e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 cgaagagccatgaacaact 20  
||||| ||||||| ||  
DB 73043 CCAAGAGCATGAACAACCT 73024

RESULT 15  
US-09-803-110-214/c  
Sequence 214, Application US/09803110  
GENERAL INFORMATION:  
APPLICANT: Hinkle, Gregory J.  
APPLICANT: Slater, Steven C.  
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof  
FILE REFERENCE: 38-10(115490)D  
CURRENT FILING DATE: 2001-03-12  
PRIOR APPLICATION NUMBER: US 09/803,110  
PRIOR APPLICATION NUMBER: US 09/739,449

PRIOR FILING DATE: 2000-12-19  
PRIOR APPLICATION NUMBER: US 09/514,000  
PRIOR FILING DATE: 2000-02-23  
PRIOR APPLICATION NUMBER: US 60/168,139  
PRIOR FILING DATE: 1999-12-01  
NUMBER OF SEQ ID NOS: 13351  
SEQ ID NO 214  
LENGTH: 308503  
TYPE: DNA  
ORGANISM: Agrobacterium tumefaciens  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (1)..(308503)  
OTHER INFORMATION: unsure at all n locations  
US-09-803-110-214

Query Match 80.0%; Score 16.8; DB 6; Length 308503;  
Best Local Similarity 90.0%; Pred. No. 2.9e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gaagagaccatgaacaact 21  
||||| ||||||| ||  
DB 262148 GAAGAGACCATGACCAATT 262129

Search completed: September 21, 2001, 02:40:59  
Job time: 15145 sec



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OM nucleic - nucleic search, using sw model

Run on: September 21, 2001, 00:35:41 : Search time 3479.37 Seconds  
(without alignments)  
93.357 Million cell updates/sec

Title: US-09-138-735-10  
Perfect score: 21  
Sequence: 1 acataatggcctcgttcacac 21

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues  
Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl:\*

- 1: gb\_ba1:\*
- 2: gb\_ba2:\*
- 3: gb\_ba3:\*
- 4: gb\_in1:\*
- 5: gb\_in2:\*
- 6: gb\_in3:\*
- 7: gb\_on:\*
- 8: gb\_ov:\*
- 9: gb\_pat1:\*
- 10: gb\_pat2:\*
- 11: gb\_ph:\*
- 12: gb\_p11:\*
- 13: gb\_p12:\*
- 14: gb\_p13:\*
- 15: gb\_p14:\*
- 16: gb\_ba1:\*
- 17: gb\_ba2:\*
- 18: gb\_fun:\*
- 19: gb\_hum:\*
- 20: gb\_hum:\*
- 21: gb\_hum:\*
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- 36: gb\_hum:\*
- 37: gb\_hum:\*
- 38: gb\_hum:\*
- 39: gb\_hum:\*
- 40: gb\_hum:\*
- 41: gb\_hum:\*
- 42: gb\_hum:\*
- 43: gb\_hum:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description          |
|------------|-------|-------------|--------|-------|----------------------|
| 1          | 21    | 100.0       | 21     | 9     | A48919 Sequence 10   |
| 2          | 21    | 100.0       | 21     | 9     | AR047928 Sequence 10 |
| 3          | 21    | 100.0       | 3402   | 9     | A48910 Sequence 1    |
| 4          | 21    | 100.0       | 3402   | 9     | AR047920 Sequence 1  |
| 5          | 21    | 100.0       | 3402   | 96    | TCU24190 Sequence 1  |
| 6          | 17.8  | 84.8        | 48369  | 63    | AC014450 Homo sapi   |
| 7          | 17.8  | 84.8        | 153929 | 62    | AC011883 Homo sapi   |
| 8          | 17.8  | 84.8        | 213892 | 60    | AC008507 Homo sapi   |

44: em\_ov:\*

45: em\_pat:\*

46: em\_ph:\*

47: em\_pl:\*

48: em\_ro:\*

49: em\_sts:\*

50: em\_sy:\*

51: em\_un:\*

52: em\_v1:\*

53: gb\_sts1:\*

54: gb\_sts2:\*

55: gb\_sts3:\*

56: gb\_sy:\*

57: gb\_un:\*

58: gb\_v11:\*

59: gb\_v12:\*

60: gb\_v13:\*

61: gb\_v14:\*

62: gb\_v15:\*

63: gb\_v16:\*

64: gb\_v17:\*

65: gb\_v18:\*

66: gb\_v19:\*

67: gb\_v20:\*

68: gb\_v21:\*

69: gb\_v22:\*

70: gb\_v23:\*

71: gb\_v24:\*

72: gb\_v25:\*

73: gb\_v26:\*

74: gb\_v27:\*

75: gb\_v28:\*

76: gb\_v29:\*

77: gb\_v30:\*

78: gb\_v31:\*

79: gb\_v32:\*

80: gb\_v33:\*

81: gb\_v34:\*

82: gb\_v35:\*

83: gb\_v36:\*

84: gb\_v37:\*

85: gb\_v38:\*

86: gb\_v39:\*

87: gb\_v40:\*

88: gb\_v41:\*

89: gb\_v42:\*

90: gb\_v43:\*

91: gb\_v44:\*

92: gb\_v45:\*

93: gb\_v46:\*

94: gb\_v47:\*

95: gb\_v48:\*

96: gb\_v49:\*

97: gb\_v50:\*

98: gb\_v51:\*

|    |      |      |        |    |             |                                |
|----|------|------|--------|----|-------------|--------------------------------|
| 9  | 17.8 | 84.8 | 257523 | 5  | AE003812    | AE003812 Drosophila            |
| 10 | 17.4 | 82.9 | 163861 | 80 | AL356099    | AL356099 Homo sapi             |
| 11 | 17.4 | 82.9 | 180530 | 65 | AC018613    | AC018613 Homo sapi             |
| 12 | 16.8 | 80.0 | 90824  | 14 | ATT26M18    | ATT26M18 Arabidops             |
| 13 | 16.8 | 80.0 | 110000 | 84 | LMFLCHR26_3 | LMFLCHR26_3 Continuation (4 of |
| 14 | 16.8 | 80.0 | 135161 | 80 | AL357494    | AL357494 Homo sapi             |
| 15 | 16.8 | 80.0 | 143092 | 72 | AC051641    | AC051641 Homo sapi             |
| 16 | 16.8 | 80.0 | 147123 | 70 | AC027030    | AC027030 Homo sapi             |
| 17 | 16.8 | 80.0 | 147945 | 77 | AC084735    | AC084735 Homo sapi             |
| 18 | 16.8 | 80.0 | 149570 | 84 | CNS01RHU    | CNS01RHU Homo sapi             |
| 19 | 16.8 | 80.0 | 164452 | 83 | CNS01RGP    | CNS01RGP Homo sapi             |
| 20 | 16.8 | 80.0 | 190000 | 60 | AC006391    | AC006391 Homo sapi             |
| 21 | 16.8 | 80.0 | 192025 | 88 | AC027129    | AC027129 Homo sapi             |
| 22 | 16.8 | 80.0 | 194140 | 2  | AF242881    | AF242881 Agrobacte             |
| 23 | 16.8 | 80.0 | 197206 | 68 | AC023757    | AC023757 Homo sapi             |
| 24 | 16.8 | 80.0 | 198788 | 13 | ATCRIV32    | ATCRIV32 Arabidops             |
| 25 | 16.8 | 80.0 | 321708 | 77 | AC087142    | AC087142 Mus muscu             |
| 26 | 16.8 | 80.0 | 338116 | 77 | AC087159    | AC087159 Mus muscu             |
| 27 | 16.4 | 78.1 | 69558  | 78 | AC090544    | AC090544 Homo sapi             |
| 28 | 16.4 | 78.1 | 70250  | 77 | AC090277    | AC090277 Homo sapi             |
| 29 | 16.4 | 78.1 | 70250  | 77 | AC090277    | AC090277 Homo sapi             |
| 30 | 16.4 | 78.1 | 127759 | 75 | AC079021    | AC079021 Oryza sat             |
| 31 | 16.4 | 78.1 | 129629 | 93 | HSJ422B11   | HSJ422B11 Human DNA            |
| 32 | 16.4 | 78.1 | 144163 | 61 | AC009885    | AC009885 Homo sapi             |
| 33 | 16.4 | 78.1 | 147700 | 83 | AP002362    | AP002362 Homo sapi             |
| 34 | 16.4 | 78.1 | 164991 | 87 | AC011088    | AC011088 Homo sapi             |
| 35 | 16.4 | 78.1 | 169168 | 83 | AP002497    | AP002497 Homo sapi             |
| 36 | 16.4 | 78.1 | 175818 | 86 | AC006257    | AC006257 Homo sapi             |
| 37 | 16.4 | 78.1 | 180234 | 82 | AP001642    | AP001642 Homo sapi             |
| 38 | 16.4 | 78.1 | 191557 | 86 | AC008506    | AC008506 Homo sapi             |
| 39 | 16.2 | 77.1 | 896    | 91 | D85291      | D85291 Pates monke             |
| 40 | 16.2 | 77.1 | 896    | 97 | MIRP45      | MIRP45 Chimpanzee              |
| 41 | 16.2 | 77.1 | 2278   | 6  | DROORA      | DROORA Drosophila              |
| 42 | 16.2 | 77.1 | 5675   | 5  | AF292113    | AF292113 Aedes aeg             |
| 43 | 16.2 | 77.1 | 10628  | 10 | AX089750    | AX089750 Sequence              |
| 44 | 16.2 | 77.1 | 10628  | 96 | PFA133811   | PFA133811 Plasmodiu            |
| 45 | 16.2 | 77.1 | 55754  | 63 | AC012694    | AC012694 Drosophila            |

## ALIGNMENTS

|                       |                                                                                                                   |       |     |     |             |  |
|-----------------------|-------------------------------------------------------------------------------------------------------------------|-------|-----|-----|-------------|--|
| RESULT                | 1                                                                                                                 |       |     |     |             |  |
| LOCUS                 | A48919                                                                                                            | 21 bp | DNA | PAT | 07-MAR-1997 |  |
| DEFINITION            | Sequence 10 from Patent WO9605312.                                                                                |       |     |     |             |  |
| ACCESSION             | A48919                                                                                                            |       |     |     |             |  |
| VERSION               | A48919.1 GI:2302578                                                                                               |       |     |     |             |  |
| KEYWORDS              | unclassified.                                                                                                     |       |     |     |             |  |
| SOURCE                | unclassified.                                                                                                     |       |     |     |             |  |
| ORGANISM              | unclassified.                                                                                                     |       |     |     |             |  |
| REFERENCE             | 1 (bases 1 to 21)                                                                                                 |       |     |     |             |  |
| AUTHORS               | Paranhos-Baccala, G., Lesenechal, M. and Jolivet, M.                                                              |       |     |     |             |  |
| TITLE                 | NOVEL TRYPA NOSOMA CRUZI ANTIGEN, AND GENE CODING THEREFOR; THEIR APPLICATION TO THE DETECTION OF CHAGAS' DISEASE |       |     |     |             |  |
| JOURNAL               | PATENT: WO 9605312-A 10 22-FEB-1996;                                                                              |       |     |     |             |  |
| COMMENT               | BIO MERIEUX (FR)                                                                                                  |       |     |     |             |  |
| OTHER PUBLICATION     | CA 2173957 960222                                                                                                 |       |     |     |             |  |
| OTHER PUBLICATION     | AU 3169195 960307                                                                                                 |       |     |     |             |  |
| OTHER PUBLICATION     | FR 2723589 960216.                                                                                                |       |     |     |             |  |
| FEATURES              | location/Qualifiers                                                                                               |       |     |     |             |  |
| source                | 1..21                                                                                                             |       |     |     |             |  |
|                       | /organism="unclassified"                                                                                          |       |     |     |             |  |
|                       | /db_xref="taxon:32644"                                                                                            |       |     |     |             |  |
| BASE COUNT            | 6 a 7 c 3 g 5 t                                                                                                   |       |     |     |             |  |
| ORIGIN                |                                                                                                                   |       |     |     |             |  |
| Query Match           | 100.0%; Score 21; DB 9; Length 21;                                                                                |       |     |     |             |  |
| Best Local Similarity | 100.0%; Pred. No. 8.4;                                                                                            |       |     |     |             |  |
| Matches               | 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                                                               |       |     |     |             |  |

|                       |                                                                                                                   |                       |      |     |             |  |
|-----------------------|-------------------------------------------------------------------------------------------------------------------|-----------------------|------|-----|-------------|--|
| QY                    | 1                                                                                                                 | acataatgacctgttacac   | 21   |     |             |  |
| Db                    | 1                                                                                                                 | ACATAATGCGCTGCTTCACAC | 21   |     |             |  |
| RESULT                | 2                                                                                                                 |                       |      |     |             |  |
| LOCUS                 | AR047928                                                                                                          | 21 bp                 | DNA  | PAT | 29-SEP-1999 |  |
| DEFINITION            | Sequence 10 from patent US 5820864.                                                                               |                       |      |     |             |  |
| ACCESSION             | AR047928                                                                                                          |                       |      |     |             |  |
| VERSION               | AR047928.1 GI:5970271                                                                                             |                       |      |     |             |  |
| KEYWORDS              | Unknown.                                                                                                          |                       |      |     |             |  |
| SOURCE                | Unknown.                                                                                                          |                       |      |     |             |  |
| ORGANISM              | Unknown.                                                                                                          |                       |      |     |             |  |
| REFERENCE             | 1 (bases 1 to 21)                                                                                                 |                       |      |     |             |  |
| AUTHORS               | Paranhos-Baccala, G., Lesenechal, M. and Jolivet, M.                                                              |                       |      |     |             |  |
| TITLE                 | TRYPA NOSOMA CRUZI ANTIGEN, GENE ENCODING THEREFOR AND METHODS OF DETECTING AND TREATING CHAGAS DISEASE           |                       |      |     |             |  |
| JOURNAL               | PATENT: US 5820864-A 10 13-OCT-1998;                                                                              |                       |      |     |             |  |
| FEATURES              | location/Qualifiers                                                                                               |                       |      |     |             |  |
| source                | 1..21                                                                                                             |                       |      |     |             |  |
|                       | /organism="unknown"                                                                                               |                       |      |     |             |  |
| BASE COUNT            | 6 a 7 c 3 g 5 t                                                                                                   |                       |      |     |             |  |
| ORIGIN                |                                                                                                                   |                       |      |     |             |  |
| Query Match           | 100.0%; Score 21; DB 9; Length 21;                                                                                |                       |      |     |             |  |
| Best Local Similarity | 100.0%; Pred. No. 8.4;                                                                                            |                       |      |     |             |  |
| Matches               | 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                                                               |                       |      |     |             |  |
| QY                    | 1                                                                                                                 | acataatgacctgttacac   | 21   |     |             |  |
| Db                    | 1                                                                                                                 | ACATAATGCGCTGCTTCACAC | 21   |     |             |  |
| RESULT                | 3                                                                                                                 |                       |      |     |             |  |
| LOCUS                 | A48910/c                                                                                                          | 3402 bp               | DNA  | PAT | 07-MAR-1997 |  |
| DEFINITION            | Sequence 1 from Patent WO9605312.                                                                                 |                       |      |     |             |  |
| ACCESSION             | A48910                                                                                                            |                       |      |     |             |  |
| VERSION               | A48910.1 GI:2302570                                                                                               |                       |      |     |             |  |
| KEYWORDS              | Trypanosoma cruzi.                                                                                                |                       |      |     |             |  |
| SOURCE                | Trypanosoma cruzi.                                                                                                |                       |      |     |             |  |
| ORGANISM              | Trypanosoma cruzi.                                                                                                |                       |      |     |             |  |
| REFERENCE             | 1 (bases 1 to 3402)                                                                                               |                       |      |     |             |  |
| AUTHORS               | Paranhos-Baccala, G., Lesenechal, M. and Jolivet, M.                                                              |                       |      |     |             |  |
| TITLE                 | NOVEL TRYPA NOSOMA CRUZI ANTIGEN, AND GENE CODING THEREFOR; THEIR APPLICATION TO THE DETECTION OF CHAGAS' DISEASE |                       |      |     |             |  |
| JOURNAL               | PATENT: WO 9605312-A 1 22-FEB-1996;                                                                               |                       |      |     |             |  |
| COMMENT               | BIO MERIEUX (FR)                                                                                                  |                       |      |     |             |  |
| OTHER PUBLICATION     | CA 2173957 960222                                                                                                 |                       |      |     |             |  |
| OTHER PUBLICATION     | AU 3169195 960307                                                                                                 |                       |      |     |             |  |
| OTHER PUBLICATION     | FR 2723589 960216.                                                                                                |                       |      |     |             |  |
| FEATURES              | location/Qualifiers                                                                                               |                       |      |     |             |  |
| source                | 1..3402                                                                                                           |                       |      |     |             |  |
|                       | /organism="Trypanosoma cruzi"                                                                                     |                       |      |     |             |  |
|                       | /strain="G"                                                                                                       |                       |      |     |             |  |
|                       | /db_xref="taxon:5693"                                                                                             |                       |      |     |             |  |
|                       | /dev_stage="EPIMASTIGOTE"                                                                                         |                       |      |     |             |  |
| BASE COUNT            | 889 a 818 c 958 g 737 t                                                                                           |                       |      |     |             |  |
| ORIGIN                |                                                                                                                   |                       |      |     |             |  |
| Query Match           | 100.0%; Score 21; DB 9; Length 3402;                                                                              |                       |      |     |             |  |
| Best Local Similarity | 100.0%; Pred. No. 4;                                                                                              |                       |      |     |             |  |
| Matches               | 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                                                               |                       |      |     |             |  |
| QY                    | 1                                                                                                                 | acataatgacctgttacac   | 21   |     |             |  |
| Db                    | 2207                                                                                                              | ACATAATGCGCTGCTTCACAC | 2187 |     |             |  |

RESULT 4  
LOCUS AR047920/c 3402 bp DNA PAT 29-SEP-1999  
DEFINITION Sequence 1 from patent US 5820864.  
ACCESSION AR047920  
VERSION AR047920.1 GI:5970263  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 3402)  
Paranhos-Baccala, G., Lesenechal, M., and Jolivet, M.  
Trypanosoma cruzi antigen, gene encoding therefor and methods of  
detecting and treating chagas disease  
Patent: US 5820864-A 1 13-Oct-1998;  
JOURNAL Location/Qualifiers  
FEATURES  
source 1..3402  
BASE COUNT 888 a 821 c 956 g 737 t  
ORIGIN  
Query Match 100.0%; Score 21; DB 9; Length 3402;  
Best Local Similarity 100.0%; Pred. No. 4;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 acataatggcctcggtcacac 21  
|||||  
Db 2207 ACATATGCGCTCGTTACAC 2187  
RESULT 5  
LOCUS TC024190/c 3402 bp mRNA INV 04-AUG-1997  
DEFINITION Trypanosoma cruzi Tc40 antigen (Tc40) mRNA, complete cds.  
ACCESSION U24190  
VERSION U24190.1 GI:790645  
KEYWORDS  
SOURCE Trypanosoma cruzi.  
ORGANISM Trypanosoma cruzi  
Eukaryota; Euzoenozoa; Kinetoplastida; Trypanosomatidae;  
Trypanosoma; Schizotrypanum.  
REFERENCE 1 (bases 1 to 3402)  
Lesenechal, M., Duret, L., Cano, M.I., Mortara, R.A., Jolivet, M.,  
Canarigo, M.E., da Silveira, J.F., and Paranhos-Baccala, G.  
Cloning and characterization of a gene encoding a novel  
immunodominant antigen of Trypanosoma cruzi  
Mol. Biochem. Parasitol. 87 (2), 193-204 (1997)  
J9791123  
JOURNAL 2 (bases 1 to 3402)  
MEDLINE  
AUTHORS Lesenechal, M., Franco Da Silveira, J., Mortara, R.A., Duret, L.,  
Canarigo, M.E., Jolivet, M., and Paranhos-Baccala, G.  
TITLE Direct Submission  
JOURNAL Submitted (06-APR-1995) Mylene Lesenechal, Biomeries, 22 rue Saint  
Jean de Dieu, Lyon 69007, France  
FEATURES  
source location/Qualifiers  
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/protein\_id="AAC47657.1"

/db\_xref="GI:790646"  
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DETENSKRPDLARLVKVFVKLDPPVTFPESEFFINAESORPDLVLETOAAILD  
SSSLIERDVESELEATLQKNCITLTLQIPVSESLCSVGSGMTPTPEPTMAACT  
LNRSTPSMACCEGEPRVALHLIDATVEENSVIAASTKGYOMLTGVEPNILRK  
FVIDGSIYAMESSERETFAVFDPRKROLAVNNHSPINPFTCHYMMCOYORNGFCNRT  
ADGSCVLADMSNRLIFILRSRREPOGOKTSYVATKPCVSSGTDASSSHRNT  
TSAAPASPRPVSAAPAKAAPAPPAARSAEPHYGSKITIANLYNIGIVTORYSVSTG  
APATTSTAVSTTTAPQRTSPYGNRPVITAGLVAAVNSGASASSPTAAKPTGEK  
ASAACETSSVAIINATRPALHNASLEPQAPDGLAAVVGSGEVSLEKESVETNT  
SRVLKLPDPTIRDOHQNLNLGAEOMTELQOSRPTPOTOPRPTSSASVEFTVY  
LIADLSRNITKRGVGVNEAIMLHDEVRRAIKNRLOTOKNIKSRIDALEKST  
TOFTLOTOYENLVKRELATVIGSINGSLISYKENSLOKELNMSISGVSLEMR  
YMLEELCTRESYAKKATMPDSSLATSFSFOGRSAPETILTATLSMVBEOYRGLG  
YMLMOPSLILRFSLITRENNVSELINVENPNCVSVLLQILEAATATEKE  
VYGVADIDILSERDQIDQNGALGSKLTTRAMRAFEROARSETTSRSLQNLNLEKLO  
S"

BASE COUNT 889 a 818 c 958 g 737 t  
ORIGIN  
Query Match 100.0%; Score 21; DB 96; Length 3402;  
Best Local Similarity 100.0%; Pred. No. 4;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 acataatggcctcggtcacac 21  
|||||  
Db 2207 ACATATGCGCTCGTTACAC 2187  
RESULT 6  
LOCUS AC014450 48369 bp DNA HTG 16-NOV-1999  
DEFINITION Drosophila melanogaster, \*\*\* SEQUENCING IN PROGRESS \*\*\*, in ordered  
pieces.  
ACCESSION AC014450  
VERSION AC014450.1 GI:6436885  
KEYWORDS HTG: HTGS\_PHASE2.  
SOURCE fruit fly.  
ORGANISM Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
REFERENCE 1 (bases 1 to 48369)  
Adams, M. and Venter, J.C.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive,  
Rockville, MD, USA  
COMMENT For further information on this sequence e-mail to fly@celera.com.  
\* NOTE: This is a 'working draft' sequence.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.  
FEATURES  
source location/Qualifiers  
1..48369  
/organism="Drosophila melanogaster"  
/db\_xref="taxon:7227"  
BASE COUNT 14352 a 10109 c 9889 g 14019 t  
ORIGIN  
Query Match 84.8%; Score 17.8; DB 63; Length 48369;  
Best Local Similarity 90.5%; Pred. No. 1; 1e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 1 acataatggcctcggtcacac 21  
|||||  
Db 32318 ACATATGCGCTCGTTACAC 32338  
RESULT 7

| LOCUS      | ACOL1883/C                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | DNA        | HTG                | 01-APR-2000        |
|------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------|--------------------|--------------------|
| DEFINITION | Homo sapiens clone Rpl1-17N20. WORKING DRAFT SEQUENCE, 13 unordered pieces                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |            |                    |                    |
| ACCESSION  | ACOL1883                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 153929 bp  |                    |                    |
| VERSION    | ACOL1883.4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | GI:7381815 |                    |                    |
| AUTHORS    | HTG; HTGS_PHASE1; HTGS_DRAFT.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |            |                    |                    |
| ORGANISM   | human.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |            |                    |                    |
| REFERENCE  | Homo sapiens                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |            |                    |                    |
| TITLE      | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eubateria; Primates; Catarrhini; Homnidae; Homo.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |            |                    |                    |
| JOURNAL    | 1 (bases 1 to 153929)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |            |                    |                    |
| REFERENCE  | Birten, B., Linton, L., Nusbaum, C. and Lander, E.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |            |                    |                    |
| AUTHORS    | Homo sapiens, clone Rpl1-17N20                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |            |                    |                    |
|            | Unpublished                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |            |                    |                    |
|            | 2 (bases 1 to 153929)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |            |                    |                    |
|            | Birten, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckert, R., Boguslavsky, L., Boukhalter, B., Brown, A., Casle, A., Colangelo, M., Collins, S., Collamore, A., Cooke, P., DeArrellano, K., Dewar, K., Domingo, M., Donegan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lebecky, J., Lieu, C., Locke, K., MacDonald, P., Marquis, N., McMan, P., McGuck, A., McKernan, K., McLaughlin, J., Meldrum, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thoman, N., Stojanovic, N., Subramanian, A., Talamas, J., Teafaye, S., Tirelli, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M. |            |                    |                    |
| TITLE      | Direct Submission                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |            |                    |                    |
| JOURNAL    | Submitted (15-OCT-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |            |                    |                    |
| COMMENT    | On Apr 1, 2000 this sequence version replaced g1:653591.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |            |                    |                    |
|            | All repeats were identified using RepeatMasker:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |            |                    |                    |
|            | Smit, A.F.A. & Green, P. (1996-1997)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |            |                    |                    |
|            | http://ftp.genome.washington.edu/RM/RepeatMasker.html                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |            |                    |                    |
|            | ----- Genome Center                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |            |                    |                    |
|            | Center: Whitehead Institute/ MIT Center for Genome Research                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |            |                    |                    |
|            | Center code: WIBR                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |            |                    |                    |
|            | Web site: http://www.seq.wi.mit.edu                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |            |                    |                    |
|            | Contact: sequence_submissions@genome.wi.mit.edu                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |            |                    |                    |
|            | ----- Project Information                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |            |                    |                    |
|            | Center project name: L3671                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |            |                    |                    |
|            | Center clone name: 17_N_20                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |            |                    |                    |
|            | ----- Summary Statistics                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |            |                    |                    |
|            | Sequencing Vector: M13; M77815; 100% of reads                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |            |                    |                    |
|            | Chemistry: Dye-terminator Big Dye; 100% of reads                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |            |                    |                    |
|            | Assembly program: Phrap; version 0.960731                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |            |                    |                    |
|            | Consensus quality: 146450 bases at least Q40                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |            |                    |                    |
|            | Consensus quality: 149447 bases at least Q30                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |            |                    |                    |
|            | Consensus quality: 150837 bases at least Q20                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |            |                    |                    |
|            | Insert size: 151000; agarose-fp                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |            |                    |                    |
|            | Insert size: 152729; sum-of-contrigs                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |            |                    |                    |
|            | Quality coverage: 6.0 in Q20 bases; agarose-fp                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |            |                    |                    |
|            | Quality coverage: 5.9 in Q20 bases; sum-of-contrigs                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |            |                    |                    |
|            | -----                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |            |                    |                    |
|            | NOTE: This is a 'working draft' sequence. It currently                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |            |                    |                    |
|            | consists of 13 contrigs. The true order of the pieces                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |            |                    |                    |
|            | is not known and their order in this sequence record is                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |            |                    |                    |
|            | arbitrary. Gaps between the contrigs are represented as                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |            |                    |                    |
|            | runs of N, but the exact sizes of the gaps are unknown.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |            |                    |                    |
|            | This record will be updated with the finished sequence                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |            |                    |                    |
|            | as soon as it is available and the accession number will                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |            |                    |                    |
|            | be preserved.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |            |                    |                    |
|            | -----                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |            |                    |                    |
|            | 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 1414:      | contrig of 1414 bp | in length          |
|            | *                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 1415       | 1514:              | gap of 100 bp      |
|            | *                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 1515       | 3704:              | contrig of 2190 bp |
|            | *                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 3705       | 3804:              | gap of 100 bp      |
|            | *                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 3805       | 8775:              | contrig of 4971 bp |
|            | *                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 8776       | 8875:              | gap of 100 bp      |
|            | *                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 8876       | 13172:             | contrig of 4297 bp |
|            | *                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 13173      | 13272:             | gap of 100 bp      |

| FEATURES                 | source                | Location/Qualifiers                         |
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| *                        | misc-feature          | /db_xref="taxon:9606"                       |
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| *                        | misc-feature          | /clone_id="RPC1-11 Human Male BAC"          |
| *                        | misc-feature          | 1.1414                                      |
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| *                        | misc-feature          | 42498 a 29651 c 31126 g 49445 t 1209 others |
| BASE COUNT               |                       |                                             |
| ORIGIN                   |                       |                                             |
| Query Match              |                       | 84.8% Score 17.8: DB 62: Length 153929;     |
| Best Local Similarity    |                       | 90.5%: Pred. No. 97:                        |
| Matches 19: Conservative | 0:                    | Mismatches 2: Indels 0: Gaps 0:             |
| Db 64681                 | ACATAATGACCTCGTTTACAC | 64661                                       |
| 1                        | acataatgacctgcgtcacac | 21                                          |
| 11                       |                       |                                             |
| AC008507                 | 213892 bp             | DNA                                         |
| AC008507                 | 11 ordered pieces.    | HTG                                         |
| AC008507                 | GI:7711281            | 06-MAY-2000                                 |
| AC008507                 | GI:7711281            | WORKING DRAFT SEQUENCE                      |

KEYWORDS HTG: HTGS\_PHASE2; HTGS\_DRAFT.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS 1 (bases 1 to 213892)  
TITLE DOE Joint Genome Institute.  
JOURNAL Sequencing of Human Chromosome 19  
REFERENCE Unpublished  
AUTHORS 2 (bases 1 to 213892)  
TITLE DOE Joint Genome Institute.  
JOURNAL Direct Submission  
REFERENCE Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
COMMENT On May 6, 2000 this sequence version replaced gi:7689761.

-----Genome Center  
Center: Joint Genome Institute  
Center Code: JGI  
Web site: http://www.jgi.doe.gov.

-----Project Information  
Center Project Name: 357334, BC322358  
Center Clone Name: CIT-HSPC\_448F2

-----Summary Statistics  
Consensus quality: 195366 bases at least Q40  
Consensus quality: 206085 bases at least Q30  
Consensus quality: 210129 bases at least Q20  
Estimated insert size: 217290; agarose-fp estimation  
Estimated insert size: 212892; sum-of-contigs estimation  
Quality coverage: 7.58 in Q20 bases; agarose-fp estimation  
Quality coverage: 7.71 in Q20 bases; sum-of-contigs estimation.  
\* NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.  
\* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 43108: contig of 43108 bp in length  
\* 43109 43208: gap of unknown length  
\* 43209 124836: contig of 81628 bp in length  
\* 124837 124936: gap of unknown length  
\* 124937 129045: contig of 4109 bp in length  
\* 129046 129145: gap of unknown length  
\* 129146 138110: contig of 8965 bp in length  
\* 138111 147488: gap of unknown length  
\* 147489 147588: gap of unknown length  
\* 147589 150480: contig of 2892 bp in length  
\* 150481 150580: gap of unknown length  
\* 150581 154788: contig of 4208 bp in length  
\* 154789 154888: gap of unknown length  
\* 154889 157934: contig of 3046 bp in length  
\* 157935 158034: gap of unknown length  
\* 158035 160157: contig of 2123 bp in length  
\* 160158 160257: gap of unknown length  
\* 160258 165114: contig of 4857 bp in length  
\* 165115 165214: gap of unknown length  
\* 165215 213892: contig of 48678 bp in length.

-----FEATURES  
SOURCE  
1. 213892  
Location/Qualifiers

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Query Match 84.8%; Score 17.8; DB 60; Length 213892;  
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Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 9  
AE003812

LOCUS 257523 bp DNA INV 04-OCT-2000  
DEFINITION Drosophila melanogaster genomic scaffold 142000013386047 section 31  
of 52 complete sequences.

ACCESSION AE003812 AE002787  
VERSION AE003812.2 GI:10727533

KEYWORDS HTG.  
SOURCE fruit fly.  
ORGANISM Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE  
AUTHORS

1 (bases 1 to 257523)  
Adams,M.D., Celinker,S.E., Holt,R.A., Evans,C.A., Gocayne,J.D.,  
Amanatides,P.G., Scherer,S.E., Li,P.W., Hoskins,R.A., Galie,R.F.,  
George,R.A., Lewis,S.E., Richards,S., Ashburner,M., Henderson,S.N.,  
Sutton,G.G., Wortman,J.R., Yandell,M.D., Zhang,Q., Chen,L.X.,  
Brannon,R.C., Rogers,Y.H., Blazey,R.G., Champs,M., Pfeiffer,B.D.,  
Wan,K.H., Doyle,C., Baxter,E.G., Helt,G., Nelson,C.R., Gabor  
Miklos,G.L., Abril,J.F., Agbayani,A., An,H.J.,  
Andrews-Plamkoc,C., Baldwin,D., Bailey,R.M., Beeson,K.Y.,  
Baxendale,J., Bayraktaroglu,L., Beasley,E.M., Beeson,K.Y.,  
Benos,P.V., Berman,B.P., Bhandari,D., Bolshakov,S., Borkova,D.,  
Botchan,M.R., Bouck,J., Brokstein,P., Brotler,P., Butts,K.C.,  
Busam,D.A., Butler,H., Cadieu,E., Center,A., Candia,I.,  
Cherry,J.M., Cawley,S., Dahlke,C., Davenport,L.B., Davies,P., de  
Pablo,B., Delcher,A., Deng,Z., Mays,A.D., Dew,I., Dietz,S.M.,  
Dodson,K., Doup,L.E., Downes,M., Dugan-Rocha,S., Dunkov,B.C.,  
Dunn,P., Durbin,K.J., Evangelista,C.C., Ferraz,C., Ferreira,S.,  
Fleischmann,W., Foster,C., Gabrielian,A.E., Garg,N.S.,  
Gelbart,W.M., Glasser,K., Glodek,A., Gong,F., Gorrell,J.H., Gu,Z.,  
Guan,P., Harris,M., Harris,N.L., Harvey,D., Helman,T.J.,  
Hernandez,J.R., Houck,J., Hostin,D., Houston,K.A., Howland,T.J.,  
Wel,M.H., Ibegwam,C., Jalali,M., Kalush,F., Karpen,G.H., Ke,Z.,  
Kensler,J.A., Ketchum,K.A., Kimmel,B.E., Kodira,C.D., Kraft,C.,  
Kravitz,S., Kulp,D., Lai,Z., Lasko,P., Lei,Y., Levitsky,A.A.,  
Li,J., Li,Z., Liang,Y., Lin,X., Liu,X., Matel,I., McIntosh,T.C.,  
McLeod,M.P., McPherson,D., Merkulov,G., Milshina,N.V., Mobarry,C.,  
Morrison,J., Moshrefi,A., Mount,S.M., Moy,M., Murphy,B., Murphy,L.,  
Muzny,D.M., Nelson,D.L., Nelson,D.R., Nelson,K.A., Nixon,K.,  
Nuskern,D.R., Pacib,J.M., Palazolo,M., Pittman,G.S., Pan,S.,  
Pollard,J., Puri,Y., Reese,M.G., Reinert,K., Remington,K.,  
Saunders,R.D., Scheeler,F., Shen,H., Shue,B.C., Siden-Kiamos,I.,  
Simpson,M., Skupski,M.P., Smith,T., Spler,E., Spidling,A.C.,  
Stapleton,M., Strong,R., Sun,E., Svitskas,R., Tector,C., Turner,R.,  
Venier,E., Wang,A.H., Wang,X., Wang,Z.Y., Wasserman,D.A.,  
Weinstock,G.M., Weissbach,J., Williams,S.M., Woodde,T.,  
Wortley,K.C., Wu,D., Yang,S., Yao,Q.A., Ye,J., Yeh,R.F.,  
Zaveri,J.S., Zhan,M., Zhang,G., Zhao,Q., Zheng,L., Zheng,X.H.,  
Zhong,F.N., Zhong,W., Zhou,X., Zhu,S., Zhu,X., Smith,H.O.,  
Gibbs,R.A., Myers,E.W., Rubin,G.M., and Venter,J.C.  
The genome sequence of *Drosophila melanogaster*  
Science 287 (5461), 2185-2195 (2000)

TITLE JOURNAL  
JOURNAL MEDLINE  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive,  
Rockville, MD, USA

COMMENT On Oct 9, 2000 this sequence version replaced gi:7303102.  
FEATURES  
SOURCE  
1. 257523  
Location/Qualifiers

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Best Local Similarity 90.5%: Pred. No. 90;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 acataatgctcgctcacac 21

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Db 49929 ACATGATGCGCATCGTTCCAC 49949



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RESULT 10
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LOCUS      AL356099
DEFINITION Homo sapiens chromosome 10 clone RP11-357A18, *** SEQUENCING IN
ACCESSION  AL356099
VERSION     AL356099.8
KEYWORDS   HTGS_PHASE1; HTGS_DRAFT; HTGS_FULFILL.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 163861)
AUTHORS    Burton, J.
JOURNAL    Direct Submission
            Submitted (07-APR-2001) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
            Requests: clonerequest@sanger.ac.uk
            On Apr 9, 2001 this sequence version replaced gi:11321947.
COMMENT    ----- Genome Center
            Center: Sanger Centre
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: humquerry@sanger.ac.uk
            ----- Project Information
            Center project name: BA357A18
            ----- Summary Statistics
            Assembly program: XGAP; Version 4.5
            Sequencing vector: plasmid; L08752; 100% of reads
            Chemistry: Dye-terminator Big Dye; 100% of reads
            Consensus quality: 16190 bases at least Q40
            Consensus quality: 16280 bases at least Q20
            Insert size: 163561; sum-of-contrigs
            Insert size: 157608; 9.7% error; agarose-fp
            Quality coverage: 5.63x in Q20 bases; sum-of-contrigs Quality
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            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 4 contrigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contrigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
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            * 1 42344: contrig of 42344 bp in length
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Best Local Similarity 94.7%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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RESULT 11
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VERSION     AC018613.3
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SOURCE     human.
ORGANISM   Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 180530)
AUTHORS    Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
            Anderson, S., Baldwin, J., Barna, N., Beckert, R., Beda, F.,
            Boguslavsky, L., Boukhgalter, B., Brown, A., Burnett, G., Castle, A.,
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            Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A.,
            Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J., Zimmer, A.
            and Zody, M.
            Direct Submission
            Submitted (14-DEC-1999) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
            On Apr 5, 2000 this sequence version replaced gi:6648226.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            ----- Genome Center
            Center: Whitehead Institute/ MIT Center for Genome Research
            Center code: WMR
            Web site: http://www-seq.wi.mit.edu
            Contact: sequence_submissions@genome.wi.mit.edu
            ----- Project Information
            Center project name: L5152
            Center clone name: 55_D_24
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            Chemistry: Dye-terminator Big Dye; 100% of reads
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            TITLE
            JOURNAL
            COMMENT

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\* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 14 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

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Query Match 82.9% Score 17.4; DB 65; Length 180530;  
 Best Local Similarity 94.7% Pred. No. 1.5e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 catatagcctcgttccca 20  
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RESULT 12  
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 DEFINITION Arabidopsis thaliana DNA chromosome 4, BAC clone T26M18 (ESSA  
 project).  
 ACCESSION AL078606  
 VERSION AL078606  
 KEYWORDS GI:5002514

ORGANISM  
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 Arabidopsis thaliana

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
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 Brassicales; Brassicaceae; Arabidopsis.

REFERENCE  
 1 (bases 38390 to 39150): 59320 to 59877; 60154 to 60701)  
 Bevan,M., Volckaert,G., Gymnopoulos,B., Voelt.M., Robben,J.,  
 Bancroft,I., Mewes,H.W., Lemcke,K. and Mayer,K.F.X.

JOURNAL  
 2 (bases 1 to 90824)  
 Bevan,M., Hilbert,H., Braun,M., Holzer,E., Brandt,A.,  
 Duesterhoeft,A., Bancroft,I., Mewes,H.W., Lemcke,K. and  
 Mayer,K.F.X.  
 Unpublished

REFERENCE  
 3 (bases 1 to 90824)  
 EU Arabidopsis sequencing project.  
 AUTHORS  
 Direct Submision  
 JOURNAL  
 Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer  
 Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:  
 lemcke@mps.blochem.mpg.de,mayer@mps.blochem.mpg.de Project  
 Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge  
 Laboratory, John Innes Centre, Colney Lane, NR4 7UT Norwich, UK,  
 E-mail: michael.bevan@bsrc.ac.uk

COMMENT  
 Information on performance of analysis and a more detailed  
 annotation of this entry and other sequences of chromosomes 3, 4  
 and 5 can be viewed at: <http://www.mips.blochem.mpg.de/proj/thal/>.

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| intron | /number=11<br>/complement(9653. .9852)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |  |
| exon   | /number=12<br>/complement(9853. .9914)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |  |
| intron | /number=13<br>/complement(9915. .10138)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |  |
| exon   | /number=14<br>/complement(10139. .10219)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| intron | /number=15<br>/complement(10220. .10449)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| exon   | /number=16<br>/complement(10450. .10559)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| intron | /number=17<br>/complement(10560. .10647)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| exon   | /number=18<br>/complement(10648. .10761)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| intron | /number=19<br>/complement(10762. .10860)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| exon   | /number=20<br>/complement(10861. .10990)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| intron | /number=21<br>/complement(10991. .11106)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| exon   | /number=22<br>/complement(11107. .11192)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| intron | /number=23<br>/complement(11193. .11441)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| exon   | /number=24<br>/complement(11442. .11551)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| intron | /number=25<br>/complement(11552. .11777)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| exon   | /number=26<br>/complement(11778. .11862)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| intron | /number=27<br>/complement(11863. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| exon   | /number=28<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| intron | /number=29<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| exon   | /number=30<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| intron | /number=31<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| exon   | /number=32<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| intron | /number=33<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| exon   | /number=34<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| intron | /number=35<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| exon   | /number=36<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| intron | /number=37<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| exon   | /number=38<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| intron | /number=39<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| exon   | /number=40<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| intron | /number=41<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| exon   | /number=42<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| intron | /number=43<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| exon   | /number=44<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| intron | /number=45<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| exon   | /number=46<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| intron | /number=47<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| exon   | /number=48<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| intron | /number=49<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| exon   | /number=50<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| intron | /number=51<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| exon   | /number=52<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| intron | /number=53<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| exon   | /number=54<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| intron | /number=55<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| exon   | /number=56<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| intron | /number=57<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| exon   | /number=58<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| intron | /number=59<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| exon   | /number=60<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| intron | /number=61<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| exon   | /number=62<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| intron | /number=63<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| exon   | /number=64<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| intron | /number=65<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| exon   | /number=66<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| intron | /number=67<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| exon   | /number=68<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| intron | /number=69<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| exon   | /number=70<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| intron | /number=71<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| exon   | /number=72<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| intron | /number=73<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| exon   | /number=74<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| intron | /number=75<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| exon   | /number=76<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| intron | /number=77<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| exon   | /number=78<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| intron | /number=79<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| exon   | /number=80<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| intron | /number=81<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| exon   | /number=82<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| intron | /number=83<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| exon   | /number=84<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| intron | /number=85<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| exon   | /number=86<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| intron | /number=87<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| exon   | /number=88<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| intron | /number=89<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| exon   | /number=90<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| intron | /number=91<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| exon   | /number=92<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| intron | /number=93<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| exon   | /number=94<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| intron | /number=95<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| exon   | /number=96<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| intron | /number=97<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| exon   | /number=98<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| intron | /number=99<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |  |
| exon   | /number=100<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=101<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=102<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=103<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=104<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=105<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=106<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=107<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=108<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=109<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=110<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=111<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=112<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=113<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=114<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=115<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=116<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=117<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=118<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=119<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=120<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=121<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=122<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=123<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=124<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=125<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=126<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=127<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=128<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=129<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=130<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=131<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=132<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=133<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=134<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=135<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=136<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=137<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=138<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=139<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=140<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=141<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=142<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=143<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=144<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=145<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=146<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=147<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=148<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=149<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=150<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=151<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=152<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=153<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=154<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=155<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=156<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=157<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=158<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
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| exon   | /number=160<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=161<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=162<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=163<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=164<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=165<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=166<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=167<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=168<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=169<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=170<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=171<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=172<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=173<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=174<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=175<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=176<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=177<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=178<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=179<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=180<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=181<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=182<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=183<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=184<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=185<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=186<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=187<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=188<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=189<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=190<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=191<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=192<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=193<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=194<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=195<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=196<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=197<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=198<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=199<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=200<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=201<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| exon   | /number=202<br>/complement(12111. .12110)<br>/gene="At4g11800"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| intron | /number=203<br>/complement(12111. .12110)<br>/gene="                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |  |

Best Local Similarity 90.0%; Pred. No. 3.3e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 2 cataatgcctcgttcacac 21  
|||||  
Db 43650 CATATATGCTCTTAACTC 43631

RESULT 13  
LMFLCHR26\_3/c  
WPCOMMENT

Sequence split into 7 fragments LOCUS LMFLCHR26 Accession AL160493

| Fragment Name | Begin  | End    |
|---------------|--------|--------|
| LMFLCHR26_0   | 1      | 110000 |
| LMFLCHR26_1   | 100001 | 210000 |
| LMFLCHR26_2   | 200001 | 310000 |
| LMFLCHR26_3   | 300001 | 410000 |
| LMFLCHR26_4   | 400001 | 510000 |
| LMFLCHR26_5   | 500001 | 610000 |
| LMFLCHR26_6   | 600001 | 677114 |

Continuation (4 of 7) of LMFLCHR26 from base 300001 (AL160493 Leishmania major chromosome)

Query Match 80.0%; Score 16.8; DB 84; Length 110000;  
Best Local Similarity 90.0%; Pred. No. 3.3e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 cataatgcctcgttcacac 21  
|||||  
Db 13686 CATGATGCTCTTAACTC 13667

RESULT 14  
AL357494/c  
LOCUS  
DEFINITION Homo sapiens chromosome 9 clone RP11-544D16, \*\*\* SEQUENCING IN  
PROGRESS \*\*\*  
ACCESSION AL357494  
VERSION AL357494.2  
KEYWORDS HTG; HTGS\_PHASE1.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 135161)  
Plumb,B.  
Direct Submission  
Submitted (20-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk  
requests: clonerequest@sanger.ac.uk  
On Aug 27, 2000 this sequence version replaced gi:9214117.  
----- Genome Center  
Center: Sanger Centre  
Center code: SC  
Web site: http://www.sanger.ac.uk  
Contact: humquerry@sanger.ac.uk  
----- Project Information  
Center project name: BA544D16  
----- Summary Statistics  
Assembly program: XGAP4; version 4.5  
Sequencing vector: plasmid; L08752; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Consensus quality: 115360 bases at least Q40  
Consensus quality: 127769 bases at least Q30  
Consensus quality: 131161 sum-of-contigs  
Insert size: 291859; 6.0% error; agarose-fp  
Quality coverage: 2.72x in Q20 bases; sum-of-contigs quality  
coverage: 1.97x in Q20 bases; agarose-fp

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 41 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is

\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
1  
2004 2103: gap of 100 bp  
2104 4562: contig of 2459 bp in length  
4563 4662: gap of 100 bp  
4663 7077: contig of 2415 bp in length  
7078 7177: gap of 100 bp  
7178 11551: contig of 4374 bp in length  
11552 11651: gap of 100 bp  
11652 15679: contig of 4028 bp in length  
15680 15779: gap of 100 bp  
15780 18624: contig of 2845 bp in length  
18625 18724: gap of 100 bp  
18725 20904: contig of 2180 bp in length  
20905 21004: gap of 100 bp  
21005 23239: contig of 2235 bp in length  
23240 23339: gap of 100 bp  
23340 25954: contig of 2615 bp in length  
25955 26054: gap of 100 bp  
26055 29157: contig of 3103 bp in length  
29158 29257: gap of 100 bp  
29258 34391: contig of 5144 bp in length  
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96672 96771: gap of 100 bp  
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101432 101531: gap of 100 bp  
101532 105517: contig of 3986 bp in length  
105518 105617: gap of 100 bp  
105618 108670: contig of 3053 bp in length  
108671 108770: gap of 100 bp

|                     |                                                                    |         |         |                   |           |  |  |  |
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|                     | *                                                                  | 115364  | 115463: | gap of 100 bp     |           |  |  |  |
|                     | *                                                                  | 115464  | 118107: | contig of 2644 bp | in length |  |  |  |
|                     | *                                                                  | 118108  | 118207: | gap of 100 bp     |           |  |  |  |
|                     | *                                                                  | 118208  | 123149: | contig of 4942 bp | in length |  |  |  |
|                     | *                                                                  | 123150  | 123249: | gap of 100 bp     |           |  |  |  |
|                     | *                                                                  | 123250  | 127306: | contig of 4057 bp | in length |  |  |  |
|                     | *                                                                  | 127307  | 127406: | gap of 100 bp     |           |  |  |  |
|                     | *                                                                  | 127407  | 129514: | contig of 2108 bp | in length |  |  |  |
|                     | *                                                                  | 129515  | 129614: | gap of 100 bp     |           |  |  |  |
|                     | *                                                                  | 129615  | 132808: | contig of 3294 bp | in length |  |  |  |
|                     | *                                                                  | 132809  | 133008: | gap of 100 bp     |           |  |  |  |
|                     | *                                                                  | 133009  | 135161: | contig of 2153 bp | in length |  |  |  |
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| Query Match                       | 80.0%                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Score 16.8        | DB 80    | Length 135161 |
|-----------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------|----------|---------------|
| Best Local Similarity             | 90.0%                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Pred. No. 3.2e+02 |          |               |
| Matches 18: Conservative          | 0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | Mismatches 2      | Indels 0 | Gaps 0        |
| 2 cataatgacctcttcacac 21          |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |                   |          |               |
| Db 71926 CATGATGACCTGTCACAC 71907 |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |                   |          |               |
| RESULT 15                         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |                   |          |               |
| AC051641                          | 143092 bp                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | DNA               | HTG      | 28-MAY-2000   |
| LOCUS                             | Homo sapiens chromosome 8 clone RP11-458L9 map 8, LOW-PASS SEQUENCE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |                   |          |               |
| DEFINITION                        | AC051641                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |                   |          |               |
| ACCESSION                         | AC051641                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |                   |          |               |
| VERSION                           | AC051641.2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | GI:8099851        |          |               |
| KEYWORDS                          | HTG: HTGS_PHASE0.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |                   |          |               |
| SOURCE                            | human.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |                   |          |               |
| ORGANISM                          | Homo sapiens                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                   |          |               |
| REFERENCE                         | Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |                   |          |               |
| AUTHORS                           | 1 (bases 1 to 143092)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                   |          |               |
| TITLE                             | Biren,B., Linton,L., Nusbaum,C. and Lander,E.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |                   |          |               |
| JOURNAL                           | Homo sapiens chromosome 8, clone RP11-458L9                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |                   |          |               |
| REFERENCE                         | 2 (bases 1 to 143092)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                   |          |               |
| AUTHORS                           | Biren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,D., Baria,N., Bastien,V., Beda,F., Boguslavsky,L., Boukhgalter,B., Brown,A., Burkett,G., Campoliano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Colliamore,A., Cooke,P., DeArnellou,K., Dewar,K., Diaz,J.S., Dodge,S., Domino,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S., Glinde,S., Goyette,M., Graham,L., Grand-Pierre,N., Grant,G., Hagos,B., Heatford,A., Hooton,L., Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., Larocque,K., Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,C., Liu,G., Locke,K., Macdonald,P., Marguis,N., McCarthy,M., McMan,P., McGurk,A., McKernan,K., McPheeters,R., Meldrum,T., Menus,L., Mihova,T., Miranda,C., Mlenda,V., Morrow,J., Murphy,T., Naylor,T., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Olivier,T.M., Oliver,T., Peterson,K., Pierre,N., Pisanic,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Stange-Roman,N., Stojanovic,N., Subramanian,A., Talamas,J., Teffaye,S., Theodore,J., Tirrell,A., Travers,M., Triggillo,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,T., Zimmer,A. and Zody,M. |                   |          |               |
| JOURNAL                           | Direct Submission                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |                   |          |               |
| COMMENT                           | Submitted (15-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02144, USA<br>On May 28, 2000 this sequence version replaced gi:7574860.<br>All repeats were identified using RepeatMasker:<br>Smt, A.F.A. & Green, P. (1996-1997)<br>http://ftp.genome.washington.edu/RM/RepeatMasker.html<br>Genome Center<br>Center: Whitehead Institute/ MIT Center for Genome Research<br>Center code: WIBR                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |                   |          |               |

Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
----- Project Information  
Center project name: L8717  
Center clone name: 458\_L<sub>9</sub>

NOTE: This record contains 158 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.

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Query Match      80.0%; Score 16.8; DB 72; Length 143092;
Best Local Similarity 90.0%; Pred. No. 3.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 cataatggcctcgttcacac 21
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Db 2303 CAGAAATGCCCTTGTTCACAC 2322

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Search completed: September 21, 2001, 00:36:20  
 Job time: 29635 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 21, 2001, 02:42:41 : Search time 330.77 Seconds  
(without alignments)  
39.864 Million cell updates/sec

Title: US-09-138-735-10

Perfect score: 21  
Sequence: 1 acataatgcctcgttcacac 21

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID       | Description           |
|------------|-------|-------------|--------|-------------|-----------------------|
| 1          | 21    | 100.0       | 21     | AA727314    | T. cruzi epimastigote |
| 2          | 21    | 100.0       | 21     | AA864096    | PCR primer for T.     |
| 3          | 21    | 100.0       | 3402   | 17 AA727310 | Trypanosoma cruzi     |
| 4          | 21    | 100.0       | 3402   | 20 AA84092  | T. cruzi PTC40 cod    |
| 5          | 16.2  | 77.1        | 10628  | 22 AAF57301 | P. falciparum FC93    |
| 6          | 15.8  | 75.2        | 296    | 14 AAO59461 | Human brain Expro     |
| 7          | 15.8  | 75.2        | 1354   | 20 AAX60584 | Human secreted pro    |
| 8          | 15.8  | 75.2        | 2344   | 14 AAO51427 | Human FACC CDNA c1    |
| 9          | 15.8  | 75.2        | 3150   | 14 AAO51428 | Human FACC CDNA c1    |
| 10         | 15.8  | 75.2        | 4488   | 14 AAO51426 | Human FACC CDNA c1    |
| 11         | 15.8  | 75.2        | 4567   | 20 AAV33945 | Fanconi anaemia co    |

|      |      |      |       |             |                    |
|------|------|------|-------|-------------|--------------------|
| C 12 | 15.2 | 72.4 | 3417  | 17 AAT39622 | Human DNA ligase I |
| C 13 | 15.2 | 72.4 | 3417  | 20 AAV82491 | Human DNA ligase I |
| C 14 | 15.2 | 72.4 | 9775  | 20 AAX77721 | N. crassa his-3 co |
| C 15 | 15.2 | 72.4 | 9934  | 20 AAX77722 | N. crassa his-3 co |
| C 16 | 15   | 71.4 | 226   | 19 AAF12686 | Xylanase activity  |
| C 17 | 14.8 | 70.5 | 771   | 21 AAF12686 | Aspergillus oryzae |
| C 18 | 14.8 | 70.5 | 1310  | 21 AA240662 | Murine serine/thre |
| C 19 | 14.8 | 70.5 | 1671  | 21 AAC79977 | Human secreted pro |
| C 20 | 14.8 | 70.5 | 2126  | 19 AAV41999 | Human GPR14 (G-pro |
| C 21 | 14.8 | 70.5 | 2126  | 20 AA211174 | Human GPR14 coding |
| C 22 | 14.8 | 70.5 | 4466  | 17 AAT39662 | Esterase secretory |
| C 23 | 14.8 | 70.5 | 6178  | 20 AAV80182 | Nucleic acid seque |
| C 24 | 14.8 | 70.5 | 11141 | 17 AAT15820 | TBE virus strain N |
| C 25 | 14.8 | 70.5 | 13907 | 20 AAX33247 | PEBP2 alpha A gene |
| C 26 | 14.6 | 69.5 | 300   | 21 AAA01343 | Human colon cancer |
| C 27 | 14.6 | 69.5 | 301   | 21 AAA06463 | Human immunogenic  |
| C 28 | 14.6 | 69.5 | 320   | 21 AAA30132 | Human chromosome 2 |
| C 29 | 14.6 | 69.5 | 338   | 18 AAX83281 | Breast cancer tumo |
| C 30 | 14.6 | 69.5 | 338   | 19 AAV69003 | DNA molecule encod |
| C 31 | 14.6 | 69.5 | 338   | 19 AAC80804 | Human breast tumou |
| C 32 | 14.6 | 69.5 | 375   | 22 AAF65970 | Novel human polyu  |
| C 33 | 14.6 | 69.5 | 435   | 21 AAA16513 | Human colon cancer |
| C 34 | 14.6 | 69.5 | 520   | 20 AAX81415 | Constitutive ferre |
| C 35 | 14.6 | 69.5 | 594   | 15 AAQ7871  | CNS neural thread  |
| C 36 | 14.6 | 69.5 | 594   | 17 AAT27753 | HB4 partial cDNA s |
| C 37 | 14.6 | 69.5 | 601   | 21 AA280323 | Human colon cancer |
| C 38 | 14.6 | 69.5 | 624   | 21 AAA16354 | Human colon cancer |
| C 39 | 14.6 | 69.5 | 732   | 22 AAF22909 | Human prostate can |
| C 40 | 14.6 | 69.5 | 755   | 21 AAA16531 | Human colon cancer |
| C 41 | 14.6 | 69.5 | 757   | 22 AAF22908 | Human prostate can |
| C 42 | 14.6 | 69.5 | 771   | 22 AAF22905 | Human prostate can |
| C 43 | 14.6 | 69.5 | 792   | 21 AAC69676 | Human NMDH ubiquin |
| C 44 | 14.6 | 69.5 | 840   | 20 AAX81417 | Constitutive ferre |
| C 45 | 14.6 | 69.5 | 1263  | 18 AAT67413 | H. pylori putative |

#### ALIGNMENTS

|           |                                                                           |
|-----------|---------------------------------------------------------------------------|
| RESULT 1. |                                                                           |
| AA727314  | AA727314 standard; CDNA; 21 BP.                                           |
| XX        | AA727314:                                                                 |
| AC        | 26-NOV-1996 (first entry)                                                 |
| XX        |                                                                           |
| DE        | T. cruzi epimastigote PTC100t antigen primer corresp. to bases 2187-2207. |
| XX        |                                                                           |
| KM        | Antigen: Trypanosoma cruzi; epimastigote; serum; Chagas disease; probe;   |
| KW        | Primer: PCR; polymerase chain reaction; amplification; antibody; ss.      |
| XX        |                                                                           |
| OS        | Synthetic.                                                                |
| XX        |                                                                           |
| PN        | FR2723589-A1.                                                             |
| XX        |                                                                           |
| PD        | 16-FEB-1996.                                                              |
| XX        |                                                                           |
| PF        | 12-AUG-1994; 94FR-0010132.                                                |
| XX        |                                                                           |
| PR        | 12-AUG-1994; 94FR-0010132.                                                |
| XX        |                                                                           |
| PA        | (INMR ) BIO MERIEUX.                                                      |
| XX        |                                                                           |
| PI        | Jolivet M, Lesenechal M, Paranhos-Bacala G;                               |
| XX        |                                                                           |
| DR        | WPI, 1996-190287/20.                                                      |
| XX        |                                                                           |
| PT        | New nucleic acid encoding Trypanosoma cruzi epimastigote antigen -        |
| PT        | useful for diagnosis, monitoring and therapy of Chagas disease            |
| XX        |                                                                           |
| PS        | Claim 29; Page 38; 55pp; French.                                          |

CC The primers AAT27311-5 were used to PCR amplify the sequence encoding a  
CC novel isolated antigenic protein from Trypanosoma cruzi epimastigotes,  
CC designated PTC100t (AAT27310). The primers, derived from the sequences  
CC of a 594 and 1041 bp fragment of PTC100t, amplified the gene as 3  
CC fragments. This primer corresponds to nucleotides 2187-2207 of the PTC100t  
CC sequence, derived from the 1041 bp fragment. The 594 bp fragment was  
CC isolated from a T. cruzi genomic expression library in lambda gtl1, using  
CC a mixture of sera from patients with Chagas disease. It corresponds to  
CC nucleotides 1232-1825 of PTC100t. The 1041 bp fragment was isolated from  
CC a lambda gtl10 library using the 594 bp fragment as a probe. The protein,  
CC or antibodies raised against it, can be used in the detection and  
CC monitoring of T. cruzi infection i.e. Chagas disease.  
XX  
SQ Sequence 21 BP; 6 A; 7 C; 3 G; 5 T; 0 other;

Query Match 100.0%; Score 21; DB 17; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0.061;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 acataatgctcgttcacac 21  
|||||  
Db 1 acataatgctcgttcacac 21

RESULT 2  
AAX84096  
ID AAX84096 standard; DNA; 21 BP.  
XX  
AC AAX84096;  
XX  
DT 27-AUG-1999 (first entry)  
XX  
DE PCR primer for T. cruzi PTC40 coding sequence.  
XX  
Ptc40: Tc40; infection; diagnosis; immune complex; antigenic determinant;  
KM therapy; antibody; PCR primer; ss.  
XX  
OS Synthetic.  
OS Trypanosoma cruzi.  
XX  
PN MO92929867-A1.  
XX  
PD 17-JUN-1999.  
XX  
PF 10-DEC-1998; 98WO-IB01987.  
XX  
PR 10-DEC-1997; 97US-0988242.  
XX  
PA (INMR ) BIO MERIEUX.  
XX  
PI Jolivet M, Lesenechal M, Mandrand B, Paranhos-Baccala G;  
XX WPI; 1999-394978/33.  
XX  
DR New Trypanosoma cruzi antigen  
XX  
PT  
PS Disclosure; Page 21; 65pp; English.  
XX  
XX This sequence is a PCR primer for DNA encoding the Trypanosoma cruzi  
CC PTC40 protein of the invention. The PTC40 antigenic determinant is  
CC useful as a reagent for detection and/or monitoring of Trypanosoma cruzi  
CC infection from samples including blood serum or plasma, urine, saliva, or  
CC tears, by contacting with the sample and detecting an immune complex. The  
CC PTC40 antigenic determinant, the vector, expression cassette, cell or  
CC antibody are useful for treatment or prevention (vaccine) of a  
CC Trypanosoma cruzi infection in a man or animal. Current Trypanosoma cruzi  
CC antigens are obtained from protein fractions of the noninfectious stage  
CC of the parasite, and these do not allow sufficient production of antigens  
CC for use in reliable serological diagnostic tests. The strain to strain  
CC polymorphism reduces reliability of the tests.  
XX  
SQ Sequence 21 BP; 6 A; 7 C; 3 G; 5 T; 0 other;

Query Match 100.0%; Score 21; DB 20; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0.061;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 acataatgctcgttcacac 21  
|||||  
Db 1 acataatgctcgttcacac 21

RESULT 3  
AAT27310/c  
ID AAT27310 standard; cDNA; 3402 BP.  
XX  
AC AAT27310;  
XX  
DT 26-NOV-1996 (first entry)  
XX  
DE Trypanosoma cruzi epimastigotic PTC100t antigen gene.  
XX  
KM Antigen; Trypanosoma cruzi; epimastigote; serum; Chagas disease; probe;  
KM Primer; PCR; polymerase chain reaction; amplification; antibody; ds.  
XX  
OS Trypanosoma cruzi.  
XX  
XX Key Location/Qualifiers  
FT CDS 266..3013  
FT /\*tag- a  
FT /product- PTC100t epimastigotic antigen  
XX  
PN FR2723589-A1.  
XX  
PD 16-FEB-1996.  
XX  
PF 12-AUG-1994; 94FR-0010132.  
XX  
PR 12-AUG-1994; 94FR-0010132.  
XX  
PA (INMR ) BIO MERIEUX.  
XX  
PI Jolivet M, Lesenechal M, Paranhos-Baccala G;  
XX WPI; 1996-190287/20.  
XX  
DR P-PSDB; AAR91615.  
XX  
PT New nucleic acid encoding Trypanosoma cruzi epimastigotic antigen  
XX useful for diagnosis, monitoring and therapy of Chagas disease  
XX  
PS Claim 1; Page 24-26; 55pp; French.  
XX  
XX This is the nucleotide sequence encoding a novel isolated antigenic  
CC protein from Trypanosoma cruzi epimastigotes, designated PTC100t.  
CC The clone Tc50 was isolated from a T. cruzi genomic expression library in  
CC lambda gtl1, using a mixture of sera from patients with Chagas disease.  
CC Clone Tc50 contained an 594 bp insert corresp. to nucleotides 1232-1825  
CC of this sequence. The Tc50 sequence was subsequently used to probe a  
CC Southern blot of restriction enzyme digested T. cruzi DNA and also screen  
CC a lambda gtl10 library to isolate a 1041 bp EcoRI fragment corresp. to  
CC nucleotides 1403-2443 of PTC100t. Primers (AAT27311-5) were synthesised  
CC based on the sequences of the 594 and 1041 bp fragments and used to  
CC amplify the PTC100t clone as 3 fragments from cDNA derived from mRNA  
CC purified from T. cruzi epimastigotes. The protein or antibodies raised  
CC against it can be used in the detection and monitoring of T. cruzi  
CC infection i.e. Chagas disease.  
XX  
SQ Sequence 3402 BP; 889 A; 818 C; 958 G; 737 T; 0 other;

Query Match 100.0%; Score 21; DB 17; Length 3402;  
Best Local Similarity 100.0%; Pred. No. 0.13;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 acataatggcctcggtcacac 21  
 |||  
 DB 2207 ACATATATGGCCTCGTTCACAC 2187

## RESULT 4

AAx84092/C  
 ID AAX84092 standard; CDNA: 3402 BP.

AC AAX84092;

DT 27-AUG-1999 (first entry)

DE T. cruzi PTC40 coding sequence.

KW PTC40: Tc40: infection; diagnosis; immune complex; antigenic determinant; therapy; antibody; ds.

OS Trypanosoma cruzi.

PN WO929867-A1.

PD 17-JUN-1999.

PF 10-DEC-1998; 98WO-1B01987.

PR 10-DEC-1997; 97US-0988242.

PA (INMR ) BIO MERIEUX.

PI Jolivet M, Lesenechal M, Mandrand B, Paranhos-Baccala G;

DR WPI: 1999-394978/33.

PS P-PSDB: AAY22124.

PT New Trypanosoma cruzi antigen

PS Claim 1: Page 52-56; 65pp; English.

CC This sequence encodes the Trypanosoma cruzi PTC40 protein of the invention, and is designated Tc40. The PTC40 antigenic determinant is useful as a reagent for detection and/or monitoring of Trypanosoma cruzi infection from samples including blood serum or plasma, urine, saliva, or tears, by contacting with the sample and detecting an immune complex. The PTC40 antigenic determinant, the vector, expression cassette, cell or antibody are useful for treatment or prevention (vaccine) of a Trypanosoma cruzi infection in a man or animal. Current Trypanosoma cruzi antigens are obtained from protein fractions of the noninfectious stage of the parasite, and these do not allow sufficient production of antigens for use in reliable serological diagnostic tests. The strain to strain polymorphism reduces reliability of the tests.

CC Sequence 3402 BP: 888 A; 821 C; 956 G; 737 T; 0 other;

Query Match 100.0%; Score 21; DB 20; Length 3402;

Best Local Similarity 100.0%; Pred. No. 0.13;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 acataatggcctcggtcacac 21  
 |||  
 DB 2207 ACATATATGGCCTCGTTCACAC 2187

## RESULT 5

AAf57301  
 ID AAF57301 standard; DNA: 10628 BP.

AC AAF57301;

DT 29-MAY-2001 (first entry)

DE P. falciparum FCR3.varCSA protein encoding DNA.

XX FCR3.varCSA protein; chondroitin sulfate A; CSA; var gene; PFEMP1;  
 KW erythrocyte membrane protein 1; parasitized red blood cell; PRBC;  
 KM malaria; protozoasidae; ds.

OS Plasmodium falciparum.

Key Location/Qualifiers  
 FT 1.10626  
 CDS /tag= a  
 /note= "the stop codon is not indicated"

WO200116326-A2.

PD 08-MAR-2001.

PF 01-SEP-2000; 2000WO-US24195.

PR 01-SEP-1999; 99US-0152023.

PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

PI Scherf A, Miller LH, Gamain B, Baruch DI, Buffet P, Scheidig C;  
 PI Gysin J, Pouvelle B, Fujii N, Smith J;

DR WPI: 2001-235109/24.

PS P-PSDB: AAB62142.

PT Novel FCR3.varCSA protein, useful for modulating parasitized red blood cell binding, sequestration and onset of maternal malaria -  
 Claim 3; Page 60-63; 78pp; English.

CC The invention relates to a P. falciparum FCR3.varCSA protein, that is capable of binding to chondroitin sulfate A (CSA). The var gene and the corresponding P.falciparum erythrocyte membrane protein 1 (PFEMP1) CC modulate adhesion of parasitized red blood cell (PRBC) to CSA. The CC protein and the encoding gene are useful for treating and preventing CC maternal malaria in a patient afflicted at a risk for contracting CC maternal malaria or in a patient afflicted with maternal malaria. The CC present sequence represents the DNA encoding the P. falciparum FCR3.varCSA protein.

CC Sequence 10628 BP: 4341 A; 1375 C; 2094 G; 2818 T; 0 other;

Query Match 77.1%; Score 16.2; DB 22; Length 10628;

Best Local Similarity 85.7%; Pred. No. 47;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 acataatggcctcggtcacac 21  
 |||  
 DB 9358 acaaatgctccgttcacac 9378

## RESULT 6

AAO59461  
 ID AAO59461 standard; CDNA: 296 BP.

AC AAO59461;

DT 16-MAR-1994 (first entry)

DE Human brain Expressed Sequence Tag EST01451.

KW Gene transcription product; genetic markers; tagging; in vivo;  
 KM transcription; mapping; locations; chromosomes; chromosomal; ss.

OS Homo sapiens.

PN WO9316178-A.

PD 19-AUG-1993.

```

XX 12-FEB-1993: 93WO-US01294.
PF
XX
XX 12-FEB-1992: 92US-0837195.
PR
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICE.
PI Adams MD, Moreno RF, Venter CJ;
XX
XX WPI: 1993-272882/34.
DR
XX Enriched oligonucleotides and corresp. sequences - used as
PT markers for human genes transcribed in-vivo, facilitate tagging
PT of most human genes
PS
XX Example 4: Page 178; 500pp; English.
XX
XX The Expressed Sequence Tag was isolated from a human brain cDNA
CC library as part of a large set of ESTs which can be used as markers
CC for human genes transcribed in vivo. They can be used to facilitate
CC tagging of most human genes, for mapping locations of expressed genes
CC on chromosomes, for individual or forensic identification, for mapping
CC locations of disease-associated genes, for identification of tissue
CC type, and for prep. of antisense sequences, probes and constructs.
CC EST01451 has a "poor" coding probability as evaluated using the
CC coding-region prediction program CRM. See also AA059041-061440.
CC
XX
XX Sequence 296 BP; 63 A; 72 C; 80 G; 78 T; 3 other:
SQ
Query Match 75.2%; Score 15.8; DB 14; Length 296;
Best Local Similarity 89.5%; Pred. No. 45;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 ataatggcctcgtcacac 21
1 |||||
Db 170 agaatggcctcgtcacac 188
RESULT 7
AA050584
ID AAX60584 standard; DNA: 1354 BP.
XX
XX AAX60584;
AC
XX
XX 27-JUL-1999 (first entry)
DT
XX
XX Human secreted protein encoding DNA (clone c01000_1).
DE
XX
XX Secreted protein; human; tissue marker; genetic disease; gene therapy;
KM veterinary medicine; cell proliferation; immunostimulant; infection;
KW immunosuppressant; autoimmune disease; organ rejection; tumour; anemia;
KM haematopoiesis; wound healing; fertility control; chemotaxis; analgesic;
KM thrombolytic; haemophilia; infarction; antimicrobial agent; cancer; ss.
XX
XX Homo sapiens.
OS
XX
XX WO924469-A1.
PN
XX
XX 20-MAY-1999.
PD
XX
XX 06-NOV-1998: 98WO-US23829.
PF
XX
XX 04-NOV-1998: 98US-0185936.
PR
XX
XX 07-NOV-1997: 97US-0965789.
PR
XX
XX (GEMV ) GENETICS INST INC.
PA
XX
XX Agostino MJ, Evans C, Jacobs K, Lavallie ER, McCoy JM;
PI Werberg D, Racie LA, Treacy M;
XX
XX WPI: 1999-327362/27.
DR
XX
XX P-PSDB; AAY16784.

```

```

XX Nucleic acid encoding secreted human proteins
PT
XX
XX Claim 28; Page 97; 107pp; English.
PS
XX
XX The invention provides polynucleotides (AAX60579-X60687) encoding
CC specific secreted human proteins (AAY16779-Y16787). The nucleic acid
CC sequences are deposited under the accession number ATCC 98580. The
CC polynucleotides are used as tissue markers, chromosomal tags, for
CC diagnosis of genetic diseases, to generate anti-protein or anti-DNA
CC antibodies, also as nutritional sources and supplements and in gene
CC therapy. The secreted proteins are useful therapeutically, in human or
CC veterinary medicine, e.g. for modulating cell proliferation or
CC differentiation, as immunostimulants or immunosuppressants (for treating
CC infections, autoimmune disease, organ rejection, or to induce tumour
CC immunity), as regulators of haematopoiesis (e.g. for treating anemia or
CC in conjunction with tumour therapy), to stimulate growth of tissue for
CC wound healing, as fertility control agents, for regulating chemotaxis or
CC chemokines (e.g. for directing cells to tumours or sites of infection), as
CC haemostatic and thrombolytic agents (e.g. in treatment of haemophilia or
CC infarctions), as antimicrobial agents, for modifying biorythms,
CC appetite, or metabolism, as analgesics and many other uses. The proteins
CC are also used to raise antibodies, used as diagnostic immunoassay
CC reagents also (when neutralizing) for treating e.g. cancer.
CC
XX
XX Sequence 1354 BP; 344 A; 369 C; 287 G; 350 T; 4 other:
SQ
Query Match 75.2%; Score 15.8; DB 20; Length 1354;
Best Local Similarity 89.5%; Pred. No. 57;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 ataatggcctcgtcacac 21
1 |||||
Db 29 agaatggcctcgtcacac 47
RESULT 8
AA051427/c
ID AA051427 standard; cDNA to mRNA: 2344 BP.
XX
XX AA051427;
AC
XX
XX 20-MAY-1994 (first entry)
DT
XX
XX Human FACC cDNA clone #2.
DE
XX
XX Fanconi Anemia Group C; FACC; complementing cDNA; variant; diagnosis;
KM open reading frame; Fanconi anemia; gene therapy; ss.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 256..1935
FT CDS /tag= a
FT /product= Human FACC
FT misc-difference 1894..1896
FT /tag= b
FT /note= "Apparent duplication of CTG codon, causing the
FT polyA_signal 2325..2330 protein encoded to be one amino acid longer
than the protein given in ARA44139"
FT /tag= c
XX
XX WO9322435-A.
PN
XX
XX 11-NOV-1993.
PD
XX
XX 27-APR-1993: 93WO-CA00178.
PF
XX
XX 29-APR-1992: 92US-0876285.
PR
XX
XX 21-JUL-1992: 92US-0918313.
PR
XX
XX 15-JAN-1993: 93US-0003963.

```

XX (HOSP-) HOSPITAL FOR SICK CHILDREN.  
PA (UNME-) UNITED MEDICAL & DENTAL SCHOOL GUYS.  
XX Buchwald M, Mathew CG, Strathdee CA, Wevrick R;  
XX WPI; 1993-368794/46.  
DR P-PSDB; AAR44139.  
XX  
XX Human CDNA which complements Fanconi Anaemia gp. C - used to  
PT develop prods. for use in diagnosis, study and therapy of Fanconi  
PT Anaemia  
XX  
XX Claim 1; Page 101-04; 137pp; English.  
XX  
XX The sequences given in AA051426-28 represent CDNA variants from the  
CC Fanconi Anemia Group C Complementing (FACC) CDNA. These three CDNA  
CC molecules are cellular variants of a single CDNA transcribed from the  
CC same gene. The three cDNAs each contain an identical open reading  
CC frame encoding the FACC protein. The FACC protein may be used for  
CC the diagnosis and study of Fanconi anemia.  
XX  
SQ Sequence 2344 BP; 597 A; 594 C; 567 G; 586 T; 0 other;

Query Match 75.2%; Score 15.8; DB 14; Length 2344;  
Best Local Similarity 89.5%; Pred. No. 61;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 cataatgacctgtcaca 20  
|||  
DB 939 CAAATGGCCTGTTACA 921

## RESULT 9

AA051428/c  
ID AA051428 standard; CDNA to mRNA; 3150 BP.

AC AA051428;

XX 20-MAY-1994 (first entry)

XX Human FACC CDNA clone #3.

XX Fanconi Anemia Group C; FACC; complementing CDNA; variant; diagnosis;  
KW open reading frame; Fanconi anemia; gene therapy; ss.  
XX

OS Homo sapiens.

XX Key Location/Qualifiers

XX CDS 256..1935

XX /tag= a

XX /product= Human FACC

XX misc\_difference 1894..1896

XX /tag= b

XX /note= "Apparent duplication of CUG codon, causing the  
FT protein encoded to be one amino acid longer  
FT than the protein given in AAR44139"

FT polyA\_signal 2325..2330

FT /tag= c

FT polyA\_signal 3127..3132

FT /tag= d

XX MO9322435-A.

XX 11-NOV-1993.

XX 27-APR-1993; 93WO-CA00178.

XX 29-APR-1992; 92US-0876285.

XX 21-JUL-1992; 92US-0918313.

XX 15-JAN-1993; 93US-0003963.

PA (HOSP-) HOSPITAL FOR SICK CHILDREN.  
PA (UNME-) UNITED MEDICAL & DENTAL SCHOOL GUYS.  
XX Buchwald M, Mathew CG, Strathdee CA, Wevrick R;  
XX WPI; 1993-368794/46.  
DR P-PSDB; AAR44139.  
XX  
XX Human CDNA which complements Fanconi Anaemia gp. C - used to  
PT develop prods. for use in diagnosis, study and therapy of Fanconi  
PT Anaemia  
XX  
XX Claim 1; Page 104-07; 137pp; English.  
XX  
XX The sequences given in AA051426-28 represent CDNA variants from the  
CC Fanconi Anemia Group C Complementing (FACC) CDNA. These three CDNA  
CC molecules are cellular variants of a single CDNA transcribed from the  
CC same gene. The three cDNAs each contain an identical open reading  
CC frame encoding the FACC protein. The FACC protein may be used for  
CC the diagnosis and study of Fanconi anemia.  
XX  
SQ Sequence 3150 BP; 801 A; 772 C; 771 G; 806 T; 0 other;

Query Match 75.2%; Score 15.8; DB 14; Length 3150;  
Best Local Similarity 89.5%; Pred. No. 64;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 cataatgacctgtcaca 20  
|||  
DB 939 CAAATGGCCTGTTACA 921

## RESULT 10

AA051426/c  
ID AA051426 standard; CDNA; 4488 BP.

AC AA051426;

XX 20-MAY-1994 (first entry)

XX Human FACC CDNA clone #1.

XX Fanconi Anemia Group C; FACC; complementing CDNA; variant;  
KW open reading frame; diagnosis; Fanconi anemia; ss.  
XX

OS Homo sapiens.

XX Key Location/Qualifiers

XX CDS 174..1850

XX /tag= a

XX /product= Human FACC

XX polyA\_signal 2240..2245

XX /tag= b

XX polyA\_signal 3042..3047

XX /tag= c

XX repeat\_unit 3163..3175

XX /tag= d

XX /rpl\_type= OTHER

XX /note= "palindrome"

XX repeat\_unit 3289..3322

XX /tag= e

XX /rpl\_type= TANDEM

XX repeat\_unit 3323..4455

XX /tag= f

XX /rpl\_type= TANDEM

XX MO9322435-A.

XX 11-NOV-1993.

XX 27-APR-1993; 93WO-CA00178.

PR 29-APR-1992; 9205-0876285.  
 PR 21-JUL-1992; 9205-0918313.  
 PR 15-JAN-1993; 9305-0003963.  
 XX  
 PA (HOSP-) HOSPITAL FOR SICK CHILDREN.  
 PA (UNME-) UNITED MEDICAL & DENTAL SCHOOL GUYS.  
 PI Buchwald M, Mathew CG, Strathdee CA, Wevrick R;  
 XX  
 DR WPI; 1993-368794/46.  
 DR P-PSDB; AAR44139.  
 XX  
 PT Human cDNA which complements Fanconi Anaemia gp. C - used to  
 PT develop prods. for use in diagnosis, study and therapy of Fanconi  
 PT Anaemia  
 PS  
 XX Claim 1; Page 97-101; 137pp; English.  
 CC The sequences given in AA051426-28 represent cDNA variants from the  
 CC Fanconi Anaemia Group C Complementing (FACC) cDNA. These three cDNA  
 CC molecules are cellular variants of a single cDNA transcribed from the  
 CC same gene. The three cDNAs each contain an identical open reading  
 CC frame encoding the FACC protein. The FACC protein may be used for  
 CC the diagnosis and study of Fanconi anemia.  
 CC  
 SQ Sequence 4488 BP; 1052 A; 1092 C; 1168 G; 1176 T; 0 other;  
 XX  
 Query Match 75.2%; Score 15.8; DB 14; Length 4488;  
 Best Local Similarity 89.5%; Pred. No. 67;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 OY 2 cataatgacctgtcaca 20  
 II |||||  
 DB 857 CAAATGCGCTCGTTTACA 839  
 XX  
 RESULT 11  
 AAV33945/C  
 ID AAV33945 standard; cDNA; 4567 BP.  
 AC  
 XX AAV33945;  
 AC  
 XX  
 DT 15-FEB-1999 (first entry)  
 XX  
 DE Fanconi anaemia complementation group C (FAC) cDNA.  
 XX  
 KW Fanconi anaemia complementation group C; FAC; apoptosis;  
 KW haematopoiesis; bone marrow; chemotherapy; gene therapy; human; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FH FT 256..1929  
 FT CDS /\*tag- a  
 FT  
 FT  
 PN W09851792-A1.  
 XX  
 PD 19-NOV-1998.  
 XX  
 PE 15-MAY-1998; 98MO-US09975.  
 XX  
 PR 15-MAY-1997; 97US-0046546.  
 XX  
 PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.  
 PA  
 PI Yousoufian H;  
 XX  
 DR WPI; 1999-009774/01.  
 DR P-PSDB; AAW68546.  
 XX  
 PT New conjugate of Fanconi anaemia molecule and peptide selective for  
 PT haematopoietic precursor cells - inhibits apoptosis of these cells,  
 XX

PT for treating Fanconi anaemia and patients undergoing high-dose  
 PT chemotherapy for cancer  
 XX  
 PS Claim 6; Page 40-45; 72pp; English.  
 CC  
 CC This cDNA clone includes a coding region for human Fanconi anaemia  
 CC complementation group C (FAC; see AAW68546), a protein that modulates  
 CC apoptosis in haematopoietic progenitor cells (HPC). The invention  
 CC provides conjugates, including fusion proteins, comprising FAC  
 CC and a targeting molecule which binds to a cell surface protein of  
 CC the HPC and is internalised. Such targeting molecules include  
 CC interleukin-3 (see AAW68547) and antibodies which recognise CD33 (see  
 CC AAW6548-49). The conjugate, or a nucleic acid encoding it, can be  
 CC used to deliver FAC to an HPC, specifically to inhibit apoptosis,  
 CC particularly in patients exposed to high doses of chemotherapy for  
 CC treatment of non-myeloid cancers, also to treat Fanconi anaemia (by  
 CC complementation of the genetic defect). Treatment of HPC is done  
 CC in vitro, ex vivo (e.g. for recombinant production of conjugate in  
 CC cell cultures) or in vivo. Treatment with FAC may eliminate the  
 CC need for extensive bone marrow transplants to restore  
 CC haematopoiesis after chemotherapy.  
 CC  
 SQ Sequence 4567 BP; 1080 A; 1135 C; 1177 G; 1175 T; 0 other;  
 XX  
 Query Match 75.2%; Score 15.8; DB 20; Length 4567;  
 Best Local Similarity 89.5%; Pred. No. 68;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 OY 2 cataatgacctgtcaca 20  
 II |||||  
 DB 939 CAAATGCGCTCGTTTACA 921  
 XX  
 RESULT 12  
 AAT39622/C  
 ID AAT39622 standard; cDNA; 3417 BP.  
 AC  
 XX AAT39622;  
 AC  
 XX  
 DT 30-DEC-1996 (first entry)  
 XX  
 DE Human DNA ligase III cDNA.  
 XX  
 KW DNA ligase III; tumour; cancer; immunosuppression; diagnosis;  
 KW gene therapy; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FH FT 334..3102  
 FT CDS /\*tag- a  
 FT 1810..1812  
 FT FT /\*tag- b  
 FT FT /transl\_except- (1810..1812, aa:His)  
 FT FT /note- "CAC encodes His, as shown in Fig 1"  
 FT FT 1813..1815  
 FT FT /\*tag- c  
 FT FT /transl\_except- (1813..1815, aa:Lys)  
 FT FT /note- "AAG encodes Lys, as shown in Fig 1"  
 PN W09630524-A1.  
 XX  
 PD 03-OCT-1996.  
 XX  
 PE 31-MAR-1995; 95MO-US03939.  
 XX  
 PR 31-MAR-1995; 95MO-US03939.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA  
 PI Haseltine WA, Wei Y, Yu G;  
 XX

DR WPI: 1996-455369/45.  
DR P-PSDB: AAM05295.  
XX  
PT New isolated human DNA ligase III polynucleotide(s) - used to  
PT develop prods. for diagnosis or treatment of disorders such as  
PT tumours and severe immunosuppression  
XX  
PS Claim 6; Page 46; 78pp: English.  
XX  
CC A CDNA clone (AAT39622) codes for human DNA ligase III (AAM05295), an  
CC enzyme that repairs single strand breaks in DNA. It was isolated  
CC from a CDNA library derived from human testis, and may also be obt.  
CC from prostate, heart and thymus. The CDNA clone can be used to  
CC detect mutant DNA ligase genes, and to produce recombinant DNA  
CC ligase III in transformed host (e.g. bacterial, COS, insect) cells.  
CC It can also be used in gene therapy to treat disorders associated  
CC with a defect in DNA ligase III; antisense sequences can be used to  
CC destroy undersized (e.g. cancer) cells.  
XX  
SQ Sequence 3417 BP; 899 A; 854 C; 912 G; 752 T; 0 other;

Query Match 72.4%; Score 15.2; DB 17; Length 3417;  
Best Local Similarity 85.0%; Pred. No. 1.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 cataatggcctcgtcacac 21  
DB 2275 CATCATGGCCTCTGCACAC 2256  
||| ||||| ||||| |||||

RESULT 13  
AAV82491/C  
ID AAV82491 standard; CDNA; 3417 BP.  
XX  
AC AAV82491;  
XX  
DT 19-MAR-1999 (first entry)  
XX  
DE Human DNA ligase III encoding cDNA.  
XX  
KW Human; DNA ligase III; abnormal cellular proliferation; leukaemia;  
KW cancer; tumour; immunosuppression; stunted growth; lymphoma;  
KW cellular hypersensitivity; DNA-damaging agent; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 334..3102  
FT /\*tag= a  
XX  
PN US5858705-A.  
XX  
PD 12-JAN-1999.  
XX  
PF 05-JUN-1995; 95US-0464402.  
XX  
PR 05-JUN-1995; 95US-0464402.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Haseltine WA, Wei Y, Yu G;  
XX  
DR WPI: 1999-119875/10.  
DR P-PSDB: AAM89575.  
XX  
PT DNA that codes for the DNA ligase III polypeptide - useful for  
PT producing recombinant polypeptides  
XX  
PS Claim 14; Fig 1; 39pp; English.  
XX  
CC The present sequence encodes human DNA ligase III. Human DNA ligase III  
CC is located within bands 1/911.2-12. The human DNA ligase III gene can be

CC used to treat conditions related to insufficient human DNA ligase III  
CC activity via gene therapy by inserting the DNA ligase III into a  
CC patients cells either in vivo or ex vivo. The gene is expressed in  
CC transduced cells and as a result the protein may be used therapeutically  
CC to prevent disorders associated with defects in DNA e.g. abnormal  
CC cellular proliferation such as leukaemia, cancer and tumour; to treat  
CC severe immunosuppression; stunted growth and lymphoma, as well as  
CC cellular hypersensitivity to DNA-damaging agents.  
XX  
SQ Sequence 3417 BP; 900 A; 852 C; 912 G; 753 T; 0 other;

Query Match 72.4%; Score 15.2; DB 20; Length 3417;  
Best Local Similarity 85.0%; Pred. No. 1.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 cataatggcctcgtcacac 21  
DB 2275 CATCATGGCCTCTGCACAC 2256  
||| ||||| ||||| |||||

RESULT 14  
AAV77721/C  
ID AAV77721 standard; DNA; 9775 BP.  
XX  
AC AAV77721;  
XX  
DT 10-AUG-1999 (first entry)  
XX  
DE N. crassa his-3 cog1 lpl region DNA.  
XX  
KW Cog1: his-3; haploid; fungal cell; recombinant hot-spot; diploid;  
KW diversification; sequence diversity; heterokaryon; transfection;  
KW discontinuous conversion tract; frequency; ss.  
XX  
OS Neurospora crassa.  
XX  
PN W09927072-A1.  
XX  
PD 03-JUN-1999.  
XX  
PF 23-NOV-1998; 98WO-A000971.  
XX  
PR 24-NOV-1997; 97US-0977171.  
XX  
PA (FLIN-) FLINDERS TECHNOLOGIES PTY LTD.  
XX  
PI Catchside DE;  
XX  
DR WPI: 1999-357826/30.  
XX  
PT Haploid fungal cells comprising heterologous DNA coupled to a  
PT recombination hot spot  
XX  
PS Example 4; Fig 7; 103pp; English.  
XX

This invention describes a novel haploid fungal cell comprising a  
CC recombinant genome, comprising a heterologous DNA functionally coupled  
CC to a recombinant hot-spot. The haploid fungal cell is capable of being  
CC converted to a diploid fungal cell, where the heterologous DNA is adapted  
CC and configured in the recombinant genome for recombination in the diploid  
CC fungal cell. The methods and compositions of the invention are useful for  
CC the diversification of heterologous DNA sequences in vivo. The process  
CC generates new versions of the foreign DNA by recombining their  
CC differences in new combinations. Errors in recombination generate  
CC additional sequence diversity. The strains containing diversified  
CC heterologous sequences are used directly for expression of the variant  
CC gene or/are combined in pairwise or higher order combinations in  
CC heterokaryons where a heteromeric protein, such as an immunoglobulin is  
CC the product. The DNA variants can be derived from genes of different  
CC species having homologous genes that produce proteins with equivalent  
CC function but differing properties such as pH tolerance, thermostability  
CC and substrate range, or for monoclonal antibodies derived from different







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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 20, 2001, 23:28:18 : Search time 4309.39 Seconds  
(without alignments)  
46.065 Million cell updates/sec

Title: US-09-138-735-10  
Perfect score: 21  
Sequence: 1 acataatgcctcgttcacac 21

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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8: gb\_est8:\*  
9: gb\_est9:\*  
10: gb\_est10:\*  
11: gb\_est11:\*  
12: gb\_est12:\*  
13: gb\_est13:\*  
14: gb\_est14:\*  
15: gb\_est15:\*  
16: gb\_est16:\*  
17: gb\_est17:\*  
18: gb\_est18:\*  
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20: gb\_est20:\*  
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB       | ID        | Description          |
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| 1          | 17.8  | 84.8        | 508    | AZ109064 | RPCT-23-4 | AZ109064 RPCT-23-4   |
| 2          | 16.8  | 80.0        | 156    | BF171313 | PCL2451.M | BF171313 PCL2451.M   |
| 3          | 16.8  | 80.0        | 501    | 22       | A1588710  | A1588710 fb98e05.y   |
| 4          | 16.8  | 80.0        | 540    | 219      | CNS000CN  | AL082829 Arabidops   |
| 5          | 16.8  | 80.0        | 548    | 232      | AQ728515  | AQ728515 HS_5481_A   |
| 6          | 16.8  | 80.0        | 551    | 123      | AW993866  | AW993866 RC3-BN003   |
| 7          | 16.8  | 80.0        | 574    | 162      | BE019806  | BE019806 b559b03.y   |
| 8          | 16.8  | 80.0        | 618    | 222      | FR0008179 | FR0008179 F_rubripes |
| 9          | 16.8  | 80.0        | 674    | 228      | AQ390364  | AQ390364 CTBT-EL1    |
| 10         | 16.8  | 80.0        | 683    | 104      | A1958169  | A1958169 fc91f07.y   |
| 11         | 16.8  | 80.0        | 852    | 220      | CNS021D5  | AL213026 Tetradodon  |
| 12         | 16.8  | 80.0        | 882    | 221      | CNS03GLR  | AL243144 Tetradodon  |
| 13         | 16.4  | 78.1        | 665    | 120      | AW766833  | AW766833 da71g12.x   |
| 14         | 16.4  | 78.1        | 937    | 169      | BF793589  | BF793589 602254242   |
| 15         | 16.2  | 77.1        | 135    | 21       | A1537376  | A1537376 tp07h11.x   |
| 16         | 16.2  | 77.1        | 175    | 23       | A1708599  | A1708599 as62a04.x   |
| 17         | 16.2  | 77.1        | 182    | 19       | A1351780  | A1351780 qt09b06.x   |
| 18         | 16.2  | 77.1        | 199    | 124      | BB053373  | BB053373 BB053373    |
| 19         | 16.2  | 77.1        | 211    | 24       | A1749861  | A1749861 ac33d04.x   |
| 20         | 16.2  | 77.1        | 235    | 120      | AW793754  | AW793754 MRI-TM000   |
| 21         | 16.2  | 77.1        | 253    | 17       | A1198558  | A1198558 qf49h06.x   |
| 22         | 16.2  | 77.1        | 292    | 8        | AA483447  | AA483447 nef5909.s   |
| 23         | 16.2  | 77.1        | 298    | 24       | A1749187  | A1749187 at40d03.x   |
| 24         | 16.2  | 77.1        | 302    | 104      | A1968537  | A1968537 wt38d11.x   |
| 25         | 16.2  | 77.1        | 310    | 23       | A1708151  | A1708151 as38c05.x   |
| 26         | 16.2  | 77.1        | 318    | 103      | A1866989  | A1866989 wnl4b02.x   |
| 27         | 16.2  | 77.1        | 318    | 128      | BB208297  | BB208297 BB208297    |
| 28         | 16.2  | 77.1        | 383    | 110      | AV741908  | AV741908 AV741908    |
| 29         | 16.2  | 77.1        | 402    | 239      | A2157187  | A2157187 SP_0022_A   |
| 30         | 16.2  | 77.1        | 441    | 148      | BF431250  | BF431250 naa42h09.   |
| 31         | 16.2  | 77.1        | 447    | 142      | BE968472  | BE968472 601649532   |
| 32         | 16.2  | 77.1        | 458    | 21       | A1521229  | A1521229 t066e09.x   |
| 33         | 16.2  | 77.1        | 458    | 223      | AQ039278  | AQ039278 CTF-HSP-2   |
| 34         | 16.2  | 77.1        | 531    | 163      | BE115460  | BE115460 UT-R-B51-   |
| 35         | 16.2  | 77.1        | 554    | 22       | A1571873  | A1571873 t020e10.x   |
| 36         | 16.2  | 77.1        | 559    | 23       | A1680156  | A1680156 tw65e05.x   |
| 37         | 16.2  | 77.1        | 571    | 156      | C18439    | C18439 C18439        |
| 38         | 16.2  | 77.1        | 595    | 9        | AA574062  | AA574062 nk14d08.s   |
| 39         | 16.2  | 77.1        | 640    | 146      | BF215276  | BF215276 601846322   |
| 40         | 16.2  | 77.1        | 643    | 168      | BF694071  | BF694071 602082675   |
| 41         | 16.2  | 77.1        | 673    | 32       | AV713711  | AV713711 AV713711    |
| 42         | 16.2  | 77.1        | 708    | 24       | AV721846  | AV721846 fc26a10.y   |
| 43         | 16.2  | 77.1        | 717    | 110      | AV762205  | AV762205 AV762205    |
| 44         | 16.2  | 77.1        | 774    | 147      | BF338092  | BF338092 602035967   |
| 45         | 16.2  | 77.1        | 826    | 168      | BF690968  | BF690968 602246993   |

## ALIGNMENTS

|            |                                                                                                                                                                   |            |                            |                |             |
|------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------|----------------------------|----------------|-------------|
| RESULT 1   | AZ109064                                                                                                                                                          | 508 bp     | DNA                        | GSS            | 09-MAY-2000 |
| LOCUS      | RPCT-23-471L14.TV                                                                                                                                                 | RPCT-23    | Mus musculus genomic clone | RPCT-23-471L14 |             |
| DEFINITION | DNA sequence.                                                                                                                                                     |            |                            |                |             |
| ACCESSION  | AZ109064                                                                                                                                                          |            |                            |                |             |
| VERSION    | AZ109064.1                                                                                                                                                        | GI:7762122 |                            |                |             |
| KEYWORDS   | GSS.                                                                                                                                                              |            |                            |                |             |
| SOURCE     | house mouse.                                                                                                                                                      |            |                            |                |             |
| ORGANISM   | Mus musculus                                                                                                                                                      |            |                            |                |             |
| REFERENCE  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 508)           |            |                            |                |             |
| AUTHORS    | Zhao, S., Nierman, W., Feldblum, T., Malek, J., Shatsman, S., Alinet, B., Levins, M., McGann, S., Isegaye, G., Geer, K., Kroll, M., de Jong, P., and Fraser, C.M. |            |                            |                |             |
| TITLE      | Mouse BAC End Sequences from Library RPCT-23                                                                                                                      |            |                            |                |             |

## JOURNAL COMMENT

Unpublished (1999)  
Other GSSs: RPCT-23-471L14.TV  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhaoc@igf.org

Clones are derived from the mouse BAC library RPCT-23. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>) or from Resea ch Genetics (info@resgen.com). BAC end page: [http://www.tigr.org/tdb/bac\\_ends/mouse/bac\\_end\\_intro.html](http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html)  
plate: 471 row: L column: 14  
Seq primer: SP6  
Class: BAC ends.

FEATURES

source

1..508

Location/Qualifiers

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="RPCT-23-471L14"

/clone\_lib="RPCT-23"

/sex="Female"

/lab\_host="DH10B"

/note="Organ: Kidney/Brain; Vector: pBAC3.6; Site: 1: EcORI; Site 2: EcORI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcORI and EcoRI Methylase. Site selected DNA was cloned into the pBAC3.6 vector at the EcORI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."

## BASE COUNT

120 a 91 c 102 g 195 t

Query Match 84.8%; Score 17.8; DB 238; Length 508;  
Best Local Similarity 90.5%; Pred. No. 76;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 acataatggccttcacac 21  
|||||  
Db 215 ACATGATGCCCTTTCAC 195

|             |                                                                                                                                                                                                                                  |               |              |              |             |
|-------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------|--------------|--------------|-------------|
| RESULT 2    | BF171313                                                                                                                                                                                                                         | 156 bp        | mRNA         | EST          | 23-MAR-2001 |
| LOCUS       | PCL2451                                                                                                                                                                                                                          | Myeloma (PCL) | CDNA Library | Homo sapiens | CDNA, mRNA  |
| DEFINITION  | sequence.                                                                                                                                                                                                                        |               |              |              |             |
| ACCESSION   | BF171313                                                                                                                                                                                                                         |               |              |              |             |
| VERSION     | BF171313.1                                                                                                                                                                                                                       | GI:13437527   |              |              |             |
| KEYWORDS    | EST.                                                                                                                                                                                                                             |               |              |              |             |
| SOURCE      | human.                                                                                                                                                                                                                           |               |              |              |             |
| ORGANISM    | Homo sapiens                                                                                                                                                                                                                     |               |              |              |             |
| REFERENCE   | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 156)                                                                                   |               |              |              |             |
| AUTHORS     | Claudio, J.O., Tang, H., Khan, E.M., Vorella, M., Li, Z., Cukerman, E., Francisco-Pabalan, O., Liew, C.C. and Stewart, A.K.                                                                                                      |               |              |              |             |
| TITLE       | The transcriptional phenotype of myeloma cells                                                                                                                                                                                   |               |              |              |             |
| JOURNAL     | Unpublished (2000)                                                                                                                                                                                                               |               |              |              |             |
| COMMENT     | Contact: A. Keith Stewart, M.D.<br>Oncology Research<br>University Health Network<br>610 University Ave., 5-126, Toronto, Ontario, M5G 2M9, Canada<br>Tel: (416) 946-4639<br>Fax: (416) 946-6546<br>Email: k.stewart@utoronto.ca |               |              |              |             |
| PCR PRIMERS | FORWARD: 5'-GCCAAGCTCGAATTAACCTCCTACATAAGG-3'                                                                                                                                                                                    |               |              |              |             |

BACKWARD: 5'-CCAGTGATGTGAATACGACGTCATATAGGCGC-3'  
Seq primer: 5'-GAAATTAACCTCCTCATTAAGG-3'.  
Location/Qualifiers

# FEATURES

source

1. 156  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="Myeloma (PCL) cDNA library"  
/sex="male"  
/tissue\_type="Blood"  
/cell\_type="myeloma"  
/dev\_stage="Plasma cell leukemia"  
/note="Vector: lambda Zap Express; Site\_1: EcoRI; Site\_2: XhoI; mRNA was purified from plasma cell leukemia patient's peripheral blood containing >95% myeloma. An oligo d(T)18 primer containing XhoI restriction site was used to prime first strand synthesis using M-MLV reverse transcriptase. To protect the cDNAs from XhoI digestion in subsequent cloning step, the nucleotide analogue 5-methyl-dCTP was added to the nucleotide mixture and a-32P dATP was added to monitor the quantity and quality of first strand synthesis. After second-strand synthesis and blunting of cDNA termini, EcoRI adapters were ligated, followed by kinase treatment and digestion with XhoI. The cDNAs were then size-fractionated using Sephacryl S-500 column and then ligated into EcoRI and XhoI digested Lambda Zap Express vector. The ligation product was packaged using Gigapack II packaging extract. The library had primary titre of approx. 1x10<sup>6</sup>. Clones from the primary library were randomly selected for single pass sequencing."

BASE COUNT 34 a 41 C 48 g 33 t  
ORIGIN

Query Match 80.0%; Score 16.8; DB 145; Length 156;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 cataatgacctgctcacac 21  
|||||

Db 148 CATATAGGCTCCTGCACAC 129

## RESULT 3

LOCUS A1588710 501 bp mRNA EST 21-APR-1999  
DEFINITION FB98605.y1 zebrafish washu mpimg EST Danio rerio cDNA 5' similar to  
FB:EM11.RAT P24942 EXCITATORY AMINO ACID TRANSPORTER 1 ;, mRNA  
sequence.

ACCESSION A1588710 GI:4597757

VERSION A1588710.1

KEYWORDS EST.

SOURCE zebrafish.

ORGANISM Danio rerio

REFERENCE 1 (bases 1 to 501)  
Eukaryota: Chordata: Craniata: Vertebrata: Euteleostomi:  
Actinopterygii: Neopterygii: Teleostei: Euteleostei: Ostariophysi:  
Cypriniformes: Cyprinidae: Rasbora: Danio.

AUTHORS Clark, M., Johnson, S.L., Lehnach, H., Lee, R., Li, F., Marra, M., Eddy,  
S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood,  
K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B.,  
Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk, R., Ritter, E.,  
Kohn, S., Shih, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.  
and Wilson, R.

TITLE Washu Zebrafish EST Project 1998

JOURNAL Unpublished (1998)

COMMENT Contact: Stephen L. Johnson  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: zbrfish@wustl.edu  
CDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by:

# FEATURES

source

Matthew Clark. DNA Sequencing by: Washington University Genome  
Sequencing Center Clone distribution: Genome Systems, St. Louis,  
Missouri (web address: www.genomesystems.com) (email contact:  
info@genomesystems.com) and Research Genetics, Huntsville, Alabama  
(web address: www.resgen.com) (email contact: info@resgen.com) and  
Ressourcen/zentrum/primardatenbank, Berlin, Germany (web address:  
www.rzpd.de)  
Seq primer: T3 ET from Amersham  
High quality sequence stop: 477.  
Location/Qualifiers

1. 501  
/organism="Danio rerio"  
/db\_xref="taxon:7955"  
/clone\_lib="Zebrafish Washu MPIMG EST"  
/sex="mixed"  
/tissue\_type="26 somite embryos, adult livers, shield  
stage embryos"  
/lab\_host="X11-blue MRP"  
/note="Vector: pSPORT1; Site\_1: NotI; Site\_2: SalI; 1st  
strand cDNA was primed with a Not I - oligo(dt)18 primer  
[5'-GACATGTCCTAGATCGGAGCGCGCCCTTTTCTTTT3'];  
double-stranded cDNA was ligated to Sal I adapters (BRL),  
digested with Not I and cloned into the Not I and Sal I  
sites of the pSPORT1 vector (BRL). Library was constructed  
by Matthew Clark (Lehnach lab, ICRF, London and Max Planck  
Institut fuer Molekulare Genetik, Berlin). cDNAs for EST  
analysis were selected following oligonucleotide  
hybridization fingerprinting of arrayed clones from  
zebrafish late somitogenesis (26 ss), adult liver or  
embryonic shield stage (5.6 h) libraries. Fingerprint  
data were used to computationally cluster cDNAs, and a  
single cDNA from each cluster was chosen for sequencing.  
In some cases multiple members of the same cluster were  
sequenced to assess clustering parameters or single clones  
were sequenced additional times to assess quality  
control."

BASE COUNT 134 a 122 C 131 g 114 t  
ORIGIN

Query Match 80.0%; Score 16.8; DB 22; Length 501;  
Best Local Similarity 90.0%; Pred. No. 2.5e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 cataatgacctgctcacac 21  
|||||

Db 464 CATGATGGCTCCTGTCAGAC 445

## RESULT 4

LOCUS CNS0006N 540 bp DNA GSS 28-JUN-1999  
DEFINITION Arabidopsis thaliana genome survey sequence T7 end of BAC F5J23 of  
IGF library from strain Columbia of Arabidopsis thaliana, genomic  
survey sequence.

ACCESSION AL082829 GI:5283969

VERSION AL082829.1

KEYWORDS GSS.

SOURCE thale cress.

ORGANISM Arabidopsis thaliana

REFERENCE 1 (bases 1 to 540)  
Eukaryota: Viridiplantae: Embryophyta: Tracheophyta: Spermatophyta:  
Magnoliophyta: eudicotyledons: core eudicots: Rosidae: eurosids II:  
Brassicales: Brassicaceae: Arabidopsis.

AUTHORS Samson, D., Saurin, W., Choisme, N., Artiguenave, F., Brotlier, P., Wincker, P.,  
Salamon, D., Saurin, W., Weissbach, J. and Quetier, F.

TITLE Unpublished

JOURNAL 2 (bases 1 to 540)

REFERENCE Genoscope.

AUTHORS Direct Submission

TITLE Submitted (25-JUN-1999) Genoscope - Centre National de Sequencage :

JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

FEATURES  
Source  
Location/Qualifiers  
1. 548  
/organism="Arabidopsis thaliana"  
/strain="Columbia"  
/db\_xref="taxon:3702"  
/clone\_1ib="IGF"  
/clone="F5J23"  
/note="end : T7"  
BASE COUNT 171 a 105 c 104 g 160 t  
ORIGIN

Query Match 80.0%; Score 16.8; DB 219; Length 540;  
Best Local Similarity 90.0%; Pred. No. 2.6e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 cataatgacctgtcacac 21  
|||||  
Db 321 CATATAGCGCTGTTACTGC 340

RESULT 5  
LOCUS A0728515 548 bp DNA GSS 15-JUL-1999  
DEFINITION HS\_5481\_A2\_F05\_77A RPCI-11 Human Male BAC Library Homo sapiens  
ACCESSION A0728515  
VERSION A0728515.1 GI:5500067  
KEYWORDS GSS.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 548)  
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,  
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and  
Hood,L.  
TITLE Sequence-tagged connectors: A sequence approach to mapping and  
scanning the human genome  
JOURN. Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)  
MEDLINE 99380589  
COMMENT Contact: Mahairas GG, Wallace JC, Hood L  
High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: jwallace@u.washington.edu  
Clones are derived from the human BAC library RPCI-11. For BAC  
library availability, please contact Pieter de Jong  
(pieter@dejong.med.buffalo.edu). Clones may be purchased from  
BACPAC Resources ([http://bacpac.med.buffalo.edu/ordering\\_bac.htm](http://bacpac.med.buffalo.edu/ordering_bac.htm))  
or from Resear h Genetics (<http://www.htsc.washington.edu>)  
<http://www.htsc.washington.edu>  
Plate: 1057 row: K column: 10  
Seq primer: T7  
Class: BAC ends  
High quality sequence stop: 548.  
Location/Qualifiers  
1. 548  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="Plate=1057 Col=10 Row=K"  
/clone\_1ib="RPCI-11 Human Male BAC Library"  
/sex="Male"  
/note="Vector: pBACe3.6; Site\_1: EcoRI; Site\_2: EcoRI;  
Male blood DNA was isolated from one randomly chosen donor  
and partially digested with a combination of EcoRI and  
EcoRI Methylase. Size selected DNA was cloned into the  
pBACe3.6 vector at EcoRI sites"  
BASE COUNT 167 a 114 c 108 g 148 t 11 others  
ORIGIN

Query Match 80.0%; Score 16.8; DB 232; Length 548;  
Best Local Similarity 90.0%; Pred. No. 2.6e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 acataatgacctgtcacac 20  
|||||  
Db 425 ACATATAGCGCTGTTACACA 444

RESULT 6  
LOCUS AW93866 551 bp mRNA EST 05-JUN-2000  
DEFINITION RC3-BN0034-240400-017-a07 BN0034 Homo sapiens CDNA, mRNA sequence.  
ACCESSION AW93866  
VERSION AW93866.1 GI:8254053  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 551)  
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,  
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.  
TITLE Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
JOURN. Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
MEDLINE 20202663  
COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?cl=kt2-RC3-BN0034-240>)  
400-017-a07&cl=2000-04-24&cl=1)  
Seq primer: puc 18 forward  
High quality sequence start: 15  
High quality sequence stop: 551.  
Location/Qualifiers  
1. 551  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_1ib="BN0034"  
/dev\_stage="Adult"  
/note="Organ: breast\_normal; Vector: puc18; Site\_1: SmaI;  
Site\_2: SmaI; A mini-library was made by cloning products  
derived from ORESRES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the puc 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."  
BASE COUNT 157 a 123 c 100 g 171 t  
ORIGIN

Query Match 80.0%; Score 16.8; DB 123; Length 551;  
Best Local Similarity 90.0%; Pred. No. 2.6e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 acataatgacctgtcacac 20  
|||||  
Db 258 ACAGATAGCGCTGTTACACA 277

```

RESULT 7
LOCUS BE019806/c 574 bp mRNA EST 06-JUN-2000
DEFINITION bb59h03.y1 NIH.MGC.9 Homo sapiens cDNA clone IMAGE:3029813 5',
similar to SW:RS_MOUSE P97461 40S RIBOSOMAL PROTEIN S5. ;, mRNA
sequence.
ACCESSION BE019806
VERSION BE019806.1 GI:8279893
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 574)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@b5-remail.nih.gov
Tissue Procurement: DCTD/DTF
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
Image.lnl.gov/Image/humi/lresources.shtml
Seq primer: -40RP from Gibco
High quality sequence stop: 337.
location/Qualifiers
1. 574
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NIH-MGC.9"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: ovary; Vector: pORF7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT 133 a 105 c 165 g 110 t 1 others
ORIGIN

Query Match 80.0%; Score 16.8; DB 162; Length 574;
Best Local Similarity 90.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 cataatgacctgtcacac 21
|||||
Db 481 CATGATGCGCTGTTACAC 462

RESULT 8
LOCUS FR0008179/c 618 bp DNA GSS 02-MAR-1997
DEFINITION F.rubripes GSS sequence, clone 188G03AD3, genomic survey sequence.
ACCESSION 291989
VERSION 291989.1 GI:1869203
KEYWORDS GSS: genome survey sequence.
SOURCE Takifugu rubripes.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
REFERENCE 1 (bases 1 to 618)
AUTHORS Elgar,G., Clark,M., Smith,S., Week,S., Warner,S., Umranta,Y.,
Williams,G. and Brenner,S.

```

```

TITLE Direct Submission
JOURNAL Submitted (18-FEB-1997) MRC Human Genome Mapping Project Resource
Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hmp.mrc.ac.uk
COMMENT Vector: m13mp18
V.type: phage
PRIMER: M13
DESCR: One pass dye-terminator sequencing of cosmid cloned genomic
sequence.
FEATURES
source location/Qualifiers
1. 618
/organism="Takifugu rubripes"
/db_xref="taxon:31033"
/clone_lib="cosmid 188G03"
/clone="188G03AD3"
BASE COUNT 161 a 154 c 145 g 152 t 6 others
ORIGIN

Query Match 80.0%; Score 16.8; DB 222; Length 618;
Best Local Similarity 90.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 cataatgacctgtcacac 21
|||||
Db 269 CCTAATGCGCTGTTACAC 250

RESULT 9
LOCUS AO390364/c 674 bp DNA GSS 06-MAR-1999
DEFINITION CITBI-E1-2545M12.TF CITBI-E1 Homo sapiens genomic clone 2545M12,
DNA sequence.
ACCESSION AO390364
VERSION AO390364.1 GI:4361387
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 674)
AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
Ventor,J.C
TITLE Use of BAC End Sequences from Caltech Libraries for Sequence-Ready
Map Building
JOURNAL Unpublished (1997)
COMMENT Other_GSSs: CITBI-E1-2545M12.TF
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@ligr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.ligr.org/tldb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.
FEATURES
source location/Qualifiers
1. 674
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2545M12"
/clone_lib="CITBI-E1"
/sex="male"
/cell_type="sperm"
/note="Vector: pBeloBAC11, Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC Library D"
BASE COUNT 200 a 138 c 162 g 174 t
ORIGIN

```





RESULT 12  
LOCUS CNS03GLR 882 bp DNA GSS 17-MAY-2000  
DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone  
024H22 of library G from Tetraodon nigroviridis, genomic survey  
sequence.  
ACCESSION AL243144.1 GI:7964156  
VERSION AL243144.1  
KEYWORDS GSS; genome survey sequence.  
SOURCE Tetraodon nigroviridis.  
ORGANISM Tetraodon nigroviridis.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
Tetraodontidae; Tetraodon.  
REFERENCE 1 (bases 1 to 882)  
AUTHORS Roest-Crollius, H., Jallion, O., Dasilva, C., Fizames, C., Fisher, C.,  
Bonneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and  
Weissenbach, J.  
TITLE Characterization and repeat analysis of the compact genome of the  
freshwater pufferfish Tetraodon nigroviridis  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 882)  
AUTHORS Roest-Crollius, H., Jallion, O., Dasilva, C., Bonneau, L., Fisher, C.,  
Bernot, A., Fizames, C., Wincker, P., Brothier, P., Quetier, F.,  
Saurin, W. and Weissenbach, J.  
TITLE Human gene number estimate provided by genome wide analysis using  
Tetraodon nigroviridis DNA sequence  
JOURNAL Unpublished  
REFERENCE 3 (bases 1 to 882)  
AUTHORS Genoscope.  
TITLE Direct Submission  
JOURNAL Submitted (12-Apr-2000) to the EMBL/Genbank/DBJ databases  
COMMENT This sequence is a single read and was generated as part of a large  
scale clone-end sequencing project of the Tetraodon nigroviridis  
genome. For more information, please take a look at  
http://www.genoscope.cns.fr/Tetraodon.  
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/db\_xref="taxon:99883"  
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/clone\_1lb="G"  
/note="Genoscope sequence ID : COB024DD11LP1-end : T7"  
BASE COUNT 176 a 204 c 200 g 300 t 2 others  
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Query Match 80.0%; Score 16.8; DB 221; Length 882;  
Best Local Similarity 90.0%; Pred. No. 2.8e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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Db 270 CATCATGCGTCTGCTTCACAC 289  
RESULT 13  
LOCUS AW766833 665 bp mRNA EST 16-FEB-2001  
DEFINITION da71g12.x1 Harland strage 19-23 Xenopus laevis cDNA clone  
IMAGE:3200422.3, similar to SW:CA24\_MOUSE P08122 COLLAGEN ALPHA  
2(IV) CHAIN PRECURSOR. [1] ;, mRNA sequence.  
ACCESSION AW766833.1 GI:7698826  
VERSION AW766833  
KEYWORDS EST.  
SOURCE African clawed frog.  
ORGANISM Xenopus laevis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
Xenopodinae; Xenopus.  
REFERENCE 1 (bases 1 to 665)  
AUTHORS Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D.

TITLE Martlin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., Person  
JOURNAL B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R.,  
Waterston, R. and Wilson, R.  
COMMENT Washu Xenopus EST project, 1999  
Unpublished (1999)  
Contact: Sandy Clifton, Ph.D.  
Washu Xenopus EST project, 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: estewatson.wustl.edu  
Library constructed by R. Harland, PhD. (University of California,  
Berkeley)  
DNA sequencing by: Washington University Genome Sequencing Center  
Clone distribution: Xenopus clones from this library are available  
through the I.M.A.G.E. Consortium/LLNL at:  
image.llnl.gov/image/html/tresources.shtml  
Seq primer: -400P from Gibco  
High quality sequence stop: 459.  
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Location/Qualifiers  
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/db\_xref="taxon:8355"  
/clone="IMAGE:3200422"  
/clone\_1lb="Harland stage 19-23"  
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/dev\_stage="stage 19-23"  
/lab\_host="DH10B (phage-resistant)"  
/note="Vector: PCS107 (custom); Site\_1: NotI; Site\_2: SalI  
; cDNA made by oligo-OT priming. Library constructed by  
Dr. Francesca Martini in the laboratory of R. Harland,  
Ph.D. (University of California, Berkeley). References:  
XBF-2 is a transcriptional repressor that converts  
development into neural tissue. Martini, F.V. Harland, R.M.,  
99030283; Use of large-scale expression cloning screens in  
the Xenopus laevis tadpole to identify gene function.  
Graham TC, Liu KJ, Martini FV, Harland RM, Dev Biol.  
2000 Dec 15;228(2):197-210. PMID: 11112324; UI: 20564075;  
Note: This is a Xenopus Gene Collection (XGC) library."  
BASE COUNT 145 a 219 c 123 g 178 t  
ORIGIN  
Query Match 78.1%; Score 16.4; DB 120; Length 665;  
Best Local Similarity 94.4%; Pred. No. 4.3e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 2 cataatgacctgctcac 19  
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Db 104 CATATGCGCTCTTCAC 121  
RESULT 14  
LOCUS BF793589 937 bp mRNA EST 12-JAN-2001  
DEFINITION 602254242F1 NIH\_MGC\_84 Homo sapiens cDNA clone IMAGE:4346435 5',  
mRNA sequence.  
ACCESSION BF793589  
VERSION BF793589.1 GI:12098643  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 937)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LLM9968 row: c column: 12  
High quality sequence stop: 667.  
Location/Qualifiers

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/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
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/note="Organ: adrenal gland; Vector: PCMV-SPORT6; Site\_1:  
NotI; Site\_2: SalI; Cloned unidirectionally; oligo-dT  
primed. Average insert size 1.229 kb. Library enriched for  
full-length clones and constructed by Life Technologies.  
Note: this is a NIH\_MGC Library."  
BASE COUNT 262 a 168 c 182 g 325 t  
ORIGIN

Query Match 78.1%; Score 16.4; DB 169; Length 937;  
Best Local Similarity 94.4%; Pred. NO. 4.6e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 taatgacctgctcacac 21  
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Db 846 TATGGCCTCTTCACAC 863

RESULT 15  
AI537376 135 bp mRNA EST 13-MAY-1999  
LOCUS tp07h11.x1 NCI-CGAP-Gas4 Homo sapiens CDNA IMAGE:2187141 3'  
DEFINITION similar to TR:021697 021697 NADH DEHYDROGENASE SUBUNIT 4. ;, mRNA  
sequence.  
ACCESSION AI537376 GI:4451511  
VERSION AI537376  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 135)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaaps-r@mail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
www-bio.llnl.gov/bdrrp/image/image.html  
Insert Length: 449 Std Error: 0.00  
Seq primer: -40UP from GIBCO  
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POLYA-No.

## FEATURES

source

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/clone\_id="NCI-CGAP\_Gas4"  
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Location/Qualifiers

signet ring cell features"  
/lab\_host="DH10B"  
/note="Organ: stomach; Vector: PCMV-SPORT6; Site\_1: SalI;  
Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.69 kb. Life Technologies catalog #:  
11549-011"  
BASE COUNT 33 a 17 c 50 g 35 t  
ORIGIN

Query Match 77.1%; Score 16.2; DB 21; Length 135;  
Best Local Similarity 85.7%; Pred. NO. 4e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 acataatgacctgctcacac 21  
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Db 104 ACATAAGCCCTCAATTCACAC 84

Search completed: September 20, 2001, 23:28:33  
Job time: 25573 sec

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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 21, 2001, 02:16:39 : Search time 164.23 Seconds  
(without alignments)  
24.207 Million cell updates/sec

Title: US-09-138-735-10

Perfect score: 21

Sequence: 1 acataatgacctcttcacac 21

Scoring table: IDENTITY\_NUC

Searched: Gapop 10.0, Gapext 1.0

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_NA:\*

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- 2: /cgnl\_7/ptodata/1/ina/5B.COMB.seq:\*
- 3: /cgnl\_7/ptodata/1/ina/6A.COMB.seq:\*
- 4: /cgnl\_7/ptodata/1/ina/6B.COMB.seq:\*
- 5: /cgnl\_7/ptodata/1/ina/PCtUS.COMB.seq:\*
- 6: /cgnl\_7/ptodata/1/ina/Backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
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| 2          | 21    | 100.0       | 3402   | 1  | US-08-480-917-1    |
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| 4          | 15.8  | 75.2        | 3147   | 1  | US-08-441-430-3    |
| 5          | 15.8  | 75.2        | 4488   | 1  | US-08-441-430-1    |
| 6          | 15.2  | 72.4        | 3417   | 2  | US-08-464-402-1    |
| 7          | 15.2  | 72.4        | 9775   | 4  | US-08-977-171-1    |
| 8          | 15.2  | 72.4        | 9934   | 4  | US-08-977-171-2    |
| 9          | 14.8  | 70.5        | 2126   | 2  | US-08-789-354-1    |
| 10         | 14.8  | 70.5        | 2126   | 3  | US-09-110-937-1    |
| 11         | 14.8  | 70.5        | 2126   | 3  | US-09-058-725B-1   |
| 12         | 14.8  | 70.5        | 2126   | 3  | US-09-232-857-1    |
| 13         | 14.8  | 70.5        | 4465   | 2  | US-08-620-605D-1   |
| 14         | 14.8  | 70.5        | 4547   | 2  | US-09-005-232A-1   |
| 15         | 14.6  | 69.5        | 338    | 4  | US-08-991-789A-82  |
| 16         | 14.6  | 69.5        | 501    | 2  | US-08-454-557C-34  |
| 17         | 14.6  | 69.5        | 501    | 2  | US-08-340-426D-44  |
| 18         | 14.6  | 69.5        | 501    | 2  | US-08-450-673C-34  |
| 19         | 14.6  | 69.5        | 501    | 2  | PCT-US95-17111A-34 |
| 20         | 14.6  | 69.5        | 594    | 5  | US-08-454-557C-29  |
| 21         | 14.6  | 69.5        | 594    | 2  | US-08-340-426D-29  |
| 22         | 14.6  | 69.5        | 594    | 2  | US-08-450-673C-29  |
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| 24         | 14.6  | 69.5        | 16569  | 4  | US-09-097-889-2    |
| 25         | 14.2  | 67.6        | 270    | 2  | US-08-921-382-16   |
| 26         | 14.2  | 67.6        | 1158   | 4  | US-09-198-092-1    |
| 27         | 14.2  | 67.6        | 3240   | 4  | US-09-262-773-7    |

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|----|------|------|-------|---|--------------------|--------------------|
| 28 | 14.2 | 67.6 | 3244  | 4 | US-09-262-773-3    | Sequence 3, Appli  |
| 29 | 14.2 | 67.6 | 3264  | 4 | US-09-262-773-5    | Sequence 5, Appli  |
| 30 | 14.2 | 67.6 | 3268  | 4 | US-09-262-773-1    | Sequence 1, Appli  |
| 31 | 14.2 | 67.6 | 4652  | 2 | US-07-861-800-1    | Sequence 1, Appli  |
| 32 | 14.2 | 67.6 | 20137 | 4 | US-09-262-773-206  | Sequence 206, App  |
| 33 | 14.2 | 67.6 | 20138 | 4 | US-09-262-773-9    | Sequence 9, Appli  |
| 34 | 14.2 | 67.6 | 23071 | 4 | US-09-262-773-210  | Sequence 210, App  |
| 35 | 13.8 | 65.7 | 491   | 1 | US-08-133-711-38   | Sequence 38, Appli |
| 36 | 13.8 | 65.7 | 2047  | 4 | US-09-345-468-1    | Sequence 1, Appli  |
| 37 | 13.8 | 65.7 | 2520  | 1 | US-08-087-016-1    | Sequence 1, Appli  |
| 38 | 13.6 | 64.8 | 384   | 3 | US-09-284-782-33   | Sequence 33, Appli |
| 39 | 13.6 | 64.8 | 554   | 2 | US-08-454-557C-31  | Sequence 31, Appli |
| 40 | 13.6 | 64.8 | 554   | 2 | US-08-340-426D-31  | Sequence 31, Appli |
| 41 | 13.6 | 64.8 | 554   | 2 | US-08-450-673C-31  | Sequence 31, Appli |
| 42 | 13.6 | 64.8 | 554   | 5 | PCT-US95-17111A-31 | Sequence 31, Appli |
| 43 | 13.6 | 64.8 | 569   | 2 | US-08-485-778-5    | Sequence 5, Appli  |
| 44 | 13.6 | 64.8 | 1296  | 5 | PCT-US91-00909-5   | Sequence 5, Appli  |
| 45 | 13.6 | 64.8 | 1425  | 3 | US-09-009-494-5    | Sequence 5, Appli  |

## ALIGNMENTS

RESULT 1  
US-08-480-917-10  
Sequence 10, Application US/08480917  
Patent No. 5620864  
GENERAL INFORMATION:  
APPLICANT: PARANHOS-BACCALA, Glaucia  
APPLICANT: LESENECHAL, Mylene  
APPLICANT: JOLIVET, Michel  
TITLE OF INVENTION: NEW TRYPAANOSOMA CRUZI ANTIGEN, AND GENE  
TITLE OF INVENTION: ENCODING THE LATTER, THEIR APPLICATION TO THE DETECTION OF  
TITLE OF INVENTION: CHAGAS DISEASE  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Oliff & Berridge  
STREET: 700 South Washington Street, Suite 300  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22314  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,917  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Berridge, William P.  
REGISTRATION NUMBER: 30,024  
REFERENCE/DOCKET NUMBER: MPB 36400  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6400  
TELEFAX: 703-836-2787  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-480-917-10  
Query Match 100.0% Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0.02; Mismatches 0; Gaps 0;  
Matches 21; Conservative 0; Indels 0;

Db 1 ACATATGCGCTCGTCACAC 21

## RESULT 2

US-08-480-917-1/C  
Sequence 1, Application US/08480917  
Patent No. 5820864  
GENERAL INFORMATION:  
APPLICANT: PARANHOS-BACALA, Glaucia  
APPLICANT: LESENECHAL, Mylene  
APPLICANT: JOLIVET, Michel  
TITLE OF INVENTION: NEW TRYPAOSOMA CRUZI ANTIGEN, AND GENE  
TITLE OF INVENTION: ENCODING THE LATTER; THEIR APPLICATION TO THE DETECTION OF  
TITLE OF INVENTION: CHAGAS DISEASE  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Oliff & Berridge  
STREET: 700 South Washington Street, Suite 300  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22314  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,917  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Berridge, William P.  
REGISTRATION NUMBER: 30,024  
REFERENCE/DOCKET NUMBER: WPA 36400  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6400  
TELEFAX: 703-836-2787  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3402 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-480-917-1

Query Match 100.0%; Score 21; DB 1; Length 3402;

Best Local Similarity 100.0%; Pred. No. 0.046;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 acataatgacctcgttcacac 21  
Db 2207 ACATATGCGCTCGTCACAC 2187

## RESULT 3

US-08-441-430-2/C  
Sequence 2, Application US/08441430  
Patent No. 5681942  
GENERAL INFORMATION:  
APPLICANT: Buchwald, Manuel  
APPLICANT: Strathdee, Craig A.  
APPLICANT: Wevick, Rachel  
APPLICANT: Mathew, Christopher George Porter  
TITLE OF INVENTION: Fanconi Anemia Type C Gene  
NUMBER OF SEQUENCES: 73  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Richard J. Polley, Esq.  
ADDRESSEE: Klarquist, Sparkman, Campbell, Leigh &  
ADDRESSEE: Winston, LLP

STREET: 121 S.W. Salmon, Suite 1600  
CITY: Portland  
STATE: Oregon  
COUNTRY: U.S.A.  
ZIP: 97204

COMPUTER READABLE FORM:  
MEDIUM TYPE: Disk, 3+1-inch  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: MS DOS  
SOFTWARE: WordPerfect 5.1/ASCII Text File  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,430  
FILING DATE: May 15, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 07/876,285  
FILING DATE: April 29, 1992  
APPLICATION NUMBER: U.S. 07/918,313  
FILING DATE: July 21, 1992  
APPLICATION NUMBER: U.S. 08/003,963  
FILING DATE: January 15, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Richard J. Polley, Esq.  
REGISTRATION NUMBER: 28,107  
REFERENCE/DOCKET NUMBER: 3812-42824  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (503) 226-7391  
TELEFAX: (503) 228-9446  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2341 base pairs  
TYPE: Nucleic Acid  
STRANDEDNESS: Double stranded  
TOPOLOGY: Linear  
MOLECULE TYPE: CDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
LIBRARY: Human CDNA  
POSITION IN GENOME: (of corresponding genomic  
POSITION IN GENOME: gene)  
CHROMOSOME/SEGMENT: 9q  
MAP POSITION: 22.3  
UNITS:  
US-08-441-430-2

Query Match 75.2%; Score 15.8; DB 1; Length 2341;

Best Local Similarity 89.5%; Pred. No. 21;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 cataatgacctcgttcaca 20  
Db 939 CAAATGCGCTCGTTACA 921

## RESULT 4

US-08-441-430-3/C  
Sequence 3, Application US/08441430  
Patent No. 5681942  
GENERAL INFORMATION:  
APPLICANT: Buchwald, Manuel  
APPLICANT: Strathdee, Craig A.  
APPLICANT: Wevick, Rachel  
APPLICANT: Mathew, Christopher George Porter  
TITLE OF INVENTION: Fanconi Anemia Type C Gene  
NUMBER OF SEQUENCES: 73  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Richard J. Polley, Esq.  
ADDRESSEE: Klarquist, Sparkman, Campbell, Leigh &  
ADDRESSEE: Winston, LLP

```

1 STREET: 121 S.W. Salmon, Suite 1600
2
3 CITY: Portland
4 STATE: Oregon
5 COUNTRY: U.S.A.
6 ZIP: 97204
7
8 COMPUTER READABLE FORM:
9 MEDIUM TYPE: Disk, 3+-inch
10 COMPUTER: IBM PC compatible
11 OPERATING SYSTEM: MS DOS
12 SOFTWARE: Wordperfect 5.1/ASCII Text File
13
14 CURRENT APPLICATION DATA:
15 APPLICATION NUMBER: US/08/441.430
16 FILING DATE: May 15, 1995
17 CLASSIFICATION: 435
18
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: U.S. 07/876,285
21 FILING DATE: April 29, 1992
22 APPLICATION NUMBER: U.S. 07/918,313
23 FILING DATE: July 21, 1992
24 APPLICATION NUMBER: U.S. 08/003,963
25 FILING DATE: January 15, 1993
26 ATTORNEY/AGENT INFORMATION:
27 NAME: Richard J. Polley, Esq.
28 REGISTRATION NUMBER: 28,107
29 REFERENCE/DOCKET NUMBER: 3812-42824
30 TELECOMMUNICATION INFORMATION:
31 TELEPHONE: (503) 226-7391
32 TELEFAX: (503) 228-9446
33 INFORMATION FOR SEQ ID NO: 3:
34 SEQUENCE CHARACTERISTICS:
35 LENGTH: 3147 base pairs
36 TYPE: Nucleic Acid
37 STRANDEDNESS: Double stranded
38 TOPOLOGY: Linear
39 MOLECULE TYPE: cDNA to mRNA
40 HYPOTHETICAL: NO
41 ANTI-SENSE: NO
42 ORIGINAL SOURCE:
43 ORGANISM: Homo sapiens
44 IMMEDIATE SOURCE:
45 LIBRARY: Human cDNA
46 POSITION IN GENOME: (of corresponding genomic gene)
47 CHROMOSOME/SEGMENT: 9q
48 MAP POSITION: 22.3
49 UNITS:
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51 US-08-441-430-3
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1 CITY: Portland
2 STATE: Oregon
3 COUNTRY: U.S.A.
4 ZIP: 97204
5 COMPUTER READABLE FORM:
6 MEDIUM TYPE: Disk, 3+1/2-inch
7 OPERATING SYSTEM: MS DOS
8 SOFTWARE: WordPerfect 5.1/ASCII Text File
9 CURRENT APPLICATION DATA:
10 APPLICATION NUMBER: US/08/441.430
11 FILING DATE: May 15, 1995
12 CLASSIFICATION: 435
13 PRIOR APPLICATION DATA:
14 APPLICATION NUMBER: U.S. 07/876,285
15 FILING DATE: April 29, 1992
16 APPLICATION NUMBER: U.S. 07/918,313
17 FILING DATE: July 21, 1992
18 APPLICATION NUMBER: U.S. 08/003,963
19 FILING DATE: January 15, 1993
20 ATTORNEY/AGENT INFORMATION:
21 NAME: Richard J. Polley, Esq.
22 REGISTRATION NUMBER: 28,107
23 REFERENCE/DOCKET NUMBER: 3812-42824
24 TELECOMMUNICATION INFORMATION:
25 TELEPHONE: (503) 226-7391
26 TELEFAX: (503) 228-9446
27 INFORMATION FOR SEQ ID NO: 1:
28 SEQUENCE CHARACTERISTICS:
29 LENGTH: 4488 base pairs
30 TYPE: Nucleic Acid
31 STRANDEDNESS: Double stranded
32 TOPOLOGY: Linear
33 MOLECULE TYPE: cDNA to mRNA
34 HYPOTHETICAL: NO
35 ANTI-SENSE: NO
36 ORIGINAL SOURCE:
37 ORGANISM: Homo sapiens
38 IMMEDIATE SOURCE:
39 LIBRARY: Human cDNA
40 POSITION IN GENOME: (of corresponding genomic gene)
41 CHROMOSOME/SEGMENT: 9q
42 MAP POSITION: 22.3
43 UNITS:
44 US-08-441-430-1.
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MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WORD PERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/464,402  
FILING DATE: June 5, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/03939  
FILING DATE: 31 MAR 95  
ATTORNEY/AGENT INFORMATION:  
NAME: FERRARO, GREGORY D.  
REGISTRATION NUMBER: 36,134  
REFERENCE/DOCKET NUMBER: 325800-388  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3417 BASE PAIRS  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: LINEAR  
MOLECULE TYPE: CDNA  
US-08-464-402-1

Query Match 72.4%; Score 15.2; DB 2; Length 3417;  
Best Local Similarity 85.0%; Pred. No. 46;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 cataatgacctgcttcacac 21  
||| ||||| ||| |||||  
Db 2275 CATCATGCGCTCCTGCACAC 2256

RESULT 7  
US-08-977-171-1/c  
Sequence 1, Application US/08977171  
Patent No. 6232112  
GENERAL INFORMATION:  
APPLICANT: CATCHESIDE, DAVID E.  
TITLE OF INVENTION: REAGENTS AND METHODS FOR DIVERSIFICATION  
TITLE OF INVENTION: OF DNA  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt  
STREET: 3100 No. 6232112west Center, 90 South 7th Street  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/977,171  
FILING DATE: 24-NOV-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: SMOOG, MARK T  
REGISTRATION NUMBER: 40,178  
REFERENCE/DOCKET NUMBER: 10552.13US01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-332-5300  
TELEFAX: 612-332-9081  
TELEX:

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9775 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
US-08-977-171-1

Query Match 72.4%; Score 15.2; DB 4; Length 9775;  
Best Local Similarity 85.0%; Pred. No. 55;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 cataatgacctgcttcacac 21  
||| ||||| ||| |||||  
Db 1397 CCGAGGCGCTCCTGCACAC 1378

RESULT 8  
US-08-977-171-2/c  
Sequence 2, Application US/08977171  
Patent No. 6232112  
GENERAL INFORMATION:  
APPLICANT: CATCHESIDE, DAVID E.  
TITLE OF INVENTION: REAGENTS AND METHODS FOR DIVERSIFICATION  
TITLE OF INVENTION: OF DNA  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt  
STREET: 3100 No. 6232112west Center, 90 South 7th Street  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/977,171  
FILING DATE: 24-NOV-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: SMOOG, MARK T  
REGISTRATION NUMBER: 40,178  
REFERENCE/DOCKET NUMBER: 10552.13US01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-332-5300  
TELEFAX: 612-332-9081  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9934 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
US-08-977-171-2

Query Match 72.4%; Score 15.2; DB 4; Length 9934;  
Best Local Similarity 85.0%; Pred. No. 55;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 cataatgacctgcttcacac 21  
||| ||||| ||| |||||  
Db 1501 CCGAGGCGCTCCTGCACAC 1482



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RESULT 9
US-08-789-354-1/c
: Sequence 1, Application US/08789354
: Patent No. 5851798
: GENERAL INFORMATION:
: APPLICANT: Shabon, Usman
: APPLICANT: Bergsma, Derk
: TITLE OF INVENTION: Cloning of Human GPR14 Re
: TITLE OF INVENTION: Ceptor
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SmithKline Beecham Corporation
: STREET: 709 Swedeland Road
: CITY: King of Prussia
: STATE: PA
: COUNTRY: USA
: ZIP: 19406
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/789,354
: FILING DATE: 27-JAN-1997
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Han, William T
: REGISTRATION NUMBER: 34,344
: REFERENCE/DOCKET NUMBER: P50610
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 610-270-5219
: TELEFAX: 610-270-4026
: TELEX:
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2126 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
:
US-08-789-354-1

Query Match 70.5%; Score 14.8; DB 2; Length 2126;
Best Local Similarity 88.9%; Pred. No. 69;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 taatgacctgattcaaac 21
1 | | | | | | | | | | | | | |
bb 558 TGATGGCCTCGTCCAC 541

RESULT 10
US-09-110-937-1/c
: Sequence 1, Application US/09110937A
: Patent No. 6005074
: GENERAL INFORMATION:
: APPLICANT: SHABON, USMAN
: APPLICANT: BERGSMÄ, DERK
: TITLE OF INVENTION: CLONING OF HUMAN GPR14 RECEPTOR
: FILE REFERENCE: P50610-1
: CURRENT APPLICATION NUMBER: US/09/110,937A
: CURRENT FILING DATE: 1998-07-06
: NUMBER OF SEQ ID NOS: 2
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 1
: LENGTH: 2126
: TYPE: DNA

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: ORGANISM: 'HOMO SAPIENS'
US-09-110-937-1

Query Match          70.5%; Score 14.8; DB 3; Length 2126;
Best Local Similarity 88.9%; Pred. No. 69;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 taatgacctgcttcacac 21
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Db 558 TGATGGCCTCGTCCAC 541

RESULT 11
US-09-058-725B-1/c
Sequence 1, Application US/09058725B
Patent No. 6133420
GENERAL INFORMATION:
APPLICANT: Ames, Robert
APPLICANT: Sarau, Henry
APPLICANT: Foley, James
APPLICANT: Chamber, Jon
TITLE OF INVENTION: A Method of Finding Angonist
TITLE OF INVENTION: and Antagonist To Human and Rat GPR 14
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSES:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: <19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/058.725B
FILING DATE: April 10, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/789,354
FILING DATE: 27-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T.
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: GP50005-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
TELEFAX: 610-270-5090
TELEX:
:
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2126 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
US-09-058-725B-1

Query Match          70.5%; Score 14.8; DB 3; Length 2126;
Best Local Similarity 88.9%; Pred. No. 69;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 taatgacctgcttcacac 21
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Db 558 TGATGGCCTCGTCCAC 541

RESULT 12
US-09-232-857-1/c

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SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/005,232A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: SVENSSON, LEONARD R  
REGISTRATION NUMBER: 30,330  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)-205-8000  
TELEFAX: (703)-205-8050  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4547 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: genomic DNA  
ORIGINAL SOURCE:  
STRAIN: Serratia marcescens Str41  
US-09-005-232A-1

Query Match 70.5%; Score 14.8; DB 2; Length 4547;  
Best Local Similarity 88.9%; Pred. No. 79;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 acataatgacctgttca 18  
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Db 1534 ACATGATGCGCTGCTCA 1517

RESULT 15  
US-08-991-789A-82  
Sequence 82, Application US/08991789A  
Patent No. 6225054  
GENERAL INFORMATION:  
APPLICANT: Fridakis, Tony N.  
Smith, John M.  
Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
TREATMENT AND DIAGNOSIS OF BREAST CANCER  
NUMBER OF SEQUENCES: 292  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed IP Law Group  
STREET: 701 Fifth Avenue, Suite 6300  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/991,789A  
FILING DATE: 11-Dec-1997  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Potter, Jane E. R.  
REGISTRATION NUMBER: 33,332  
REFERENCE/DOCKET NUMBER: 210121.419C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 82:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 338 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 82:  
US-08-991-789A-82

Query Match 69.5%; Score 14.6; DB 4; Length 338;  
Best Local Similarity 81.0%; Pred. No. 65;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
OY 1 acataatgacctgttccac 21  
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Db 234 ACATAAACCTCATTCACAC 254

Search completed: September 21, 2001, 02:16:42  
Job time: 28235 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 21, 2001, 02:19:54 : Search time 6407.28 Seconds  
(without alignments)  
48.431 Million cell updates/sec

Title: US-09-138-735-10  
Perfect score: 21  
Sequence: 1 acataatgctcgttcacac 21

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 14155048 seqs, 7388405095 residues

Total number of hits satisfying chosen parameters: 28310096

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Pending\_Patents\_NA\_Main:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description          |
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| 1          | 21    | 100.0       | 21     | 13    | US-08-988-242-6      |
| 2          | 21    | 100.0       | 21     | 13    | US-09-138-736-10     |
| 3          | 21    | 100.0       | 3402   | 15    | US-08-988-242-1      |
| 4          | 21    | 100.0       | 3402   | 15    | US-09-138-736-1      |
| 5          | 17.8  | 84.8        | 654    | 48    | US-60-167-217-19923  |
| 6          | 17.8  | 84.8        | 654    | 51    | US-60-191-637-21772  |
| 7          | 17.8  | 84.8        | 654    | 51    | US-60-191-681-17179  |
| 8          | 17.8  | 84.8        | 704    | 28    | US-09-702-134-11881  |
| 9          | 17.8  | 84.8        | 849    | 48    | US-60-173-464-17842  |
| 10         | 17.8  | 84.8        | 3382   | 48    | US-60-167-217-21922  |
| 11         | 17.8  | 84.8        | 3382   | 51    | US-60-191-637-21771  |
| 12         | 17.8  | 84.8        | 3382   | 51    | US-60-191-681-17178  |
| 13         | 17.8  | 84.8        | 3577   | 49    | US-60-173-464-17841  |
| 14         | 17.8  | 84.8        | 59140  | 19    | US-09-528-2374-1266  |
| 15         | 17.4  | 82.9        | 183411 | 53    | US-60-212-664-166    |
| 16         | 16.8  | 80.0        | 41001  | 56    | US-60-248-505-68     |
| 17         | 16.8  | 80.0        | 90824  | 20    | US-09-534-859-570    |
| 18         | 16.4  | 78.1        | 253    | 25    | US-09-684-617-160878 |
| 19         | 16.4  | 78.1        | 253    | 27    | US-09-684-616-160878 |
| 20         | 16.4  | 78.1        | 405    | 23    | US-09-605-699-20540  |
| 21         | 16.4  | 78.1        | 479    | 23    | US-09-605-699-20582  |
| 22         | 16.4  | 78.1        | 144838 | 53    | US-60-212-664-236    |
| 23         | 16.2  | 77.1        | 110    | 11    | US-08-798-074-1985   |
| 24         | 16.2  | 77.1        | 108    | 11    | PCT-US01-01334-1199  |
| 25         | 16.2  | 77.1        | 192    | 11    | US-08-798-074-1726   |
| 26         | 16.2  | 77.1        | 192    | 11    | US-08-798-074-1726   |
| 27         | 16.2  | 77.1        | 265    | 52    | US-09-628-858-604    |
| 28         | 16.2  | 77.1        | 265    | 54    | US-60-208-063-2221   |
| 29         | 16.2  | 77.1        | 267    | 51    | US-60-196-868-10176  |
| 30         | 16.2  | 77.1        | 392    | 25    | US-09-654-617-407207 |
| 31         | 16.2  | 77.1        | 392    | 27    | US-09-684-016-407207 |
| 32         | 16.2  | 77.1        | 478    | 19    | US-09-527-429-786    |
| 33         | 16.2  | 77.1        | 718    | 19    | US-09-644-871-6164   |
| 34         | 16.2  | 77.1        | 995    | 50    | US-60-182-316-337    |
| 35         | 16.2  | 77.1        | 2315   | 51    | US-60-173-464-9902   |
| 36         | 16.2  | 77.1        | 2315   | 51    | US-60-191-637-12205  |
| 37         | 16.2  | 77.1        | 2318   | 48    | US-60-191-681-15275  |
| 38         | 16.2  | 77.1        | 2318   | 48    | US-60-167-217-12139  |
| 39         | 16.2  | 77.1        | 4731   | 51    | US-60-173-464-9901   |
| 40         | 16.2  | 77.1        | 4731   | 51    | US-60-191-637-12204  |
| 41         | 16.2  | 77.1        | 4734   | 48    | US-60-191-681-9576   |
| 42         | 16.2  | 77.1        | 8886   | 54    | US-60-167-217-12198  |
| 43         | 16.2  | 77.1        | 17116  | 24    | US-09-620-392-41892  |
| 44         | 16.2  | 77.1        | 17116  | 53    | US-60-215-161-2406   |
| 45         | 16.2  | 77.1        | 17116  | 53    | US-60-215-161-2407   |
|            |       |             |        |       | US-60-215-161-2408   |

## ALIGNMENTS

## RESULT 1

US-08-988-242-6

Sequence 6, Application US/08988242  
GENERAL INFORMATION:  
APPLICANT: PARANHOS-BACCALA, GLAUCIA  
APPLICANT: LESENECHAL, MYLENE  
APPLICANT: JOLIVET, MICHEL  
APPLICANT: MANDRAND, BERNARD  
TITLE OF INVENTION: NEW TRYPANOSOMA CRUZI ANTIGEN, GENE  
TITLE OF INVENTION: ENCODING THEREFOR, AND METHODS OF DETECTING AND TREATING  
TITLE OF INVENTION: CHAGAS DISEASE  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OLIVIER & BERRIDGE, PLC  
STREET: P.O. BOX 19928  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22320

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/988,242  
FILING DATE: 10-DEC-1997  
CLASSIFICATION: 435

## ATTORNEY/AGENT INFORMATION:

NAME: Berridge, William P.  
REGISTRATION NUMBER: 30,024  
REFERENCE/DOCKET NUMBER: WPB 36400A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6400  
TELEFAX: 703-836-2787

## INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-988-242-6

Query Match 100.0%; Score 21; DB 13; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.85; Mismatches 0; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 acataatgcctcgttcacac 21  
Db 1 ACATAATGCCTCGTTCACAC 21

## RESULT 2

US-09-138-736-10

Sequence 10, Application US/09138736

GENERAL INFORMATION:

APPLICANT: PARANHOS-BACCALA, GLAUCIA  
APPLICANT: LESENECHAL, MYLENE  
APPLICANT: JOLIVET, MICHEL

TITLE OF INVENTION: NEW TRYPANOSOMA CRUZI ANTIGEN, AND GENE  
TITLE OF INVENTION: ENCODING THE LATWER, THEIR APPLICATION TO THE DETECTION OF

NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Olivier & Berridge

STREET: 700 South Washington Street, Suite 300  
CITY: Alexandria

STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22314

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/138,736  
FILING DATE:

## CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/480,917  
FILING DATE: 07-JUN-1995

## ATTORNEY/AGENT INFORMATION:

NAME: Berridge, William P.  
REGISTRATION NUMBER: 30,024  
REFERENCE/DOCKET NUMBER: WPB 36400  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6400  
TELEFAX: 703-836-2787

## INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-138-736-10

Query Match 100.0%; Score 21; DB 15; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.85; Mismatches 0; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 acataatgcctcgttcacac 21  
Db 1 ACATAATGCCTCGTTCACAC 21

## RESULT 3

US-08-988-242-1/C

Sequence 1, Application US/08988242

GENERAL INFORMATION:

APPLICANT: PARANHOS-BACCALA, GLAUCIA  
APPLICANT: LESENECHAL, MYLENE  
APPLICANT: JOLIVET, MICHEL

TITLE OF INVENTION: NEW TRYPANOSOMA CRUZI ANTIGEN, GENE  
TITLE OF INVENTION: ENCODING THEREFOR, AND METHODS OF DETECTING AND TREATING

NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:

ADDRESSEE: OLIVIER & BERRIDGE, PLC  
STREET: P.O. BOX 19928

CITY: Alexandria  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22320

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/988,242  
FILING DATE: 10-DEC-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Berridge, William P.  
REGISTRATION NUMBER: 30,024  
REFERENCE/DOCKET NUMBER: WPB 36400A

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6400  
TELEFAX: 703-836-2787  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3402 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-988-242-1

Query Match 100.0%; Score 21; DB 13; Length 3402;  
Best Local Similarity 100.0%; Pred. No. 1.8;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 acataatgctcgttcacac 21  
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DB 2207 ACATAATGCGCTCGTTACAC 2187

RESULT 4  
US-09-138-736-1/c  
Sequence 1, Application US/09138736  
GENERAL INFORMATION:  
APPLICANT: PARANHOS-BACCALA, Glaucia  
APPLICANT: LESENECHAL, Mylene  
TITLE OF INVENTION: NEW TRYPANOSOMA CRUZI ANTIGEN, AND GENE  
TITLE OF INVENTION: ENCODING THE LATTER, THEIR APPLICATION TO THE DETECTION OF  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRES:  
ADDRESSEE: Oliff & Berridge  
STREET: 700 South Washington Street, Suite 300  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22314

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/138,736  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/480,917  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Berridge, William P.  
REGISTRATION NUMBER: 30,024  
REFERENCE/DOCKET NUMBER: WPB 36400  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6400  
TELEFAX: 703-836-2787

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3402 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-09-138-736-1

Query Match 100.0%; Score 21; DB 15; Length 3402;  
Best Local Similarity 100.0%; Pred. No. 1.8;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 acataatgctcgttcacac 21  
|||||  
DB 2207 ACATAATGCGCTCGTTACAC 2187

RESULT 5  
US-60-167-217-21923  
Sequence 21923, Application US/60167217  
GENERAL INFORMATION:  
APPLICANT: LI, Peter W. D.  
TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC  
TITLE OF INVENTION: ACID MOLECULES ENCODING DROSOPHILA PROTEINS, AND USES  
FILE REFERENCE: C1000152  
CURRENT APPLICATION NUMBER: US/60/167,217  
CURRENT FILING DATE: 1999-11-24  
NUMBER OF SEQ ID NOS: 23195  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 21923  
LENGTH: 654  
TYPE: DNA  
ORGANISM: Drosophila  
US-60-167-217-21923

Query Match 84.8%; Score 17.8; DB 48; Length 654;  
Best Local Similarity 90.5%; Pred. No. 73;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 acataatgctcgttcacac 21  
|||||  
DB 546 acataatgctcgttcacac 566

RESULT 6  
US-60-191-637-21772  
Sequence 21772, Application US/60191637  
GENERAL INFORMATION:  
APPLICANT: Venter, J. Craig  
TITLE OF INVENTION: NUCLEIC ACID DETECTION KITS COMPRISING  
TITLE OF INVENTION: GENE SEQUENCES EXPRESSED FROM THE DROSOPHILA GENOME, AND  
FILE REFERENCE: C1000392  
CURRENT APPLICATION NUMBER: US/60/191,637  
CURRENT FILING DATE: 2000-03-23  
NUMBER OF SEQ ID NOS: 42660  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 21772  
LENGTH: 654  
TYPE: DNA  
ORGANISM: DROSOPHILA  
US-60-191-637-21772

Query Match 84.8%; Score 17.8; DB 51; Length 654;  
Best Local Similarity 90.5%; Pred. No. 73;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 acataatgctcgttcacac 21  
|||||  
DB 546 acataatgctcgttcacac 566

RESULT 7  
US-60-191-681-17179  
Sequence 17179, Application US/60191681  
GENERAL INFORMATION:  
APPLICANT: LI, Peter, W.D.  
TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC  
TITLE OF INVENTION: ACID MOLECULES ENCODING ISOLATED DROSOPHILA PROTEINS AND  
FILE REFERENCE: C1000390  
CURRENT APPLICATION NUMBER: US/60/191,681

;; CURRENT FILING DATE: 2000-03-23  
;; NUMBER OF SEQ ID NOS: 30973  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 17179  
;; LENGTH: 654  
;; TYPE: DNA  
;; ORGANISM: DROSOPHILA  
US-60-191-681-17179

Query Match 84.8%; Score 17.8; DB 51; Length 654;  
Best Local Similarity 90.5%; Pred. No. 73;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 acataatgctcgttcacac 21  
||||| ||||| ||||| ||||| |||||  
Db 546 acatgatgcctcgttcacac 566

RESULT 8  
US-09-702-134-41881/C  
; Sequence 41881, Application US/09702134  
; GENERAL INFORMATION:  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Kovacic, David K.  
; APPLICANT: Liu, Jingdong  
; APPLICANT: McIninch, James  
; APPLICANT: Wu, Wei  
; TITLE OF INVENTION: Plant Genome Sequence and Uses Thereof  
; FILE REFERENCE: 38-21(51237)F  
; CURRENT APPLICATION NUMBER: US/09/702.134  
; CURRENT FILING DATE: 2000-10-31  
; NUMBER OF SEQ ID NOS: 52202  
; SEQ ID NO 41881  
; LENGTH: 704  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
US-09-702-134-41881

Query Match 84.8%; Score 17.8; DB 28; Length 704;  
Best Local Similarity 90.5%; Pred. No. 74;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 acataatgctcgttcacac 21  
||||| ||||| ||||| ||||| |||||  
Db 248 ACATTAAGGCGCTCGTTCATC 228

RESULT 9  
US-60-173-464-17842  
; Sequence 17842, Application US/60173464  
; GENERAL INFORMATION:  
; APPLICANT: Li, Peter W. D.  
; TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS AND USES  
; FILE REFERENCE: CL000173  
; CURRENT APPLICATION NUMBER: US/60/173.464  
; CURRENT FILING DATE: 1999-12-29  
; NUMBER OF SEQ ID NOS: 30269  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17842  
; LENGTH: 849  
; TYPE: DNA  
; ORGANISM: Drosophila  
US-60-173-464-17842

Query Match 84.8%; Score 17.8; DB 49; Length 849;  
Best Local Similarity 90.5%; Pred. No. 76;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 acataatgctcgttcacac 21  
||||| ||||| ||||| ||||| |||||  
Db 546 acatgatgcctcgttcacac 566

RESULT 10  
US-60-167-217-21922/C  
; Sequence 21922, Application US/60167217  
; GENERAL INFORMATION:  
; APPLICANT: Li, Peter W. D.  
; TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING DROSOPHILA PROTEINS, AND USES  
; FILE REFERENCE: CL000152  
; CURRENT APPLICATION NUMBER: US/60/167.217  
; CURRENT FILING DATE: 1999-11-24  
; NUMBER OF SEQ ID NOS: 23195  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 21922  
; LENGTH: 3382  
; TYPE: DNA  
; ORGANISM: Drosophila  
US-60-167-217-21922

Query Match 84.8%; Score 17.8; DB 48; Length 3382;  
Best Local Similarity 90.5%; Pred. No. 93;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 acataatgctcgttcacac 21  
||||| ||||| ||||| ||||| |||||  
Db 1109 ACATGATGCATCGTTCACAC 1089

RESULT 11  
US-60-191-637-21771/C  
; Sequence 21771, Application US/60191637  
; GENERAL INFORMATION:  
; APPLICANT: Venter, J. Craig  
; TITLE OF INVENTION: NUCLEIC ACID DETECTION KITS COMPRISING  
; TITLE OF INVENTION: GENE SEQUENCES EXPRESSED FROM THE DROSOPHILA GENOME, AND  
; FILE REFERENCE: CL000392  
; CURRENT APPLICATION NUMBER: US/60/191.637  
; CURRENT FILING DATE: 2000-03-23  
; NUMBER OF SEQ ID NOS: 42660  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 21771  
; LENGTH: 3382  
; TYPE: DNA  
; ORGANISM: DROSOPHILA  
US-60-191-637-21771

Query Match 84.8%; Score 17.8; DB 51; Length 3382;  
Best Local Similarity 90.5%; Pred. No. 93;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 acataatgctcgttcacac 21  
||||| ||||| ||||| ||||| |||||  
Db 1109 ACATGATGCATCGTTCACAC 1089

RESULT 12  
US-60-191-681-17178/C  
; Sequence 17178, Application US/60191681  
; GENERAL INFORMATION:  
; APPLICANT: Li, Peter W. D.  
; TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING ISOLATED DROSOPHILA PROTEINS AND  
; FILE REFERENCE: CL000390



; CURRENT APPLICATION NUMBER: US/60/191,681  
; CURRENT FILING DATE: 2000-03-23  
; NUMBER OF SEQ ID NOS: 30973  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17178  
; LENGTH: 3382  
; TYPE: DNA  
; ORGANISM: DROSOPHILA  
US-60-191-681-17178

Query Match 84.8%; Score 17.8; DB 51; Length 3382;  
Best Local Similarity 90.5%; Pred. No. 93;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 acataatggcctcgctcacac 21  
||||| ||||| ||||| ||||| |||||  
Db 1109 ACATGATGCGCATGTTCCACAC 1089

RESULT 13  
US-60-173-464-17841/C  
; Sequence 17841, Application US/60173464  
; GENERAL INFORMATION:  
; APPLICANT: Li, Peter W.D.  
; TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CLO00173  
; CURRENT APPLICATION NUMBER: US/60/173,464  
; CURRENT FILING DATE: 1999-12-29  
; NUMBER OF SEQ ID NOS: 30269  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17841  
; LENGTH: 3577  
; TYPE: DNA  
; ORGANISM: Drosophila  
US-60-173-464-17841

Query Match 84.8%; Score 17.8; DB 49; Length 3577;  
Best Local Similarity 90.5%; Pred. No. 94;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 acataatggcctcgctcacac 21  
||||| ||||| ||||| ||||| |||||  
Db 1304 ACATGATGCGCATGTTCCACAC 1284

RESULT 14  
US-09-528-237A-1266  
; Sequence 1266, Application US/09528237A  
; GENERAL INFORMATION:  
; APPLICANT: Venter, J. Craig  
; TITLE OF INVENTION: The Drosophila Genome, Primary Nucleic  
; TITLE OF INVENTION: Acid Sequences, Systems Containing The Nucleic Acid  
; TITLE OF INVENTION: Sequences and Uses Thereof  
; FILE REFERENCE: CLO00284  
; CURRENT APPLICATION NUMBER: US/09/528,237A  
; CURRENT FILING DATE: 2000-03-17  
; NUMBER OF SEQ ID NOS: 2926  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1266  
; LENGTH: 59140  
; TYPE: DNA  
; ORGANISM: Drosophila  
US-09-528-237A-1266

Query Match 84.8%; Score 17.8; DB 19; Length 59140;  
Best Local Similarity 90.5%; Pred. No. 1,4e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 acataatggcctcgctcacac 21  
||||| ||||| ||||| ||||| |||||  
Db 32318 acatgatgcatgcttcacac 32338

RESULT 15  
US-60-212-664-166/C  
; Sequence 166, Application US/60212664  
; GENERAL INFORMATION:  
; APPLICANT: Ladunga, Steve  
; APPLICANT: Spier, Gene  
; APPLICANT: Greenberg, Simon  
; APPLICANT: Rabkin, Steven  
; APPLICANT: Wang, Yu  
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CLO00687  
; CURRENT APPLICATION NUMBER: US/60/212,664  
; CURRENT FILING DATE: 2000-06-20  
; NUMBER OF SEQ ID NOS: 636  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 166  
; LENGTH: 183411  
; TYPE: DNA  
; ORGANISM: HUMAN  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(183411)  
; OTHER INFORMATION: n = A,T,C or G  
US-60-212-664-166

Query Match 82.9%; Score 17.4; DB 53; Length 183411;  
Best Local Similarity 94.7%; Pred. No. 2.7e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 cataatggcctcgctcacac 20  
||||| ||||| ||||| ||||| |||||  
Db 115270 CATATGCGCTCGTTCAAA 115252

Search completed: September 21, 2001, 02:20:06  
Job time: 30478 sec

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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 21, 2001, 02:39:25 : Search time 1035.34 Seconds  
(without alignments)  
40.480 Million cell updates/sec

Title: US-09-138-735-10

Perfect score: 21

Sequence: 1 acataatgcccgttcacac 21

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1741792 seqs, 997871973 residues

Total number of hits satisfying chosen parameters: 3483584

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending\_Patents\_NA\_New:\*  
1: /cgnl\_7/ptodata/2/pna/PCr\_NEW\_COMB.seq:\*  
2: /cgnl\_7/ptodata/2/pna/US06\_NEW\_COMB.seq:\*  
3: /cgnl\_7/ptodata/2/pna/US07\_NEW\_COMB.seq:\*  
4: /cgnl\_7/ptodata/2/pna/US08\_NEW\_COMB.seq:\*  
5: /cgnl\_7/ptodata/2/pna/US09\_NEW\_COMB.seq:\*  
6: /cgnl\_7/ptodata/2/pna/US09\_NEW\_COMB.seq1:\*  
7: /cgnl\_7/ptodata/2/pna/US09\_NEW\_COMB.seq2:\*  
8: /cgnl\_7/ptodata/2/pna/US60\_NEW\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length  | DB ID | Description         |
|------------|-------|-------------|---------|-------|---------------------|
| 1          | 21    | 100.0       | 21      | 6     | US-09-138-735-10    |
| 2          | 21    | 100.0       | 3402    | 6     | US-09-138-735-1     |
| 3          | 16.8  | 80.0        | 90824   | 6     | US-09-803-736-570   |
| 4          | 16.4  | 78.1        | 227     | 8     | US-60-253-378-23517 |
| 5          | 16.4  | 78.1        | 285     | 8     | US-60-253-378-22541 |
| 6          | 16.4  | 78.1        | 320     | 8     | US-60-253-456-24803 |
| 7          | 16.4  | 78.1        | 1503841 | 6     | US-09-795-686-1     |
| 8          | 16.2  | 77.1        | 108     | 4     | US-08-798-074B-1985 |
| 9          | 16.2  | 77.1        | 108     | 4     | US-08-798-074B-1985 |
| 10         | 16.2  | 77.1        | 108     | 4     | US-08-798-074C-1985 |
| 11         | 16.2  | 77.1        | 110     | 7     | US-09-764-874-1199  |
| 12         | 16.2  | 77.1        | 149     | 4     | US-08-798-074B-1726 |
| 13         | 16.2  | 77.1        | 149     | 4     | US-08-798-074B-1726 |
| 14         | 16.2  | 77.1        | 149     | 4     | US-08-798-074C-1726 |
| 15         | 15.8  | 75.2        | 326     | 7     | US-09-834-366-48084 |
| 16         | 15.8  | 75.2        | 403     | 8     | US-60-253-652-15179 |
| 17         | 15.8  | 75.2        | 451     | 7     | US-09-834-366-50522 |
| 18         | 15.8  | 75.2        | 99008   | 6     | US-09-803-736-1399  |
| 19         | 15.4  | 73.3        | 421     | 7     | US-09-834-366-11277 |
| 20         | 15.4  | 73.3        | 452     | 6     | US-09-909-629-19092 |
| 21         | 15.4  | 73.3        | 454     | 6     | US-09-909-627-1543  |
| 22         | 15.4  | 73.3        | 794     | 6     | US-09-808-383-5722  |
| 23         | 15.4  | 73.3        | 95173   | 6     | US-09-803-736-1184  |
| 24         | 15.4  | 73.3        | 105680  | 6     | US-09-803-736-545   |
| 25         | 15.4  | 73.3        | 187892  | 6     | US-09-803-110-208   |

|      |      |      |      |   |                     |                   |
|------|------|------|------|---|---------------------|-------------------|
| c 26 | 15.2 | 72.4 | 257  | 8 | US-60-253-456-6471  | Sequence 6471, Ap |
| c 27 | 15.2 | 72.4 | 288  | 6 | US-09-866-555-2028  | Sequence 2028, Ap |
| c 28 | 15.2 | 72.4 | 296  | 7 | US-09-867-716-2330  | Sequence 2330, Ap |
| c 29 | 15.2 | 72.4 | 348  | 7 | US-09-867-716-15052 | Sequence 15052, A |
| c 30 | 15.2 | 72.4 | 376  | 1 | PCT-US01-18569-1889 | Sequence 1889, Ap |
| c 31 | 15.2 | 72.4 | 377  | 8 | US-60-256-867-486   | Sequence 486, Ap  |
| c 32 | 15.2 | 72.4 | 402  | 8 | US-60-253-457-43854 | Sequence 43854, A |
| c 33 | 15.2 | 72.4 | 410  | 6 | US-09-799-435-1341  | Sequence 1341, Ap |
| c 34 | 15.2 | 72.4 | 425  | 6 | US-09-909-637-14034 | Sequence 14034, A |
| c 35 | 15.2 | 72.4 | 470  | 6 | US-09-796-632-5529  | Sequence 5529, Ap |
| c 36 | 15.2 | 72.4 | 508  | 8 | US-60-253-652-24830 | Sequence 24830, A |
| c 37 | 15.2 | 72.4 | 598  | 8 | US-60-253-651-22731 | Sequence 22731, A |
| c 38 | 15.2 | 72.4 | 637  | 7 | US-09-910-689-189   | Sequence 189, Ap  |
| c 39 | 15.2 | 72.4 | 707  | 7 | US-09-867-716-19160 | Sequence 19160, A |
| c 40 | 15.2 | 72.4 | 717  | 7 | US-09-824-518-312   | Sequence 312, Ap  |
| c 41 | 15.2 | 72.4 | 1046 | 8 | US-60-312-544-4380  | Sequence 4380, Ap |
| c 42 | 15.2 | 72.4 | 1968 | 6 | US-09-764-891-7620  | Sequence 7620, Ap |
| c 43 | 15.2 | 72.4 | 3417 | 6 | US-09-879-228-1     | Sequence 1, Appl  |
| c 44 | 15.2 | 72.4 | 3456 | 6 | US-09-764-856-42    | Sequence 42, Appl |
| c 45 | 15.2 | 72.4 | 4208 | 8 | US-60-278-258-4178  | Sequence 4178, Ap |

#### ALIGNMENTS

```
RESULT 1
US-09-138-735-10
; Sequence 10, Application US/09138735
; GENERAL INFORMATION:
; APPLICANT: PARANHOS-BACCALA, Glaucia
; APPLICANT: LESENECHAL, Mylene
; APPLICANT: JOLIVER, Michel
; TITLE OF INVENTION: TRYPANOSOMA CRUZI ANTIGEN, GENE ENCODING THEREFOR AND METHODS
; FILE REFERENCE: WPB 36400B
; CURRENT APPLICATION NUMBER: US/09/138,735
; PRIOR FILING DATE: 1998-08-24
; PRIOR APPLICATION NUMBER: US 08/480,917
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: FR 94/10132
; PRIOR FILING DATE: 1994-08-12
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: probe/primer
US-09-138-735-10

Query Match 100.0%; Score 21; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 acataatgcccgttcacac 21
Db 1 acataatgcccgttcacac 21

RESULT 2
US-09-138-735-1/c
; Sequence 1, Application US/09138735
; GENERAL INFORMATION:
; APPLICANT: PARANHOS-BACCALA, Glaucia
; APPLICANT: LESENECHAL, Mylene
; APPLICANT: JOLIVER, Michel
; TITLE OF INVENTION: TRYPANOSOMA CRUZI ANTIGEN, GENE ENCODING THEREFOR AND METHODS
; FILE REFERENCE: WPB 36400B
; CURRENT APPLICATION NUMBER: US/09/138,735
; CURRENT FILING DATE: 1998-08-24
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PRIOR APPLICATION NUMBER: US 08/480,917  
PRIOR FILING DATE: 1995-06-07  
PRIOR APPLICATION NUMBER: FR 94/10132  
PRIOR FILING DATE: 1994-08-12  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 1  
LENGTH: 3402  
TYPE: DNA  
ORGANISM: Trypanosoma cruzi  
US-09-138-735-1

Query Match 100.0%; Score 21; DB 6; Length 3402;  
Best Local Similarity 100.0%; Pred. No. 0.24;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 acataatgacctgcttcacac 21  
DB 2207 ACATTAATGGCCTCGTTCACAC 2187

RESULT 3  
US-09-803-736-570/c  
Sequence 570, Application US/09803736  
GENERAL INFORMATION:  
APPLICANT: Bush, David F.  
APPLICANT: Levin, Irena M.  
APPLICANT: Norris, Susan R.  
APPLICANT: Rounsley, Steven D.  
APPLICANT: Wiegand, Roger C.  
TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof  
FILE REFERENCE: 38-10(15493)D  
CURRENT APPLICATION NUMBER: US/09/803,736  
CURRENT FILING DATE: 2001-03-12  
PRIOR APPLICATION NUMBER: US 09/534,859  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: Identified by Attorney Docket number 04983.0206CPUS01 38-10  
PRIOR FILING DATE: 2000-10-20  
NUMBER OF SEQ ID NOS: 1582  
SEQ ID NO 570  
LENGTH: 90824  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
US-09-803-736-570

Query Match 80.0%; Score 16.8; DB 6; Length 90824;  
Best Local Similarity 90.0%; Pred. No. 75;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 cataatgacctgcttcacac 21  
DB 43650 CATTAATGGCCTCGTTCACAC 43631

RESULT 4  
US-60-253-378-23517/c  
Sequence 23517, Application US/60253378  
GENERAL INFORMATION:  
APPLICANT: Havukkala, Ilkka J  
TITLE OF INVENTION: Polynucleotides isolated from plants  
TITLE OF INVENTION: and methods for their use.  
FILE REFERENCE: 1054P3  
CURRENT APPLICATION NUMBER: US/60/253,378  
CURRENT FILING DATE: 2000-11-27  
NUMBER OF SEQ ID NOS: 40367  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 23517  
LENGTH: 227  
TYPE: DNA  
ORGANISM: Pinus radiata  
US-60-253-378-23517

Query Match 78.1%; Score 16.4; DB 8; Length 227;  
Best Local Similarity 94.4%; Pred. No. 44;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 taatgacctgcttcacac 21  
DB 102 TAATGGCCTCGTTCACAC 85

RESULT 5  
US-60-253-378-22541/c  
Sequence 22541, Application US/60253378  
GENERAL INFORMATION:  
APPLICANT: Havukkala, Ilkka J  
TITLE OF INVENTION: Polynucleotides isolated from plants  
TITLE OF INVENTION: and methods for their use.  
FILE REFERENCE: 1054P3  
CURRENT APPLICATION NUMBER: US/60/253,378  
CURRENT FILING DATE: 2000-11-27  
NUMBER OF SEQ ID NOS: 40367  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 22541  
LENGTH: 285  
TYPE: DNA  
ORGANISM: Pinus radiata  
US-60-253-378-22541

Query Match 78.1%; Score 16.4; DB 8; Length 285;  
Best Local Similarity 94.4%; Pred. No. 46;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 taatgacctgcttcacac 21  
DB 102 TAATGGCCTCGTTCACAC 85

RESULT 6  
US-60-253-456-24803/c  
Sequence 24803, Application US/60253456  
GENERAL INFORMATION:  
APPLICANT: Havukkala, Ilkka J  
TITLE OF INVENTION: Polynucleotides, isolated from  
TITLE OF INVENTION: plants, and methods for their use.  
FILE REFERENCE: 1054P1  
CURRENT APPLICATION NUMBER: US/60/253,456  
CURRENT FILING DATE: 2000-11-27  
NUMBER OF SEQ ID NOS: 37096  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 24803  
LENGTH: 320  
TYPE: DNA  
ORGANISM: Pinus radiata  
US-60-253-456-24803

Query Match 78.1%; Score 16.4; DB 8; Length 320;  
Best Local Similarity 94.4%; Pred. No. 47;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 taatgacctgcttcacac 21  
DB 19 TAATGGCCTCGTTCACAC 2

RESULT 7  
US-09-795-686-1  
Sequence 1, Application US/09795686  
GENERAL INFORMATION:  
APPLICANT: Stefansson, Hreinn  
APPLICANT: Steinhorsdottir, Valgerdur

```

1  APPLICANT: Gulcher, Jeffrey R.
2  TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
3  FILE REFERENCE: 2345 2005-001
4  CURRENT APPLICATION NUMBER: US/09/795,686
5  CURRENT FILING DATE: 2001-02-28
6  PRIOR APPLICATION NUMBER: US 09/515,715
7  PRIOR FILING DATE: 2000-02-28
8  NUMBER OF SEQ ID NOS: 1531
9  SOFTWARE: FASTSEQ for Windows Version 4.0
10 SEQ ID NO 1
11 LENGTH: 1503841
12 TYPE: DNA
13 ORGANISM: Homo sapiens
14 FEATURE:
15 NAME/KEY: misc_feature
16 LOCATION: (1)...(1531)
17 OTHER INFORMATION: r-g or a
18 NAME/KEY: misc_feature
19 LOCATION: (1)...(1531)
20 OTHER INFORMATION: y-t/u or c
21 NAME/KEY: misc_feature
22 LOCATION: (1)...(1531)
23 OTHER INFORMATION: m-a or c
24 NAME/KEY: misc_feature
25 LOCATION: (1)...(1531)
26 OTHER INFORMATION: k-g or t/u
27 NAME/KEY: misc_feature
28 LOCATION: (1)...(1531)
29 OTHER INFORMATION: s-g or c
30 NAME/KEY: misc_feature
31 LOCATION: (1)...(1531)
32 OTHER INFORMATION: w-a or t/u
33 NAME/KEY: misc_feature
34 LOCATION: (1)...(1531)
35 OTHER INFORMATION: b-g or c or t/u
36 NAME/KEY: misc_feature
37 LOCATION: (1)...(1531)
38 OTHER INFORMATION: d-a or g or t/u
39 NAME/KEY: misc_feature
40 LOCATION: (1)...(1531)
41 OTHER INFORMATION: h-a or c or t/u
42 NAME/KEY: misc_feature
43 LOCATION: (1)...(1531)
44 OTHER INFORMATION: v-a or g or c
45 NAME/KEY: misc_feature
46 LOCATION: (1)...(1531)
47 OTHER INFORMATION: n-a or g or c or t/u
48 US-09-795-686-1
49
50 Query Match 78.1%, Score 16.4; DB 6; Length 1503841;
51 Best Local Similarity 94.4%; Pred. No. 1.8e+02;
52 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0.
53
54 Oy 1 acataatgcctcgttca 18
55 ||| ||||| ||||| |||||
56 Db 243742 acaaaatgcctcgttca 243759
57
58 RESULT 8
59 US-08-798-074B-1985
60 : Sequence 1985, Application US/08/98074B
61 : GENERAL INFORMATION:
62 : APPLICANT: Rosen, Craig A.
63 : APPLICANT: Dillon, Patrick J.
64 : APPLICANT: Li, Haodong
65 : APPLICANT: Ruben, Steven M.
66 : TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 22
67 : FILE REFERENCE: PO-22
68 : CURRENT APPLICATION NUMBER: US/08/798,074B
69 : CURRENT FILING DATE: 1997-02-12
70 : PRIOR APPLICATION NUMBER: 60/011,617
71 : PRIOR FILING DATE: 1996-02-13

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```

? NUMBER OF SEQ ID NOS: 13449
? SEQ ID NO: 1985
? LENGTH: 108
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (8)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc_feature
? LOCATION: (31)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc_feature
? LOCATION: (76)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc_feature
? LOCATION: (80)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc_feature
? LOCATION: (94)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc_feature
? LOCATION: (107)
? OTHER INFORMATION: n equals a,t,g, or c
? US-08-798-074B-1985

Query Match          77.1%; Score 16.2; DB 4; Length 108;
Best Local Similarity 85.7%; Pred. No. 50;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy      1  acataatggccctgcgtcacac 21
        |||| ||||| ||||| |||
Db      42  acattatggccctgtaacgc 62

RESULT 9
US-08-798-074B-1985
? Sequence 1985, Application US/08798074B
? GENERAL INFORMATION:
? APPLICANT: Rosen, Craig A.
? APPLICANT: Dillon, Patrick J.
? APPLICANT: Li, Haodong
? APPLICANT: Ruben, Steven M.
? TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 22
? FILE REFERENCE: PO-22
? CURRENT APPLICATION NUMBER: US/08/798,074B
? PRIOR FILING DATE: 1997-02-12
? PRIOR APPLICATION NUMBER: 60/011,617
? PRIOR FILING DATE: 1996-02-13
? NUMBER OF SEQ ID NOS: 13449
? SEQ ID NO: 1985
? LENGTH: 108
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (8)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc_feature
? LOCATION: (31)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc_feature
? LOCATION: (76)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc_feature
? LOCATION: (80)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc_feature
? LOCATION: (94)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc_feature
? LOCATION: (107)
? OTHER INFORMATION: n equals a,t,g, or c
? US-08-798-074B-1985

```

OTHER INFORMATION: n equals a,t,g, or c  
US-08-798-074B-1985

Query Match 77.1%; Score 16.2; DB 4; Length 108;  
Best Local Similarity 85.7%; Pred. No. 30;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 acataatgacctgtacac 21  
|||||  
Db 42 acatatgacctgttaacgc 62

## RESULT 10

US-08-798-074C-1985  
Sequence 1985, Application US/08798074C  
GENERAL INFORMATION:  
APPLICANT: Rosen, Craig A.  
APPLICANT: Dillon, Patrick J.  
APPLICANT: Li, Haodong  
APPLICANT: Ruben, Steven M.  
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 22  
FILE REFERENCE: PO-22  
CURRENT APPLICATION NUMBER: US/08/798,074C  
CURRENT FILING DATE: 1997-02-12  
PRIOR APPLICATION NUMBER: 60/011,617  
PRIOR FILING DATE: 1996-02-13  
NUMBER OF SEQ ID NOS: 13449  
SEQ ID NO 1985  
LENGTH: 108  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (8)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (31)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (76)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (80)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (94)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (107)  
OTHER INFORMATION: n equals a,t,g, or c  
US-08-798-074C-1985

Query Match 77.1%; Score 16.2; DB 4; Length 108;  
Best Local Similarity 85.7%; Pred. No. 30;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 acataatgacctgtacac 21  
|||||  
Db 42 acatatgacctgttaacgc 62

## RESULT 11

US-09-764-874-1199  
Sequence 1199, Application US/09764874  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: PC010  
CURRENT APPLICATION NUMBER: US/09/764,874  
CURRENT FILING DATE: 2001-01-17  
PRIOR APPLICATION NUMBER: 60/179,065

PRIOR FILING DATE: 2000-01-31  
PRIOR APPLICATION NUMBER: 60/180,628  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: 60/214,886  
PRIOR FILING DATE: 2000-06-28  
PRIOR APPLICATION NUMBER: 60/217,487  
PRIOR FILING DATE: 2000-07-11  
PRIOR APPLICATION NUMBER: 60/225,758  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/220,963  
PRIOR FILING DATE: 2000-07-26  
PRIOR APPLICATION NUMBER: 60/217,496  
PRIOR FILING DATE: 2000-07-11  
PRIOR APPLICATION NUMBER: 60/225,447  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/218,290  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: 60/225,757  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/226,868  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 60/216,647  
PRIOR FILING DATE: 2000-07-07  
PRIOR APPLICATION NUMBER: 60/225,267  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/216,880  
PRIOR FILING DATE: 2000-07-07  
PRIOR APPLICATION NUMBER: 60/225,270  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/251,869  
PRIOR FILING DATE: 2000-12-08  
PRIOR APPLICATION NUMBER: 60/235,834  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: 60/234,274  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: 60/234,223  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: 60/228,924  
PRIOR FILING DATE: 2000-08-30  
PRIOR APPLICATION NUMBER: 60/224,518  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/236,369  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/224,519  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/220,964  
PRIOR FILING DATE: 2000-07-26  
PRIOR APPLICATION NUMBER: 60/241,809  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/249,299  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/236,327  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/241,785  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/244,617  
PRIOR FILING DATE: 2000-11-01  
PRIOR APPLICATION NUMBER: 60/225,268  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/236,368  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/251,856  
PRIOR FILING DATE: 2000-12-08  
PRIOR APPLICATION NUMBER: 60/251,868  
PRIOR FILING DATE: 2000-12-08  
PRIOR APPLICATION NUMBER: 60/229,344  
PRIOR FILING DATE: 2000-09-01  
PRIOR APPLICATION NUMBER: 60/234,997  
PRIOR FILING DATE: 2000-09-25  
PRIOR APPLICATION NUMBER: 60/229,343  
PRIOR FILING DATE: 2000-09-01  
PRIOR APPLICATION NUMBER: 60/229,345  
PRIOR FILING DATE: 2000-09-01

PRIOR APPLICATION NUMBER: 60/229,287  
PRIOR FILING DATE: 2000-09-01  
PRIOR APPLICATION NUMBER: 60/229,513  
PRIOR FILING DATE: 2000-09-05  
PRIOR APPLICATION NUMBER: 60/231,413  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: 60/229,509  
PRIOR FILING DATE: 2000-09-05  
PRIOR APPLICATION NUMBER: 60/236,367  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/237,039  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 60/237,038  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 60/236,370  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/236,802  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 60/237,037  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 60/237,040  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 60/240,960  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/239,935  
PRIOR FILING DATE: 2000-10-13  
PRIOR APPLICATION NUMBER: 60/239,937  
PRIOR FILING DATE: 2000-10-13  
PRIOR APPLICATION NUMBER: 60/241,787  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/246,474  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: 60/246,532  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: 60/249,216  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,210  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/226,681  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 60/225,759  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/225,213  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/227,182  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 60/225,214  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/235,836  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: 60/230,438  
PRIOR FILING DATE: 2000-09-06  
PRIOR APPLICATION NUMBER: 60/215,135  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: 60/225,266  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/249,218  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,208  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,213  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,212  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,207  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,245  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,244  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,217  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,211

PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,215  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,264  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,214  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,297  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/232,400  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: 60/231,242  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: 60/232,081  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: 60/232,080  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: 60/231,414  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: 60/231,244  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: 60/233,064  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: 60/233,063  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: 60/232,397  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: 60/232,399  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: 60/232,401  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: 60/241,808  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/241,826  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/241,786  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/241,221  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/246,475  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: 60/231,243  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: 60/233,065  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: 60/232,398

Query Match 77.1%; Score 16.2; DB 7; Length 110;  
Best Local-Similarity 85.7%; Pred. No. 50;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 acataatgctcgttacac 21  
|||||1111111111111111  
Db 73 acataatgcccgttacac 93

RESULT 12  
US-08-798-074B-1726  
Sequence 1726, Application US/08798074B  
GENERAL INFORMATION:  
APPLICANT: Rosen, Craig A.  
APPLICANT: Dillon, Patrick J.  
APPLICANT: Li, Haodong  
APPLICANT: Ruben, Steven M.  
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 22  
FILE REFERENCE: PO-22  
CURRENT APPLICATION NUMBER: US/08/798, 074B  
PRIOR FILING DATE: 1997-02-12  
PRIOR APPLICATION NUMBER: 60/011,617  
PRIOR FILING DATE: 1996-02-13  
NUMBER OF SEQ ID NOS: 13449  
SEQ ID NO 1726  
LENGTH: 149

```
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (11)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (16)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (19)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (20)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (25)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (109)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (112)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (113)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (126)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (127)
OTHER INFORMATION: n equals a,t,g, or c
US-08-798-074B-1726
```

```
Query Match      77.1%; Score 16.2; DB 4; Length 149;
Best Local Similarity 85.7%; Pred. No. 52;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 acataatggcctcgtcacac 21
    ||||| ||||| ||||| |||
DB 78 acattatggcctcgttaacgc 98
```

```
RESULT 13
US-08-798-074B-1726
; Sequence 1726, Application US/08798074B
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Li, Haodong
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 22
; FILE REFERENCE: PO-22
; CURRENT APPLICATION NUMBER: US/08/798,074B
; PRIOR FILING DATE: 1997-02-12
; PRIOR APPLICATION NUMBER: 60/011,617
; NUMBER OF SEQ ID NOS: 13449
; SEQ ID NO 1726
; LENGTH: 149
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (16)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (19)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (20)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (25)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (109)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (112)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (113)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (126)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (127)
; OTHER INFORMATION: n equals a,t,g, or c
US-08-798-074B-1726
```

```
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (20)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (25)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (109)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (112)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (113)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (126)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (127)
OTHER INFORMATION: n equals a,t,g, or c
US-08-798-074B-1726
```

```
Query Match      77.1%; Score 16.2; DB 4; Length 149;
Best Local Similarity 85.7%; Pred. No. 52;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 acataatggcctcgtcacac 21
    ||||| ||||| ||||| |||
DB 78 acattatggcctcgttaacgc 98
```

```
RESULT 14
US-08-798-074C-1726
; Sequence 1726, Application US/08798074C
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Li, Haodong
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 22
; FILE REFERENCE: PO-22
; CURRENT APPLICATION NUMBER: US/08/798,074C
; PRIOR FILING DATE: 1997-02-12
; PRIOR APPLICATION NUMBER: 60/011,617
; NUMBER OF SEQ ID NOS: 13449
; SEQ ID NO 1726
; LENGTH: 149
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (16)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (19)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (20)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (25)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (109)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (112)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (113)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (126)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (127)
; OTHER INFORMATION: n equals a,t,g, or c
US-08-798-074C-1726
```



```

: LOCATION: (112)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc.feature
: LOCATION: (113)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc.feature
: LOCATION: (126)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc.feature
: LOCATION: (127)
: OTHER INFORMATION: n equals a,t,g, or c
US-08-798-074C-1726

```

```

Query Match 77.1%; Score 16.2; DB 4; Length 149;
Best Local Similarity 85.7%; Pred. No. 52;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy 1 acataatggcctcgttcacac 21
   ||| ||||| ||| |||
Db 78 acataatggcctcgttcacgc 98

```

```

RESULT 15
US-09-834-366-48084
: Sequence 48084, Application US/09834366
: GENERAL INFORMATION:
: APPLICANT: Benjamin, Stephane
: APPLICANT: Tanaka, Hiroaki
: APPLICANT: Dumas Milne Edwards, Jean Baptiste
: APPLICANT: Jobert, Severin
: APPLICANT: Giordano, Jean-Yves
: TITLE OF INVENTION: ESTs and Encoded Human Proteins.
: FILE REFERENCE: 81. US2. REG
: CURRENT APPLICATION NUMBER: US/09/834,366
: CURRENT FILING DATE: 2001-04-13
: PRIOR APPLICATION NUMBER: US 60/197,873
: PRIOR FILING DATE: 2000-04-18
: NUMBER OF SEQ ID NOS: 52153
: SOFTWARE: patent.pm
: SEQ ID NO 48084
: LENGTH: 326
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: LOCATION: 26..27,214
: OTHER INFORMATION: n=a, g, c or t
US-09-834-366-48084

```

```

Query Match 75.2%; Score 15.8; DB 7; Length 326;
Best Local Similarity 81.0%; Pred. NO. 98;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy 1 acataatggcctcgttcacac 21
   ||||| :||| |||||
Db 275 acataaascctcattcacac 295

```

Search completed: September 21, 2001, 02:40:43  
 Job time: 15129 sec

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